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(54) Title: **HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG**

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung is described. Also described are single exon nucleic acid probes expressed in the lung and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG

CROSS REFERENCE TO RELATED APPLICATIONS

- 5 The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 10 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, 15 the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

- 20 The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto_LUNG.txt, created 25 24 January 2001, having 25,232,785 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

- 30 The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

lung and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

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amounts of sequence data (see for example Adams et al.,
Science 252:1651. (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known a priori with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only a priori biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the lung are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
20 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are, for the most part, believed to have polygenic etiologies. There is a need for methods and apparatus that permit prediction,
25 diagnosis and prognosis of diseases of the human lung, particularly those diseases with polygenic etiology.

Summary of the Invention.

30 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
35 expression of putative genes identified within genomic

sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 12,614 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable..

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon

nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,001 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and
15 bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more
20 preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first
25 aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable
30 substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate,
35 polyacetal, polysulfone, celluloseacetate,

cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with
5 the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative
10 embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene
15 expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 12,615 - 25,001, wherein the fragment
20 hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 12,614.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for
25 measuring human gene expression in a sample derived from human lung which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 12,614 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a
30 nucleic acid expressed in the human lung.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOS.: 12,615 - 25,001 or a complementary sequence or a fragment
35 thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human lung which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,002 - 37,012 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human lung.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a
5 single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition,
10 comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to
15 prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human lung, comprising:

contacting the single exon microarray in
20 accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human lung; and then

measuring the label detectably bound to each
25 probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from
30 genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the lung of said eukaryote, said
35 probe is a single exon probe having a fragment identical in

sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at
5 high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic
10 sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe
15 with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

20 In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,001 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a
25 sequence as set out in any of SEQ ID NOS: 12,615 - 25,001, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,614.

30 In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 25,002 - 37,012.

Accordingly in a eleventh aspect of the invention
35 there is provided a peptide comprising a sequence as set

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out in any of SEQ ID NOS: 25,002 - 37,012, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

10

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, inter alia, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic

acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as

PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

5 As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the
10 larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

15 As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

20 As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9
25 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means
30 any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual
35 display in which a single genomic sequence is annotated

with predicted and experimentally confirmed functional information.

5 Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

10 FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence
15 data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

20 FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted
25 lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray.
30 The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the
35 expression of verified sequences that showed expression

with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present

invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records
5 corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector
10 sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence
15 identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence.
20 Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in
25 information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the
30 htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than
35 human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*

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brigsii, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification

and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps: Any or all process steps

can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

5 Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

10 For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process
15 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into
20 process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database
25 contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

30 Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

35 For example, if the function sought to be

identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added

relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

5 One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further
10 described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of
15 the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

 If query 20 incorporates multiple criteria, such
20 as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

25 If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query
30 20 can be generated that takes into account the initial negative result.

 When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired
35 analytical approach and the particular analytical methods

thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent
5 analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu
10 repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the
15 genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by
20 proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified
algorithmically without comparison to external databases
25 and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or
30 codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the
35 specific nucleotide references to one that is unrecognized

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by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

5 Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those
10 nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

 Preprocessing 24 can, and often will, also
15 include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence
20 database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

25 Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified
30 within the genomic sequence.

 As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after
35 transcription, of regulating message degradation, and the

like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

5 The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not
10 hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

15 Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

20 Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be
25 performed using any of a variety of known programs that identify regions with lower sequence variability.

 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in
30 Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

35 Increased reliability can be obtained when

consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

5 Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

10 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset
15 thereof suitable for assay.

 Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene
20 prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5%
25 of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

 Furthermore, consensus can be required among
30 different approaches to identifying a chosen function.

 For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset
35 thereof, with another approach, such as comparative

sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the
5 predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

10 Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

15 In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

20 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based inter alia upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that
25 have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses
30 amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully
35 to amplify. Where subsequent gene expression assay relies

upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in

process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also
5 be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic
10 sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100
15 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from
20 application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an
25 approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the
30 methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at
amplifying pieces of such ORFs is low, and that such
35 putative exons are more effectively amplified when larger

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fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can

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conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline

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silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or
5 alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose
10 certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the
15 expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed
20 using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in
25 Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography
30 techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at
35 least 1000, typically at least 2000, preferably 5000 and

upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., Cancer Res. (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays

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based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

5 Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as
10 probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other
15 expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful
20 cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the
25 genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the
30 desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

35 Thus, the genome-derived single exon microarrays

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of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes

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disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-
5 including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence
10 of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or
15 amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes
disposed upon the genome-derived single exon microarrays
20 need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific
primer sequence, useful for "universal" (that is,
25 independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the
genome-derived single exon microarray will include
30 artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would
35 contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the

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present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or
5 include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in
10 turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in
15 EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon
20 microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST
25 microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional
30 presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the
35 present invention are also quite different from *in situ*

synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

5 A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe
10 basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays
15 from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al.,
20 *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent
25 use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence
30 drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred
35 embodiments, the methods and apparatus of the present

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invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

5 After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental
10 verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon
15 microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the
20 microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous,
25 as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-
30 transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the
35 reference source is reverse transcribed in the presence of

a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial
5 purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a
10 Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the
15 genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support
20 substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention
25 provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is
30 disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates
35 having 384, 864, 1536, 3456, 6144, or 9600 wells, and

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although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

5 In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such
10 as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
15 in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers,
20 etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together
25 with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

30 In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable
35 media can be packaged with the microarray, with the ordered

probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then
5 separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification
10 sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted
15 to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than,
20 or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

25 Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and
30 more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - including information on identical sequences and
35 information on nonidentical sequences that have diffuse or

focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

5 Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully
10 relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are
15 well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present
20 invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

25 FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

30 Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual
35 nucleotides would rarely be readable in hard copy output of

display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the
5 first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a
10 convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any
15 point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point
20 in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned
25 into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the
30 sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to
35 computerized data, additional control over the first and

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last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the

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results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select

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a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example,

where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than
5 does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions
10 submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions
15 that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify
20 sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through
25 color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of
30 sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as
35 can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof.

5 As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked
10 information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

15 Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

20 Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the
25 degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for
30 respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute
35 expression (signal intensity) can be expressed using.

normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay
5 is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing
10 gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene
15 predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as
20 white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of
25 sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

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The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present
35 invention rapidly identify and confirm the expression of

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portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 12,614 of these ORFs in lung.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in lung is currently available for use in measuring the level of its ORF's expression in lung.

Diseases of the lung are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are, for the most part, believed to have polygenic etiologies.

For example, asthma affects about 5% of the adult population in the United States, making it the seventh-ranking chronic condition. The worldwide prevalence of asthma has increased more than 30% since the late 1970s, mostly in areas of increased industrialization. The yearly economic costs (including both direct and indirect

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costs) are estimated at almost \$12 billion dollars. Asthma is also one of the most common reasons to seek medical treatment, with over 1.5 million emergency room visits, 500,000 hospitalizations and over 5,500 deaths each year. 5 Outpatient visits are estimated at 15 million per year.

Patients with asthma suffer shortness of breath accompanied by cough, wheezing, and anxiety. Common features of acute asthma attacks include a rapid respiratory rate, tachycardia, and pulsus paradoxus. 10 Acute attacks can be triggered by environmental factors such as allergens, changes in temperature, and exercise; other acute exacerbations have no discernible precipitating cause. If asthma is not treated, it can be life-threatening.

15 It is now well known that genetic factors predispose to asthma, but the exact nature of this genetic component is still imprecise.

A 1986 human genetic study supported polygenic inheritance, Townley, et. al., J. Allergy Clin. Immun. 77: 20 101-107 (1986), and more recent studies have suggested that predisposing factors for asthma, if not the disease itself, are heritable. Slutsky, J. Clin. Pharmacol. 39: 246-51 (1999).

In one approach to elaborating the polygenic 25 contributions to asthma, candidate genes have been suggested based upon presumed involvement in the physiologic processes known to contribute to the asthmatic state. Huss et al., Nurs. Clin. North Am. 35: 695-705 (2000).

30 In other studies, linkages and/or associations of genetic markers with atopy, bronchial hyperresponsiveness and/or asthma have been reported in candidate regions, including the 6p region, which includes both the HLA complex and the Tumor Necrosis Factor α gene (TNF- α), the 35 11q region which includes the gene coding for the b sub-

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unit of the high-affinity IgE receptor (FcE R1), the T-cell receptor a gene on chromosome 14, the 5q region bearing numerous candidate genes among which are the interleukin (IL-3, 4, 5, 9, 13) cluster and the b2-adrenergic receptor gene, the 12q region containing the genes for interferon-gamma (IFNg), a mast cell growth factor (MGF), and an insulin-like growth factor (IGF1). The strongest of these linkages are associated with chromosomes 5 and 11. Other linkage regions have been reported on chromosomes 6, 7, 11, 12 and 13. Demenais, The European Network For Understanding Mechanisms of Severe Asthma, BIOMED 2 Program - European Commission (1998). Linkage regions have also been suggested on chromosomes 3, 16 and 14. Duffy, D., "Review of Molecular Genetics of Asthma and Allergy", (<http://www2.qimr.edu.au/davidD/asthma6.html>).

As another example, chronic obstructive pulmonary disease (COPD) is the fourth most common cause of death in the United States. Although cigarette smoking is the most common cause of COPD, with smokers having a rate 10 to 30 times higher for developing emphysema than non-smokers, genetic factors are thought to play a significant role in susceptibility to COPD; indeed, only 15-20% of long-term cigarette smokers will develop COPD, suggesting that genetic factors strongly affect outcome.

COPD includes both chronic bronchitis and emphysema, which share similar symptoms and frequently coexist. More than 16 million Americans have COPD at a cost currently estimated at \$30 billion dollars each year. Chronic obstructive lung disease is characterized by a decline in lung function resulting in difficulty in breathing and physiological changes. In severe COPD, patients breathe at very high lung volumes, having lost the lung's normal elastic recoil. Because COPD does not affect the lung uniformly, ventilation and

perfusion distribution is impaired. In areas of the lung with low ventilation-perfusion ratios, arterial hypoxia results. This can further lead to pulmonary hypertension, right ventricular failure, and, ultimately, tissue ischemia, such as coronary artery disease.

The only confirmed genetic risk factor for COPD is the inherited deficiency of alpha 1-proteinase inhibitor (familial emphysema). Familial emphysema accounts for less than 5 percent of all cases of COPD, however, and familial clustering of lung function and COPD suggest the presence of other genetic risk factors. Luisetti et al., *Mondaldi Arch. Chest Dis.* 50:28-32 (1995); Khoury et. al., *Genet Epidemiol.* 2: 155-66 (1985).

Among such additional genetic factors are the presence of the GC2 allele, which appears to exert a protective effect against COPD. Horne et. al., *Hum. Hered.* 40: 173-76 (1990). Other suspected genetic involvement includes genes coding for alpha1-antichymotrypsin, alpha2-macroglobulin, vitamin D-binding protein and blood group antigens. Sandford et. al., *Eur. Respir. J.* 10: 1380-91 (1997). Finally, the form of the enzyme microsomal epoxide hydrolase is correlated to susceptibility to COPD. Smith et al., *The Lancet* 350: 630-33 (1997). It remains uncertain, however, whether other loci contribute to predisposition and aggressiveness of COPD.

As yet a further example, lung cancer is the leading cause of cancer death in both men and women in the United States. Although smoking is the primary risk factor, genetics plays a known role in susceptibility to these bronchogenic carcinomas.

The most common of the bronchogenic carcinomas is non-small cell lung cancer (NSCLC), which accounts for 75% of all primary lung cancers. NSCLCs are divided into adenocarcinomas, squamous cell carcinomas, and large cell carcinomas. Small cell lung cancer (SCLC) comprises 20% of

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primary lung cancers, and carcinoids make up 5%. Other rare forms of lung cancer (all totaling less than 1%) include lymphoma, carcinosarcoma, mucoepidermoid carcinoma, malignant fibrous histiocyctoma, melanoma, sarcoma, and blastoma. Lung cancer is generally not associated with clinical symptoms until late in the course of the disease; this late diagnosis is likely to contribute to the poor 5-year survival rate of 14%.

Premalignant changes are thought to include a number of successive mutations in various growth regulation genes. A chromosome 3p deletion, chromosome 9p deletion, and p53 gene mutations have been identified in premalignant lesions. Chromosomal abnormalities identified in both SCLC and NSCLC include deletions involving chromosomes 3p, 5q, 9p, 11p, 13q, and 17p. Weston et. al., Proc. Nat. Acad. Sci. 86: 5099-5103 (1989). For most of these regions, suspected loci are tumor suppressor genes. Additionally, transforming oncogenes such as Ki-ras, H-ras, N-ras, myc, her2neu, c-kit, bcl-2 and cyclin D1 (prad) have also been shown to be activated in certain types of bronchogenic carcinomas. Perucho et. al., Cell 27: 467-76 (1981); Cecil Textbook of Medicine, 21st ed. (2000).

Other contributing genetic loci have been identified, including a deletion of the phosphatase and tensin homolog (PTEN) at 10q23.3. Overexpression of PTEN can inhibit invasion in lung cancer cells, and appears to downregulate integrin alpha(6), laminin beta(3), heparin-binding epidermal growth factor-like growth factor, urokinase-type plasminogen activator, myb protein B, and Akt2. Hong et. al., Am. J. Respir. Cell Mol. Biol 23: 355-63 (2000). In a recent study assessing the risk of lung cancer from environmental tobacco smoke (ETS), women who were homozygous null for glutathione S-transferase (GST)-1 (GSTM1) had a statistically significant greater risk of developing lung cancer from ETS. Bennett et. al., J. Nat.

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Cancer. Inst. 91: 2009-2014 (1999). The identified genetic factors are believed to be only a subset, however, of loci that contribute to disease.

As a still further example, the interstitial lung diseases (ILDs) share certain pathogenic mechanisms and histopathologic features. ILDs comprise more than 100 disorders characterized by diffuse inflammation and scarring of the lung interstitium, derangement of the alveolar walls and loss of functional alveolar capillary units. Symptoms include breathlessness, exercise intolerance, and progressive respiratory insufficiency. ILD is estimated to account for 100,000 hospital admissions each year.

Genetic factors are known to contribute to the development of some types of ILD. Examples are familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease and Hermansky-Pudlak syndrome. ILDs with unknown etiology include, e.g., sarcoidosis, pulmonary hemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, and nonspecific interstitial lung disease.

As an example of still undefined polygenic basis, the etiology of sarcoidosis remains enigmatic, but has long been suspected to have a genetic component. Ethnic preponderance, familial clustering and multigenerational involvement all point towards hereditary susceptibility. Rybicki et. al., Clin. Chest Med. 18: 707-717 (1997). Some studies have shown an association between susceptibility to sarcoidosis and HLA type. Nowack et al., Arch. Intern. Med. 147: 481-83 (1987); Ishihara et. al., Tissue Antigens 50: 650-53 (1997).

Other significant diseases of the lung are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, for example, Kartagener

syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension, and hyaline membrane disease.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human lung, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed at detectable levels in human lung, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as the ILDs), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given lung disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's lung to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease.

Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits

predisposition to and/or prognosis of lung disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human lung. The
5 algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which
10 stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in
15 the lung has been demonstrated are useful for both measurement in the lung and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

20 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the
25 ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was
30 measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or
35 tools for surveying gene expression, the genome-derived

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single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression

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- Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
- 10 Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
- 15 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of

20 pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

- 25 For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.
- 30 Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does
- 35 not affect the pathway of which the gene's expressed

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protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit
5 useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in
10 Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in lung.

15 The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly
20 hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or
25 additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are
30 described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the
35 hybridization reactions that probe gene expression.

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Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and

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typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention
5 will typically not contain a detectable label.

When intended for use in solution phase hybridization, however - that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may
10 indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such
15 probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset
20 of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In
25 particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,615 - 25,001, respectively, for probe SEQ ID NOS. 1 - 12,614. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or
30 microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,615 - 25,001 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described,
35 inter alia, in Ausubel et al. and Maniatis et al. For

microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes
5 of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable
10 for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

15 When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material
20 contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more
25 typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

30 It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded
35 probes must be complementary in sequence to the ORF as

present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be

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packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human lung.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human lung. In preferred embodiments, the present invention provides
5 human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 12,614.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater
10 physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single
15 exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be
20 provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among
25 the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1
30 - 12,614 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,615 - 25,001, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 12,614 can be used, or that portion thereof in SEQ ID NOS. 12,615 - 25,001 used, to express a protein domain by standard in
35 vitro recombinant techniques. See Ausubel et al. and

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Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,615 - 25,001. Such amino acid sequences are set out in SEQ ID NOS: 25,002 - 37,012. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

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EXAMPLE 1Preparation of Single Exon Microarrays from ORFs Predicted
in Human Genomic Sequence5 Bioinformatics Results

All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
10 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
15 algorithmic methods developed on independent training sets:
GRAIL uses a neural network, GENEFINDER uses a hidden
Markoff model, and DICTION, a program proprietary to
Genetics Institute, operates according to a different
heuristic. The results of all three programs were used to
20 create a prediction matrix across the segment of genomic
DNA.

The three gene finding programs yielded a range
of results. GRAIL identified the greatest percentage of
genomic sequence as putative coding region, 2% of the data
25 analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
genomic sequence called as coding region.

The consensus data were as follows. GRAIL and
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and
30 DICTION agreed on 0.5% of genomic sequence, and the three
programs together agreed on 0.25% of the data analyzed.
That is, 0.25% of the genomic sequence was identified by
all three of the programs as containing putative coding
region.

35 ORFs predicted by any two of the three programs

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("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

10 The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

15 Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to
20 approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at
25 <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single
30 set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

35 The ORFs were then PCR amplified from genomic

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DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were

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sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

5 Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

10 Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of
15 noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

20 The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular
25 Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against
30 the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known
35 mRNA (13% of sequences). A further 22% of the probe

sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5 EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10 The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, 15 placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics 20 equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg 25 of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 30 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. 35 The reaction was then purified using a Qiagen PCR cleanup

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column, increasing the number of ethanol washes to 5.

Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 μ l hybridization solution containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2 μ g/ μ l human c_{ot}1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes

was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is

novel, with gray depicting nonidentical with significant
homology (white: E values < $1e-100$; gray: E values from $1e-05$
to $1e-99$; black: E values > $1e-05$).

As FIG. 7 readily shows, heart and brain were
5 demonstrated to have the greatest numbers of genes that
were shown to be uniquely expressed in the respective
tissue. In brain, 200 uniquely expressed genes were
identified; in heart, 150. The remaining tissues gave the
following figures for uniquely expressed genes: liver, 100;
10 lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100;
HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more
"novel" genes among those that were up-regulated in only
one tissue, as compared with those that were down-regulated
15 in only one tissue. In fact, it was found that ORFs whose
expression was measurable in only a single of the tested
tissues were represented in sequencing databases at a rate
of only 11%, whereas 36% of the ORFs whose expression was
measurable in 9 of the tissues were present in public
20 databases. As for those ORFs expressed in all ten tissues,
fully 45% were present in existing expressed sequence
databases. These results are not unexpected, since genes
expressed in a greater number of tissues have a higher
likelihood of being, and thus of having been, discovered by
25 EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have
high homology to genes present in the GenBank human EST
30 database were compared to the normalized signal of those
genes not found in the GenBank human EST database. The
data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity
for all sequence-verified products with a BLAST Expect
35 ("E") value of greater than $1e-30$ (designated "unknown")

upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

25 Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR

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against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle

				filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be

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important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et

al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15

Liver	-1.62 \pm 0.22	-2.07 \pm
Lung	-4.95 \pm 0.93	-3.75 \pm 0.21
Placenta	-3.56 \pm 0.25	-3.52 \pm 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the

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region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):

- red = kallistatin protease inhibitor (P29622);
- purple = plasma serine protease inhibitor (P05154);
- turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
5 Human Gene Expression

The protocols set forth in Examples 1 and 2, supra, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique
10 exons in the human genome that could be shown to be expressed at significant levels in lung.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon
15 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
20 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 12,614 single exon probes, each fragment corresponding to an extension product from one of
25 the two amplification primers.)

The structures of the 12,614 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,614. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included
30 in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 12,615 - 25,001, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than
35 one amplicon.

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As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human lung and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human lung tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 12,615 - 25,001 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is

found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:.. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for

analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously
5 been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even
10 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent
15 a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOS.: 1 - 12,614) and probe exon (SEQ ID NOS.: 12,615 - 25,001, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

20 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST
25 query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

30 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

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Genome-Derived Single Exon Probes Useful For Measuring
Expression of Genes in Human Lung

Table 4 (523 pages) presents expression, homology, and
s functional information for the genome-derived single exon
probes that are expressed significantly in human lung.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human lung comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 12,614 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,615 - 25,001.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human lung comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,614 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human lung.

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14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 12,615 - 25,001 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human lung which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of
10 SEQ ID NOS.: 25,002 - 37,012, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human lung.

16. A single exon nucleic acid probe as claimed in any one
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one
35 of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human lung, comprising:

5 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human lung; and then measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

15 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the lung of said eukaryote, said probe is a
20 single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25

24. A method of assigning exons to a single gene, comprising:

25 identifying a plurality of exons from genomic sequence according to the method of claim 23; and
30 then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,
35 wherein a common pattern of expression of said exons in

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said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOS: 1 - 25,001 which encodes a peptide.
26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 25,001.
- 10 27. A peptide comprising a sequence as set out in any of
SEQ ID Nos: 25,002 - 37,012.

1/10

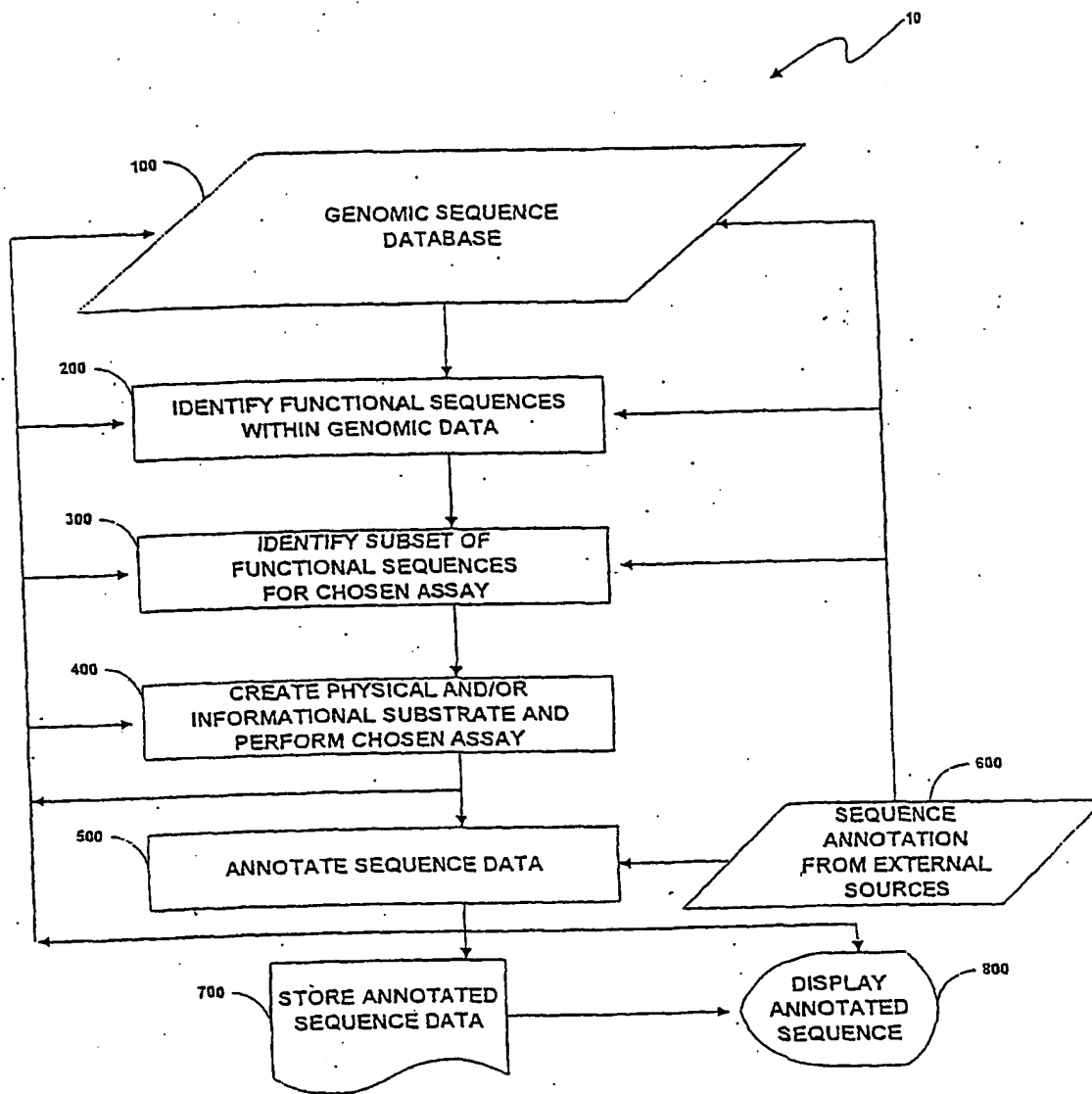


Fig. 1

2/10

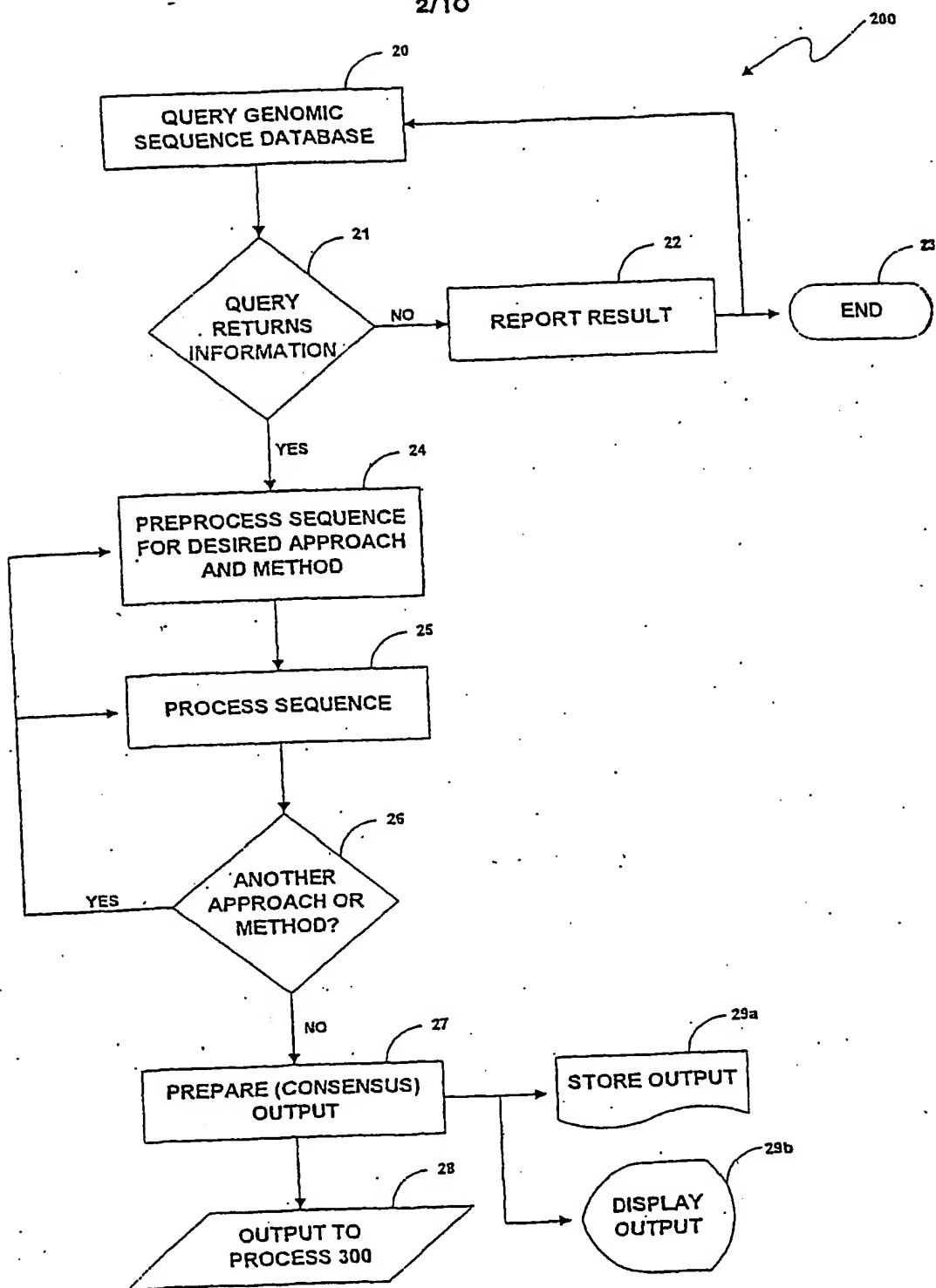


Fig. 2

3/10

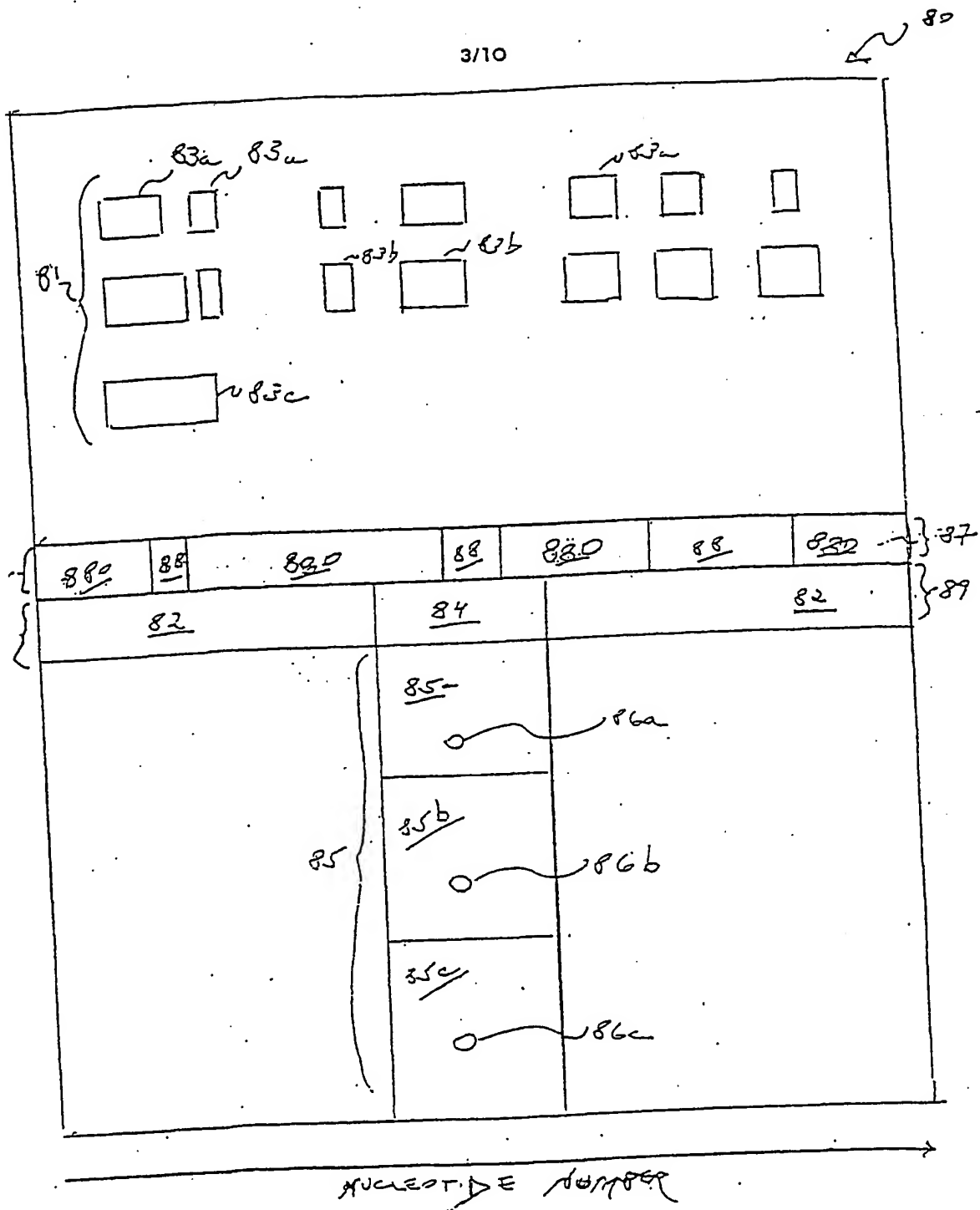


Fig. 3

4/10

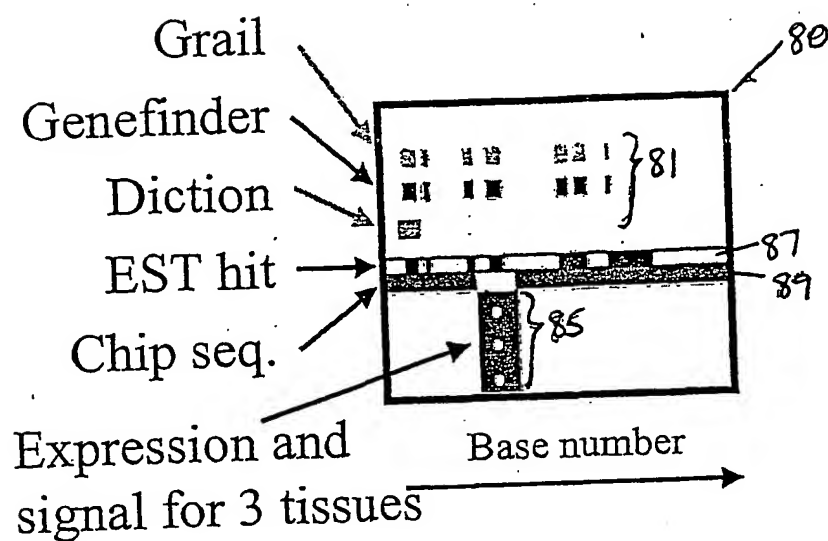


Fig. 4

5/10

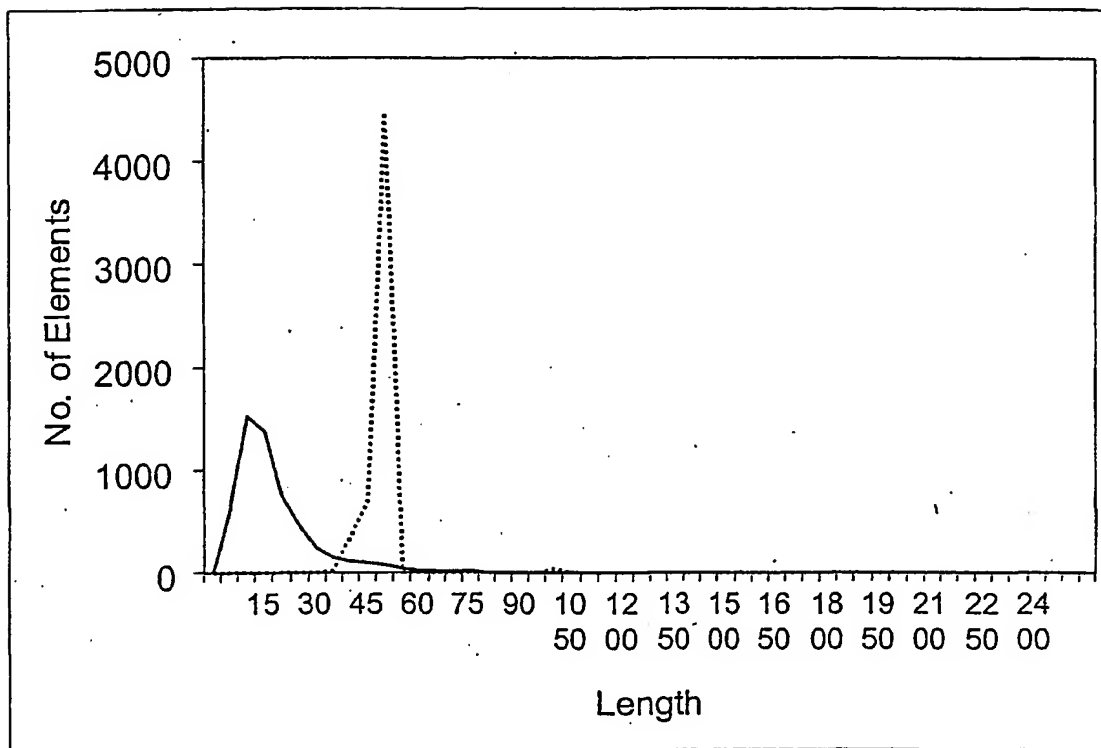


Fig. 5

6/10

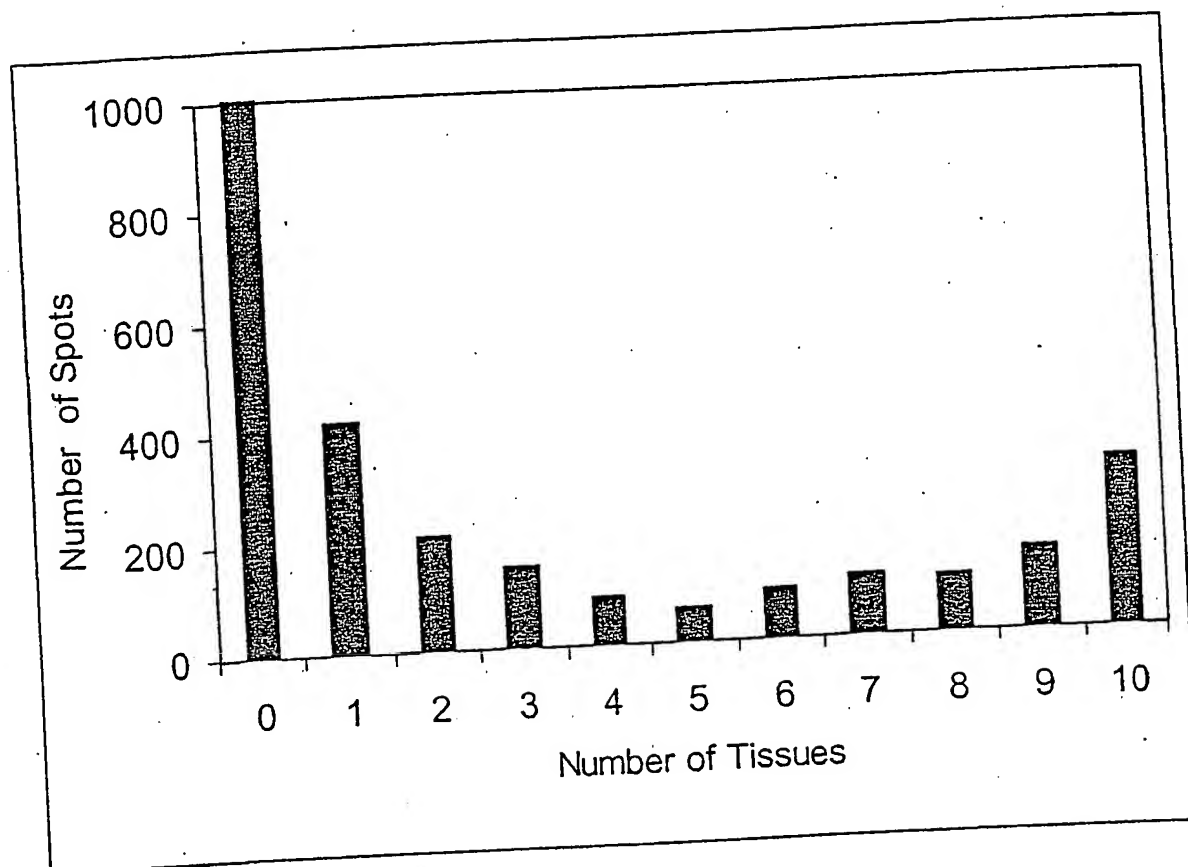
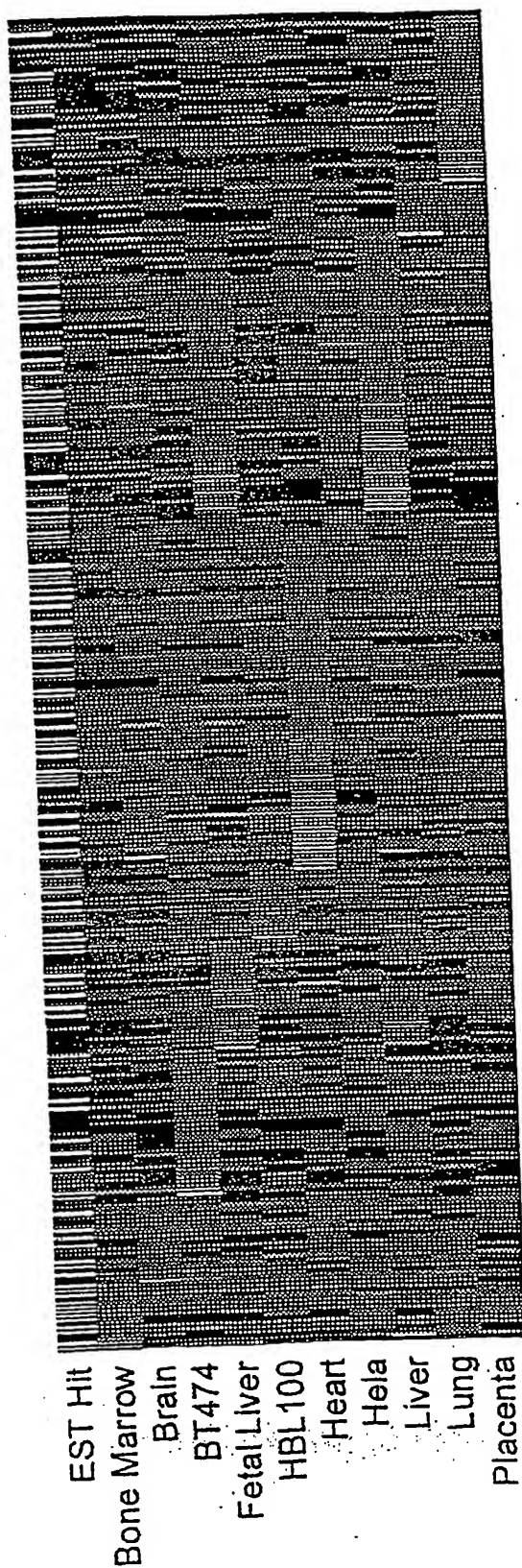


Fig. 6



EST Hit
Bone Marrow
Brain
BT474
Fetal Liver
HBL100
Heart
Hela
Liver
Lung
Placenta

Fig. 7a

ratio legend

>9
8
7
6
5
4
3
2
1



Fig. 7b

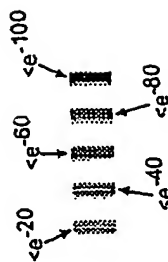


Fig. 7c

8/10

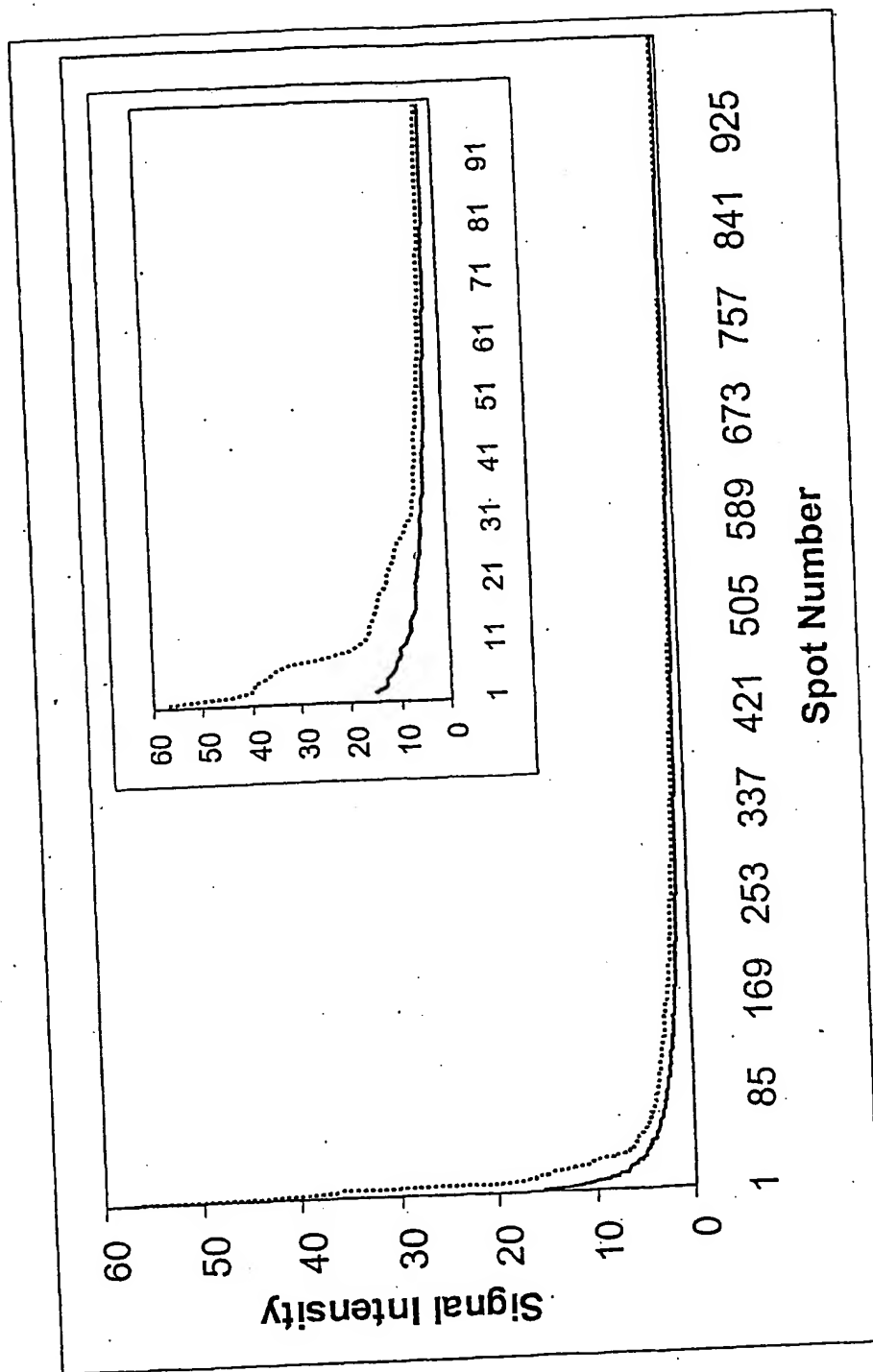


Fig. 8

9/10

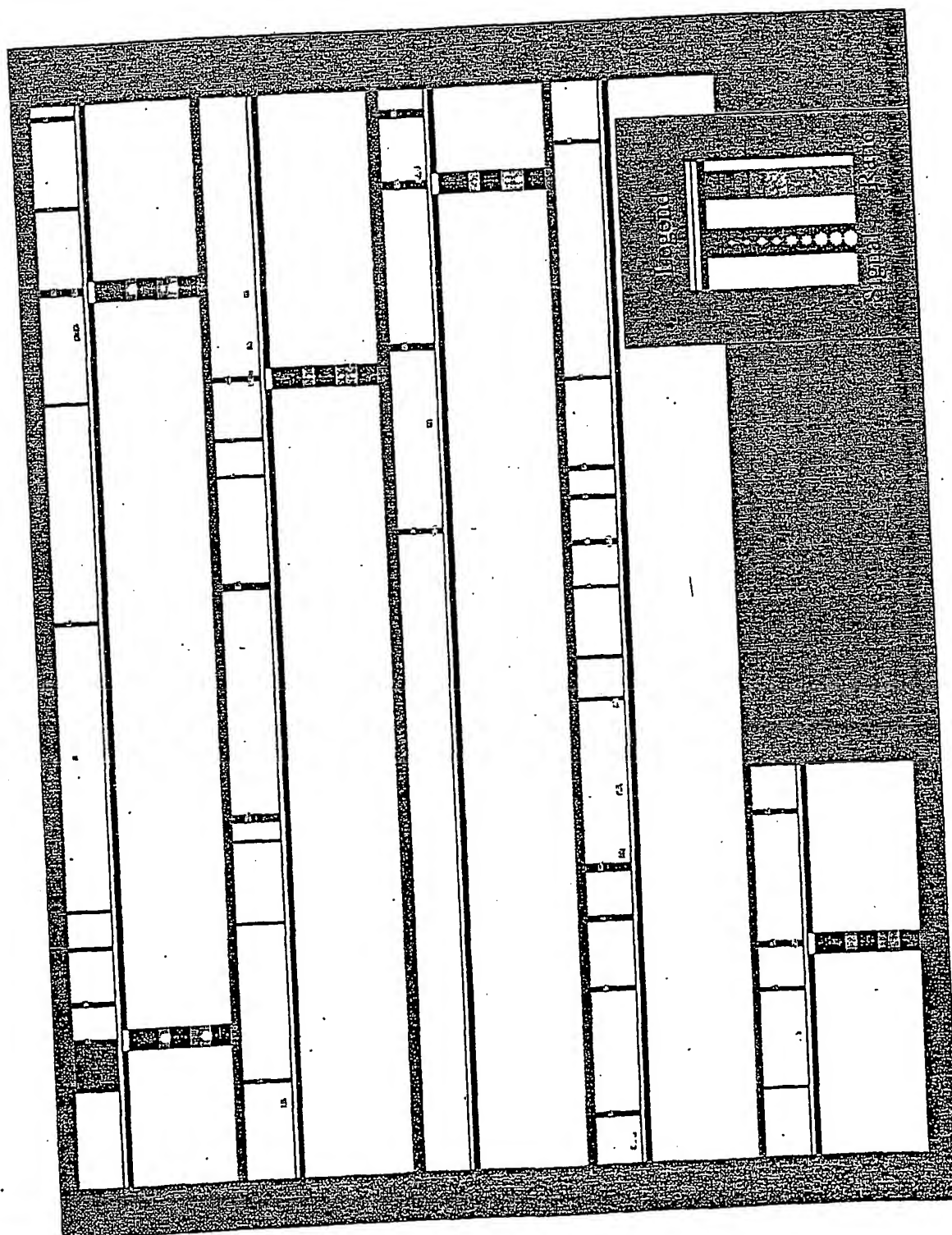


Fig. 9

10/10

Fig. 10

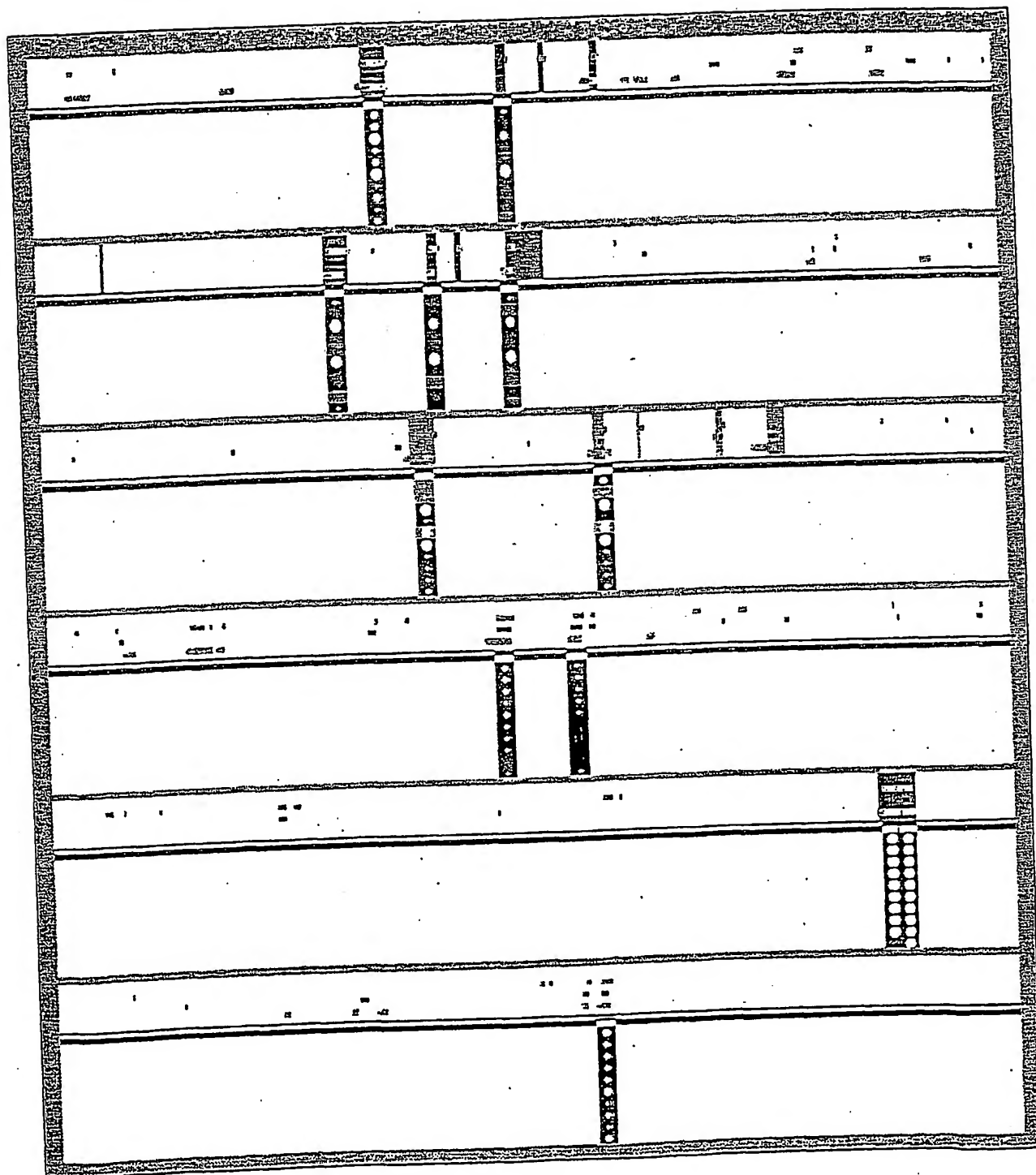


Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
467	13041	25464	6.91			
912	13466	25914	13.47			
1070	13616		2.76			
1334	13870	26321	11.77			
1628	14159	26829	1.37			
1644	14176	26844	3.67			
1722	14250	26734	0.89			
1746	14273	26768	5.47			
1854	14376	26868	1.04			
1923	14442	26945	1.45			
2073	14588	27107	1.46			
2177	14688	27212	1.12			
2488	14989	27502	1.14			
2488	14989	27503	1.14			
3143	15696	28115	3.08			
3427	15971	28384	1.22			
3495	16038	28459	16.98			
3649	16091		0.83			
4213	16738	29129	1.34			
4278	16803	29186	6.98			
4298	16823	29208	0.85			
4288	16823	29209	0.85			
4416	16937	29328	0.68			
4894	17406	29778	1.26			
5001	17511	29885	0.6			
5152	17656	30016	5.84			
5172	17876	30038	1.09			
5507	18098	30341	1.58			
5507	18098	30342	1.58			
5678	18263		3.96			
5894	18443		6.35			
5948	18263		2.9			
6010	18584	31270	0.45			
6016	18590	31276	3.48			

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6328	24607	31616	1.51				
6355	18913	31646	1.93				
6755	19298		1.01				
6901	19441	32217	1.26				
6901	19441	32218	1.26				
7555	20015	32859	0.55				
7555	20015	32860	0.55				
7892	20331	33197	1.29				
7892	20331	33198	1.29				
8678	21113	34016	1.59				
8992	21425	34336	1.48				
9718	22141	35068	5.69				
9955	22357	35505	1.07				
10052	22453	35402	1.1				
10474	22824		8.1				
10804	23240		2.07				
10872	23305	36300	3.23				
11117	23570	36613	1.78				
11213	22865	35839	1.87				
11213	22865	35840	1.87				
12042	24211		1.27				
12378	24421	30896	1.75				Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
6358	18916	31650	21.04	9.9E+00	AJ239028.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
8640	21075	33983	1.82	9.8E+00	U32716.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7419	19924	32755	0.97	9.8E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7419	19924	32758	0.87	9.8E+00	AF065630.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor ILH polypeptide 2 (Gf2h2) genes, complete cds
10317	22717	35684	1.44	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor ILH polypeptide 2 (Gf2h2) genes, complete cds
10317	22717	35685	1.44	9.6E+00	AF242432.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2604	15100	27615	6.39	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2604	15100	27616	6.39	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2878	18433	27851	3.27	9.4E+00	AB043785.1	NT	Mus musculus A13 gene for antithrombin, complete cds
6653	19201	31952	0.55	9.4E+00	P75130	SWISSPROT	HYPOTHETICAL PROTEIN MG447 HOMOLOG
8702	21137	34041	1.15	9.3E+00	AF130990.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9343	21775	34881	2.88	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
							3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(5)-STEROID DEHYDROGENASE)
							(PROGESTERONE REDUCTASE)
7954	20381	33258	0.49	9.2E+00	Q61767	SWISSPROT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5548	18138	30406	2.7	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5548	18138	30497	2.7	9.1E+00	AF095609.1	NT	RHODOPSIN
9640	22055		1.08	9.0E+00	P09241	SWISSPROT	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6340	18898	31029	6.18	8.9E+00	BE971806.1	EST_HUMAN	Cynops pyrrhogaster Cptbx3 premature mRNA, partial cds
6714	19260	32016	2.58	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cptbx3 premature mRNA, partial cds
6714	19260	32017	2.58	8.7E+00	AB019788.1	NT	Homo sapiens Insulin receptor substrate 1 (IRS1) mRNA
457	13032	26454	1.84	8.4E+00	5031804	NT	Zea mays mRNA for legumain-like protease (see 2a)
9658	20949	33948	3.7	8.1E+00	AJ131719.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
8737	21171		0.93	7.6E+00	Z21489.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
7814	20256		1.81	7.5E+00	AL445065.1	NT	THROMBOSPONDIN 1 PRECURSOR
8899	21333	34245	1.94	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8899	21333	34246	1.94	7.5E+00	P35441	SWISSPROT	602128876F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285506 5'
6084	18654	31348	3.23	7.4E+00	BF700517.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
9178	21610	34520	3.54	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
9178	21610	34521	3.54	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2932	15487	27907	3.15	7.2E+00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds
2932	15487	27908	3.15	7.2E+00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds
7458	19961	32795	0.74	7.2E+00	BE179090.1	EST_HUMAN	RCO-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA
7589	20038	32885	1.39	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7589	20038	32886	1.39	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
6763	22166		8.44	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11139	23590	36631	2.27	7.1E+00	P05950	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
10020	22422	35372	2.97	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
8838	21272	34181	3.52	6.9E+00	P35678	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10272	22873	36038	1.4	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8587	21002	33989	1.54	6.8E+00	W03412.1	EST_HUMAN	zab07c11.1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:291860 5'
8567	21002	33900	1.54	6.8E+00	W03412.1	EST_HUMAN	zab07c11.1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:291860 5'
9429	21861		1.65	6.8E+00	P39307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
10184	22585	35550	3.37	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5535	18125		0.7	6.6E+00	Q89028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6896	19436	32212	0.77	6.6E+00	BF672121.1	EST_HUMAN	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
10094	22495	35454	2.38	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10094	22495	35455	2.38	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
9460	21891	34812	7.71	6.9E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP38]
9862	22265	35204	1.81	6.2E+00	AY010901.1	NT	Schizopodium commune unknown mRNA
7465	19867	32801	1.6	6.0E+00	BE780163.1	EST_HUMAN	601488031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
6801	24593	31041	0.41	5.9E+00	AA037751.1	EST_HUMAN	zlk38p03.1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:485069 3'
6871	19411	32186	7.41	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kank6) genes, complete cds
11360	23742		1.74	5.9E+00	BE958630.1	EST_HUMAN	601645279F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930451 5'
3505	18048		1.06	5.8E+00	7681657	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7603	20052	32603	0.84	5.7E+00	AF302046.1	NT	Mus musculus Immunoglobulin scavenger receptor IgSR mRNA, complete cds
7603	20052	32604	0.84	5.7E+00	AF302046.1	NT	Mus musculus Immunoglobulin scavenger receptor IgSR mRNA, complete cds
8085	20513		1.5	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11230	22882	35860	4.48	5.6E+00	Q56276	SWISSPROT	LYCOPENE BETA CYCLASE
6573	19124	31866	0.9	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HIRCA
11228	22880	35857	2.22	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
7339	19751	32554	1.16	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7339	19751	32555	1.16	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7796	20238		0.89	5.4E+00	Q89435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8464	20877	33776	0.64	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4-R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
8540	20975		1.63	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;
10063	22464	35418	1.46	5.4E+00	Q17094	SWISSPROT	LIPOVITELLIN LV-2
10063	22464	35419	1.46	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4837	17349	29732	1.44	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6836	19377		0.77	5.3E+00	P41779	SWISSPROT	HOMEOBOX PROTEIN CEH-20
8891	21128		3.08	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11377	23739	36788	1.68	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
5722	18304		1.01	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0691-270400-186409 HT0691 Homo sapiens cDNA
10286	22687		1.04	5.2E+00	AF248070.1	NT	Drosophila orientacea RTB retrotransposable element reverse transcriptase gene, partial cds
9315	21747	34855	0.92	5.1E+00	O16005	SWISSPROT	RHODOPSIN
9912	22314	36280	1.2	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
11055	23481	36507	3.32	5.1E+00	P55200	SWISSPROT	ZINC FINGER PROTEIN HRX (ALL-1)
6611	19161	31911	0.79	5.0E+00	BF310449.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10324	22724	35691	3.76	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11060	23488	36512	3.22	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
						NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
2629	15124	27637	5.39	4.9E+00	AL021127.2	NT	
						NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10199	22600		0.89	4.8E+00	U91328.1	NT	
4075	18608		13.73	4.8E+00	AF186255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
9030	21482		5.27	4.8E+00	AW760087.1	EST_HUMAN	PM0-BT0547-310100-002404 BT0547 Homo sapiens cDNA
303	12899	25318	1.55	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
304	12899	25318	1.59	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
3236	16788	28205	1.12	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11344	23708	36763	2.2	4.7E+00	BE072352.1	EST_HUMAN	QV3-BT0537-221299-048-d11 BT0537 Homo sapiens cDNA
11344	23708	36764	2.2	4.7E+00	BE072352.1	EST_HUMAN	QV3-BT0537-221299-048-d11 BT0537 Homo sapiens cDNA
8344	20759	33654	0.75	4.6E+00	U67569.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
						EST_HUMAN	KIAA0645 PROTEIN; contains element PTR5 repetitive element;
9471	21802	34825	1.24	4.6E+00	BE646437.1	EST_HUMAN	7e86g10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140
9471	21802	34826	1.24	4.6E+00	BE646437.1	EST_HUMAN	7e86g10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140
8328	20741		0.54	4.5E+00	AF126177.1	NT	KIAA0645 PROTEIN; contains element PTR5 repetitive element;
11469	23827	36894	4.77	4.5E+00	BF688841.1	EST_HUMAN	Isoschekia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds
3000	15555	27968	0.8	4.4E+00	BF630983.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3000	15555	27969	0.8	4.4E+00	BF630983.1	EST_HUMAN	602072585F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
6516	18059		1.61	4.4E+00	X13414.1	NT	602072585F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
6567	19138	31886	0.59	4.4E+00	AF156696.1	NT	Murine I gene for MHC class II(a) associated invariant chain
8430	18986		0.76	4.3E+00	AF059879.1	NT	Nicotiana tabacum inorganic phosphate transporter (PT1) mRNA, complete cds
7923	20360	33227	1.58	4.3E+00	Y13402.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
						NT	Plasmodium falciparum R28R+var.1 gene, exon 1

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8143	20566	33443	0.81	4.3E+00	AE001222.1	NT	Troponin pallidum section 38 of 87 of the complete genome
10943	23084	36089	5.86	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
10709	23148		2.7	4.3E+00	11528311	NT	Homo sapiens complete cds
5779	18390		4.18	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE)
5861	18440	31115	0.92	4.2E+00	P61828	SWISSPROT	(RDP)
6040	18614		0.54	4.2E+00	O27830	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
7155	19888	32889	1.59	4.2E+00	P13983	SWISSPROT	PUTATIVE ATP-DEPENDENT HELICASE MTH1802
7155	19888	32690	1.59	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9314	21740	34654	4.59	4.2E+00	A1808013.1	EST_HUMAN	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9982	22384	35334	1.09	4.2E+00	P31368	SWISSPROT	wf67g03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692.3
6234	24604	31508	0.48	4.1E+00	O09185	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
9234	24604	31508	0.48	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P63
7551	20001	32843	0.99	4.1E+00	BE253668.1	EST_HUMAN	CELLULAR TUMOR ANTIGEN P63
7658	20104	32958	0.5	4.1E+00	BF247939.1	EST_HUMAN	60110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534.5
8183	20616	33502	8.13	4.1E+00	O23810	SWISSPROT	601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069768.5
8342	20757		0.75	4.1E+00	AB041523.1	NT	YY1 PROTEIN PRECURSOR
8345	20760	33655	4.19	4.1E+00	P28984	SWISSPROT	Palinopacten yessoensis mRNA for calcineurin A, complete cds
8345	20760	33656	4.19	4.1E+00	P28984	SWISSPROT	GENE 68 PROTEIN
8572	21007	33907	2.2	4.1E+00	U57503.1	NT	GENE 68 PROTEIN
9813	22216	36152	2.01	4.1E+00	BF692425.1	EST_HUMAN	Pan troglodytes novel repetitive sdo LTR element in the RNU2 locus
10688	23108		3.22	4.1E+00	P09716	SWISSPROT	602247838F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209.5
10752	23190		8.62	4.1E+00	BE886880.1	EST_HUMAN	HYPOTHETICAL PROTEIN HVLF1
11544	23901		2.69	4.1E+00	Q61193	SWISSPROT	601507610F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3808051.5
3530	18073		1.01	4.0E+00	P38229	SWISSPROT	RAL GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR-LIKE 2 (RALGDS-LIKE FACTOR)
5716	19759	32564	0.98	4.0E+00	O62653	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5716	19759	32565	0.98	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7347	19759	32564	0.86	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7347	19759	32565	0.86	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7633	20080	32933	1.24	4.0E+00	O33010	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
11227	22879	36856	1.75	4.0E+00	P14546	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
3481	16024	28445	5.55	3.9E+00	X64519.1	NT	CYTOKROM C OXIDASE POLYPEPTIDE III
4343	16865		0.74	3.9E+00	AF055466.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
							Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6927	18505	31188	3.25	3.9E+00	BE814357.1	EST_HUMAN	MF0-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6927	18505	31189	3.25	3.9E+00	BE814357.1	EST_HUMAN	MF0-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6988	18534	32317	0.83	3.9E+00	AF288209.1	NT	Dicotyledon discoidium non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
7060	18594	32388	0.58	3.9E+00	U91323.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7277	19782	32592	4.74	3.9E+00	P39289	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AID-RPSF INTERGENIC REGION
7835	20276	33137	3.63	3.9E+00	M23907.1	NT	Human MHG class II lymphocyte antigen (DPW4-beta-1) gene, exon 2
8863	21287	34207	2.17	3.9E+00	XG5955.1	NT	Xlae1s mRNA for M4 muscarinic receptor
11143	22833	35803	4.91	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2561	15080		13.68	3.9E+00	AE001662.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6727	19273	32033	1.13	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
7164	18867	32688	0.53	3.8E+00	A1493849.1	EST_HUMAN	q51107.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030437 3'
8954	21387	34289	1.3	3.8E+00	D44725.1	EST_HUMAN	HUMSUJY135 Human brain cDNA Homo sapiens cDNA clone 148
4032	16565	28958	13.41	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7509	20058		0.8	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
11681	23990		1.24	3.7E+00	AB013746.3	NT	Callus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
610	13178	25581	3.37	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone IMAGE:4131016 5'
5805	18086	30339	0.64	3.6E+00	BF316316.1	EST_HUMAN	301801866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
9099	21531	34439	3.65	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PAO1, section 8 of 629 of the complete genome
9099	21531	34440	3.65	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PAO1, section 8 of 629 of the complete genome
							Escherichia coli glycerophosphate dehydrogenase (gldD) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds
10632	23074		3.08	3.6E+00	M98795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3208	16768	28176	0.97	3.5E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
6303	18884		1.14	3.5E+00	L42898.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6529	18081	31822	1.11	3.5E+00	R18745.1	EST_HUMAN	Y94008.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
							cd37f10.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1818987 3' similar to gb:J04213
							CELLULAR RETINALDEHYDE-BINDING PROTEIN (HUMAN);
8387	20801	33688	0.6	3.5E+00	AA992102.1	EST_HUMAN	Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R) mRNA
8430	20844	33744	0.53	3.5E+00	4505294	NT	Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R) mRNA
							zps6b04.s1 Stratiogene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
9364	21786	34703	1.04	3.5E+00	AA190998.1	EST_HUMAN	

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9384	21796	34704	1.04	3.5E+00	AA180998.1	EST_HUMAN	zp86604.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
9889	22101	35030	1.1	3.5E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
1540	14071	28531	3.2	3.4E+00	AF254577.1	NT	Breescia napus RP86d mRNA, complete cds
2495	14998	27510	2.6	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7108	19841	32438	0.56	3.4E+00	U77617.1	NT	Chlorante-Aster yellows phytoplasma acetate kinase gene, complete cds
7834	20274	33136	3.14	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8242	20659	33549	0.9	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9119	21551		0.84	3.4E+00	U65408.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
10219	22620	35587	3.11	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11288	23653	36701	2.08	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6374	18932	31669	1	3.3E+00	Q09689	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6374	18932	31670	1	3.3E+00	Q09689	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
8558	20991	33888	0.91	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10351	22751	35717	1.17	3.3E+00	AP001611.1	NT	Bacillus halodurans genomic DNA, section 5/14
10351	22751	35718	1.17	3.3E+00	AP001611.1	NT	Bacillus halodurans genomic DNA, section 5/14
518	13091	25504	2.43	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4038	13091	25504	0.88	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
5833	18413	31081	1.43	3.2E+00	P64924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5833	18413	31082	1.43	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5869	18448	31123	3	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5869	18448	31124	3	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6634	19182	31933	1.73	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6634	19182	31934	1.73	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
8132	20555	33432	0.97	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8332	20747	33643	2.55	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8332	20747	33644	2.55	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
9362	21794		6.29	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE]HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9715	22138	35068	2	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (LDV1) gene, complete cds
10145	22548	35515	2.08	3.2E+00	AB016081.2	NT	Oryza latipes OIGC8 gene for guanylyl cyclase C, complete cds
11639	23983		3.08	3.2E+00	L39386.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
12574	24893		1.28	3.2E+00	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
6163	18731	31435	2.08	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7866	20305	33170	0.88	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
8278	20693		1.24	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
8072	21504	34411	4.88	3.1E+00	P48894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE-1 DEIODINASE) (DIO1) (TYPE 1 D1) (5D1)
8072	21504	34412	4.88	3.1E+00	P48894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE-1 DEIODINASE) (DIO1) (TYPE 1 D1) (5D1)
							GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9520	21983		4.24	3.1E+00	Q14957	SWISSPROT	Chlorella vulgaris chloroplast, complete genome
9967	22369	35318	0.88	3.1E+00	7524759	NT	DEOXYHYDROLYSINE SYNTHASE (DHS)
10265	22668	35829	4.14	3.1E+00	P49365	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5))
11216	22867		2.81	3.1E+00	P33515	SWISSPROT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PGC7-MZ1, mRNA, 2871 nt]
11238	23604		2.63	3.1E+00	S56660.1	NT	S. aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease
5592	18180	30545	1.43	3.0E+00	X53088.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6909	19448	32226	0.7	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6909	19448	32227	0.7	3.0E+00	X56037.1	NT	CYR61 PROTEIN PRECURSOR (3CH61)
7597	20046		8.53	3.0E+00	P18406	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
7640	20087		0.71	3.0E+00	Q13201	SWISSPROT	B. napus DNA for myosinase
9284	21716		1.49	3.0E+00	X67838.1	NT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2)
							(ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10788	23228	36208	6.33	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2)
10788	23228	36209	6.33	3.0E+00	P51842	SWISSPROT	(ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
1949	14468	26972	1.84	2.9E+00	AE002226.2	NT	Chlamydomonas reinhardtii AR39, section 63 of 94 of the complete genome
5482	17877	30321	1.94	2.9E+00	AF013187.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
9380	18937		0.65	2.8E+00	AB026033.1	NT	Bonaparitia pediculus mitochondrial DNA for 16S ribosomal RNA
7317	19729	32533	1.61	2.9E+00	Z36879.1	NT	F. pingid gdcPA gene for P-protein of the glycine cleavage system
7656	20102	32952	4.87	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7656	20102	32953	4.87	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7941	20378	33245	5.83	2.9E+00	P46599	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
1486	14018	26483	6.38	2.8E+00	AF166398.1	NT	Buxus harlandii mature K (maK) gene, partial cds; chloroplast gene for chloroplast product
1841	14172		1.55	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2687	15065	27680	2.34	2.8E+00	AF044578.1	NT	Homo sapiens putative DNA polymerase mRNA, partial cds
7771	20213	33076	5.71	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
242	12843	26266	10.9	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
242	12843	26267	10.9	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
5816	18386	31059	1.26	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
9319	21751		2.18	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T-4 cDNA library under conditions of nitrogen deprivation
10375	22775		2.06	2.7E+00	BE063527.1	EST_HUMAN	CMO-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
4718	17234	29615	5.58	2.6E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5812	18392	31084	2.04	2.6E+00	8755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5812	18392	31055	2.04	2.6E+00	8755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
8111	18680		0.85	2.6E+00	Y17062.1	NT	Mycobacterium fortuitum furA II gene
8069	24992		0.75	2.6E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
8241	20658		7.52	2.6E+00	AF235502.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8677	21112	34014	1.19	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
8677	21112	34016	1.19	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
9802	22205	35142	3.47	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10274	22675		1.72	2.6E+00	8055193	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12324	24854		2.87	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1493	14025	26487	1.51	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1493	14025	26488	1.51	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
6097	18668	31356	2.35	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6097	18668	31359	2.35	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6802	18668	31358	1.64	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6802	18668	31359	1.64	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
7107	18840	32435	0.71	2.5E+00	D30052.1	NT	Vibrio cholerae cbaA gene and cbaB gene for cholera toxin, complete cds
8314	20728	33621	1.07	2.5E+00	AW949158.1	EST_HUMAN	QV4-F70005-110500-205-g07 F70005 Homo sapiens cDNA
8388	20802	33699	0.48	2.5E+00		NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
9412	21844	34768	1.88	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
11636	23961		3.16	2.5E+00	AF286665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
2971	15526	27948	1	2.4E+00	M24262.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4976	17497	29865	5.94	2.4E+00		NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
6314	18875	31600	4.82	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7854	20294	33156	0.63	2.4E+00	BF687602.1	EST_HUMAN	602120856FT NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7854	20294	33157	0.63	2.4E+00	BF687502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
7870	20309	33175	0.51	2.4E+00	P20126	SWISSPROT	RNA REPLICASE POLYPROTEIN
7870	20309	33178	0.51	2.4E+00	P20126	SWISSPROT	RNA REPLICASE POLYPROTEIN
8730	21165	34059	2.43	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8730	21165	34070	2.43	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8786	21220		2.89	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
9104	21538		1.47	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d06 PT0004 Homo sapiens cDNA
9236	21668	34578	9.69	2.4E+00	P24091	SWISSPROT	ENDOCHITININASE B PRECURSOR (CHN-B)
10065	22468	35422	2.51	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10065	22468	35423	2.51	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10122	22523	35489	2.27	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
10207	22608		7.28	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLUKINASE)
10258	22657	35318	1.79	2.4E+00	BE326702.1	EST_HUMAN	hr63708.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10258	22657	35319	1.79	2.4E+00	BE326702.1	EST_HUMAN	hr63708.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10428	22828	35798	0.96	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN N1RQ
10957	23386		1.66	2.4E+00	AF096872.1	NT	Capra hircus alphaS2-casein type C gene, Intron 15
11116	23569	36612	2.1	2.4E+00	AF168652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
12238	24735		1.26	2.4E+00	AF275949.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
1286	13821	26273	12.19	2.3E+00	Z46724.1	NT	G domesticus artificial single chain antibody gene (L3)
4138	16866		1.39	2.3E+00	AJ401081.1	NT	Bos taurus partial cyt b gene for cytochrome b
4939	17450	29825	3.72	2.3E+00	AF134318.1	NT	Mus musculus G7c (G7c) gene, G7c-b allele, complete cds
6121	18690		1.14	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7939	20376	33243	10.66	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
8120	24893		2.16	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (GENP-B)
8340	20755	33650	1.7	2.3E+00	X60265.1	NT	M. mazel dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9454	21885	34805	1.52	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
10584	23031	36014	4.4	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11037	23464	36485	2.3	2.3E+00	P20059	SWISSPROT	ENDOCHITININASE 3 PRECURSOR
11483	23841	36908	2.33	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
11483	23841	36909	2.33	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
11872	24114	31000	6.38	2.3E+00	BE955237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4030	18563	28987	0.88	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4335	18857	29242	4.01	2.2E+00	D87071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4335	18857	29243	4.01	2.2E+00	D87071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- RECEPTOR REPEATS) (LR11) <2
5596	18184	30548	10.77	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- RECEPTOR REPEATS) (LR11) <2
5596	18184	30549	10.77	2.2E+00	O88307	SWISSPROT	BINDING REPEATS) (LR11) <2
6140	18708	31407	1.84	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
6140	18708	31408	1.84	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
6368	18926	31681	8.4	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2859777 3'
6885	19233	31983	2.51	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6952	19489	32269	3.45	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7372	18042		3.86	2.2E+00	AA594574.1	EST_HUMAN	n195b02.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7781	20223	33083	0.85	2.2E+00	AA137027.1	EST_HUMAN	zn9704.f1 Stralagens fetal retina 937202 Homo sapiens cDNA clone IMAGE:568143 5'
8134	20557	33434	14.89	2.2E+00	AA448012.1	EST_HUMAN	zn05g10.f1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
8227	20846	33538	0.76	2.2E+00	P94918	SWISSPROT	ALANINE RACEMASE
8513	20925	33821	0.54	2.2E+00	O87099	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
9578	22001		12.55	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9744	24653		2.72	2.2E+00	Q04708	SWISSPROT	TRANSPONSON TY1 PROTEIN A
10079	22480	35438	1.36	2.2E+00	A1290373.1	EST_HUMAN	qrm69b03.x1 Soares placenta 8to9weeks_2NBP8P8c9W Homo sapiens cDNA clone IMAGE:1893965 3'
10079	22480	35437	1.36	2.2E+00	A1290373.1	EST_HUMAN	qrm69b03.x1 Soares placenta 8to9weeks_2NBP8P8c9W Homo sapiens cDNA clone IMAGE:1893965 3'
10113	22514	35479	2.58	2.2E+00	BF246782.1	EST_HUMAN	similar to gb:Y00493 GLUTATHIONE PEROXIDASE (HUMAN);
10345	22745	35712	2.72	2.2E+00	AF183416.1	NT	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
11190	22842	35814	4.9	2.2E+00	P07811	SWISSPROT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11382	23725	36785	12.17	2.2E+00	P10407	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11480	23848	36917	2.52	2.2E+00	F31628.1	EST_HUMAN	EARLY E1A 28 KD PROTEIN
596	18287	25661	9.08	2.1E+00	AF132812.2	NT	HSPD22848 Hm3 Homo sapiens cDNA clone s4000123808
3580	16122		1.05	2.1E+00	AW448388.1	EST_HUMAN	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
							UI-H-B13-alt-08-0-U1.s1 NCL_CGAP_sub5 Homo sapiens cDNA clone IMAGE:2794560 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6445	19001		0.84	2.1E+00	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
7198	19009	32738	3.47	2.1E+00	O70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7453	19956	32760	0.7	2.1E+00	4503430	NT	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
7475	19979	32475	7.64	2.1E+00	N29575.1	EST_HUMAN	y08a10.s1 Scores melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
8000	21433		2.09	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1227	13766	26212	1.42	2.0E+00	AF180827.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000871 5'
1227	13766	26213	1.42	2.0E+00	AF180827.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1367	13901	26358	0.93	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1592	14124		2.77	2.0E+00	P25582	SWISSPROT	Oryctolagus cuniculus Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
2061	14576	27093	3.7	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2061	14576	27094	3.7	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4117	16647	29032	1.69	2.0E+00	AW564496.1	EST_HUMAN	R. norvegicus mRNA for collagen alpha1 type I
4117	16647	29033	1.89	2.0E+00	AW664496.1	EST_HUMAN	hi13c05.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
8064	20495		0.82	2.0E+00	P07568	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8649	21084	33989	4.08	2.0E+00	AB008676.1	NT	hi13c05.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
8649	21084	33990	4.08	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8649	21084	33991	4.08	2.0E+00	AB008676.1	NT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE
9284	21726	34634	3.11	2.0E+00	F31600.1	EST_HUMAN	GLYCOPROTEINS E1 AND E2
12225	24810	30381	6.71	2.0E+00	5834843	NT	Escherichia coli 0167 DNA, map position at 46 min., complete cds
5865	18444	31118	3.67	1.9E+00	6754389	NT	Escherichia coli 0167 DNA, map position at 46 min., complete cds
5865	18444	31119	3.67	1.9E+00	6754389	NT	Escherichia coli 0167 DNA, map position at 46 min., complete cds
6408	18965	31701	1.24	1.9E+00	BE68895.1	EST_HUMAN	Escherichia coli 0167 DNA, map position at 46 min., complete cds
7019	19555		0.74	1.9E+00	AW845688.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000177B08
7129	19662		2.16	1.9E+00	Q63627	SWISSPROT	Gallus gallus mitochondrion, complete genome
8972	21405	34319	2.3	1.9E+00	P02467	SWISSPROT	Mus musculus Inositol 1,4,5-triphosphate receptor 1 (ltp1), mRNA
8972	21405	34320	2.3	1.9E+00	P02467	SWISSPROT	Mus musculus Inositol 1,4,5-triphosphate receptor 1 (ltp1), mRNA
9111	21543		3.6	1.9E+00	BF360206.1	EST_HUMAN	601679636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
9273	21705		2.02	1.9E+00	Q51781	SWISSPROT	MRO-CT0063-071099-002-g02 CT0063 Homo sapiens cDNA
3055	15609	28018	2.16	1.9E+00	P21004	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							OM3-MT0114-010600-323-512 MT0114 Homo sapiens cDNA
							ARGININE DEMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
							PROTEIN B8 PRECURSOR

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3081	15635	28041	3.6	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3081	15635	28042	3.8	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
6155	18723		1.8	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6413	18970	31706	1.91	1.8E+00	BF311939.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6736	19281		1.69	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
7120	19653	32449	1.48	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7490	18694	32490	0.97	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7714	20159		0.83	1.8E+00	P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE-- (GLUCOSYL)UPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8715	21150	34054	0.92	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ; ENDONUCLEASE]
8715	21150	34055	0.92	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ; ENDONUCLEASE]
9257	21689	34901	2.72	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HIEFS)
9931	22333	35281	0.85	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10233	22634		2.28	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10408	22806		0.84	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE)(CDA)
12000	24779		4.81	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12088	24239		3.53	1.8E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpct1b), mRNA
12413	24875	30770	1.31	1.8E+00	BF212412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'
1135	13678	28118	1.92	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2171	14682	27207	3.64	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2266	14774	27295	5.32	1.7E+00	AI141067.1	EST_HUMAN	0243105.X1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4491	17009	29394	0.79	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5880	18459	31132	1.86	1.7E+00	BE063548.1	EST_HUMAN	CM0-BT0282-171289-127-e05 BT0282 Homo sapiens cDNA
5880	18459	31133	1.86	1.7E+00	BE063548.1	EST_HUMAN	CM0-BT0282-171289-127-e05 BT0282 Homo sapiens cDNA
6142	18710	31411	0.47	1.7E+00	R58748.1	EST_HUMAN	G4846 Fetal heart Homo sapiens cDNA clone G4846 5' end
6321	18981	31609	3.94	1.7E+00	Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6904	19443	32221	0.64	1.7E+00	P35816	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPc)
7666	20112	32964	1.19	1.7E+00	Q03703	SWISSPROT	HYPOHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7668	20112	32965	1.19	1.7E+00	Q03703	SWISSPROT	HYPOHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7716	20161	33019	0.43	1.7E+00	P20393	SWISSPROT	ORPHAN NUCLEAR RECEPTOR NR1D1 (V-ERBA RELATED PROTEIN EAR-1) (REV-ERBA-ALPHA)
8530	20985	33887	0.97	1.7E+00	AF021336.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8655	21090	33997	1.15	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tcl1), mRNA
9088	21520	34787	1.7	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
9439	24652	34787	1.6	1.7E+00	O80478	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9439	24652	34788	1.6	1.7E+00	O80478	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9769	22172	36765	1.25	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
11346	23709	36765	2.77	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retha cDNA Tsp5081-cleaved sublibrary Homo sapiens cDNA, not directional
11851	24154	30974	1.6	1.7E+00	AI678443.1	EST_HUMAN	tu82407.x1 NC1_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2267649 3' similar to contains MSR1.11
12499	24505	30855	1.76	1.7E+00	AI108573.1	EST_HUMAN	MSR1 repetitive element;
1968	14488	26995	13.63	1.6E+00	AF189339.1	NT	qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1
1974	14492	27000	2.45	1.6E+00	AF077374.1	NT	repetitive element;
2914	15489	27892	1.19	1.6E+00	W58426.1	EST_HUMAN	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
4045	16577	29277	6.9	1.6E+00	BF570077.1	EST_HUMAN	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
4374	16896	29277	1.57	1.6E+00	AF155827.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
4374	16896	29278	1.57	1.6E+00	AF155827.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
5106	17614	29975	0.88	1.6E+00	AF075394.1	NT	z22501.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
5106	17614	29976	0.88	1.6E+00	AF075394.1	NT	gb:D28805 N-ACETYL LACTOSAMINE SYNTHASE (HUMAN);
5214	17717	30082	2.62	1.6E+00	Y11344.1	NT	802186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
5214	17717	30083	2.62	1.6E+00	Y11344.1	NT	802186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
6112	18581	31378	2.61	1.6E+00	L04908.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
6208	18774	31479	0.7	1.6E+00	AF009531.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
6271	18534	31547	0.42	1.6E+00	BE971873.1	EST_HUMAN	Urothitis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial
6271	18534	31548	0.42	1.6E+00	BE971873.1	EST_HUMAN	Urothitis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial
6816	19358	32133	0.91	1.6E+00	BF380703.1	EST_HUMAN	protein, partial cds
							Urothitis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial
							protein, partial cds
							Mus musculus ST6GalNAcII gene, exon 2
							Mus musculus ST6GalNAcII gene, exon 2
							Brachydanio rerio MHC class II DA-beta-2'01 gene, 3' end
							Homo sapiens transglutaminase type I (Tgase) gene, promoter region
							601651111R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934443 3'
							601651111R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934443 3'
							IL2-UT0073-080900-145-E02 UT0073 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7082	19616	32411	1	1.6E+00	AW204881.1	EST_HUMAN	U1H-B12-shr-b-04-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7694	20139	32995	2.58	1.6E+00	BE697267.1	EST_HUMAN	RCO-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
8653	21088		1.49	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8915	21349	34266	3.5	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SGL & CYP_b genes
9278	21710	34820	1.05	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9278	21710	34821	1.05	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9663	24850	33852	1.22	1.6E+00	X52046.1	NT	Mimulus COL3A1 gene for collagen alpha-1
9663	24850	33853	1.22	1.6E+00	X52046.1	NT	Mimulus COL3A1 gene for collagen alpha-1
9955	22258	35186	1.57	1.6E+00	T41280.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV
10167	22568	35533	0.95	1.6E+00	AW835844.1	EST_HUMAN	QV4-LT0018-090200-100-d07 LT0018 Homo sapiens cDNA
10167	22568	35534	0.95	1.6E+00	AW835844.1	EST_HUMAN	QV4-LT0018-090200-100-d07 LT0018 Homo sapiens cDNA
10553	23000	35984	2.63	1.6E+00	P64817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
10921	18774	31479	7.7	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
11430	23791	36852	3.41	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
12544	24533		1.28	1.6E+00	AV764043.1	EST_HUMAN	AV764043 MDS Homo sapiens cDNA clone MDSDAH08 5'
34	12654	25044	4.43	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
243	12844	25258	2.13	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome
940	13204		2.37	1.5E+00	6752861	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2308	14815	27332	5.54	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3089	14815	27332	1.44	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3352	15888	28319	0.9	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
6003	18577	31263	0.81	1.5E+00	AI655301.1	EST_HUMAN	HKF-1.;
6003	18577	31263	0.81	1.5E+00	AI655301.1	EST_HUMAN	HKF-1.;
6003	18577	31264	0.81	1.5E+00	AI655301.1	EST_HUMAN	HKF-1.;
6650	19198		0.65	1.5E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment H921C002
6744	19288	32049	2.83	1.5E+00	R17879.1	EST_HUMAN	Y910a02.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
7288	19773	32581	0.52	1.5E+00	BE907771.1	EST_HUMAN	601602041F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903659 5'
7688	20018		1.33	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7602	20051	32801	17.68	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7602	20051	32802	17.68	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7812	20254	33115	0.58	1.5E+00	AA889259.1	EST_HUMAN	ak26f10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8117	20542	33419	0.8	1.5E+00	A003254.1	EST_HUMAN	an07b11.s1 Stralagene schizs brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
8468	20879		0.54	1.5E+00	AB039887.1	NT	gb:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8474	20887		0.43	1.5E+00	AA2851181.1	EST_HUMAN	Homo sapiens WDR4 gene for WD repeat protein, complete cds
8718	21163	34059	0.96	1.5E+00	BE887446.1	EST_HUMAN	zs02b12.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683909 5'
9088	21530	34438	1.01	1.5E+00	K02138.1	NT	601508586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
9787	22180	35128	1.33	1.5E+00	AW375897.1	EST_HUMAN	Mouse germline IgM chain gene, mu-delta region
9938	22340	35289	8.51	1.5E+00	BF378754.1	EST_HUMAN	QV3-CT0192-261089-008-d09 CT0192 Homo sapiens cDNA
10078	22478		1.38	1.5E+00	BF337944.1	EST_HUMAN	RCO-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
10174	22575	35542	2.01	1.5E+00	AA017689.1	EST_HUMAN	602035771F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:361308 5'
10174	22575	35543	2.01	1.5E+00	AA017689.1	EST_HUMAN	602035771F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:361308 5'
11153	23534	36572	11.16	1.5E+00	AL134197.1	EST_HUMAN	zs08g06.1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:361308 5'
11288	23661		9.1	1.5E+00	X07380.1	NT	zs08g06.1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:361308 5'
11788	24057		1.22	1.5E+00	D63480.1	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
11942	24878	30574	1.48	1.5E+00	D63480.1	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
12185	24305		4.61	1.5E+00	AL445065.1	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
12297	24381		1.67	1.5E+00	6978492.1	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
31	12851	25040	2.52	1.4E+00	7681685	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
31	12851	25041	2.52	1.4E+00	U67922.1	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
2229	14738		9.53	1.4E+00	X74463.1	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
2608	15103	27621	4.82	1.4E+00	X74463.1	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
2732	15222	27735	1.3	1.4E+00	AF064584.2	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
2732	15222	27738	1.3	1.4E+00	AF064584.2	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
3305	15853		0.86	1.4E+00	6453733	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
4272	16797	29179	1.14	1.4E+00	AW600455.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
4272	16797	29180	1.14	1.4E+00	AW600455.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
4624	17140		1.18	1.4E+00	BF681547.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
5468	17963	30311	14.22	1.4E+00	Y19213.1	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
5628	18215	30617	1.66	1.4E+00	AW054878.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
5780	18371		6.28	1.4E+00	AB032983.1	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
6603	19154	31902	3.75	1.4E+00	Q13472	SWISSPROT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
6620	24988		4.23	1.4E+00	AB020712.1	NT	DKFZp547P243_s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6751	19295	32057	3.23	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6751	19295	32058	3.23	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6798	19341	32112	0.61	1.4E+00	11096333	NT	Mus musculus WW domain binding protein 11 (Wbp11-pending), mRNA
6987	19524	32306	0.71	1.4E+00	BE007870.1	EST_HUMAN	QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA
6987	19524	32307	0.71	1.4E+00	BE007870.1	EST_HUMAN	QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA
7215	19827	32643	0.92	1.4E+00	AW89057.1	EST_HUMAN	CM3-NN0008-300300-132-b12 NN0008 Homo sapiens cDNA
							Homo sapiens caveolin-1/2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7743	20187	33049	2.27	1.4E+00	AJ133289.1	NT	he2305.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element
7783	20207	33070	1.32	1.4E+00	AW467760.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7830	20271	33133	0.83	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7830	20271	33134	0.83	1.4E+00	P55268	SWISSPROT	MINOR CAPSID PROTEIN L2
7859	20298	33184	0.65	1.4E+00	Q80905	SWISSPROT	Homo sapiens Xq pseudautosomal region, segment 1/2
8210	21642		5.99	1.4E+00	AJ271735.1	NT	Y93312.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:34348 5'
9404	21836	34749	1.95	1.4E+00	R20459.1	EST_HUMAN	RC1-BT0313-301290-012-05 BT0313 Homo sapiens cDNA
9472	21903	34927	1.85	1.4E+00	BE064687.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10183	22584	35549	1.07	1.4E+00	BF57545.1	EST_HUMAN	IL6-HT0198-291099-008-C04 HT0188 Homo sapiens cDNA
10214	22615	35582	0.89	1.4E+00	BE145374.1	EST_HUMAN	IL6-HT0198-291099-008-C04 HT0188 Homo sapiens cDNA
10214	22615	35583	0.89	1.4E+00	BE145374.1	EST_HUMAN	IL6-HT0198-291099-008-C04 HT0188 Homo sapiens cDNA
10390	22780	35781	0.93	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10390	22780	35782	0.93	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10996	23425	36442	2.38	1.4E+00	AB006882.1	NT	Homo sapiens APECE2 mRNA for AIRE-1, complete cds
11160	23540	36578	3.3	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11160	23540	36579	3.3	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11179	23585	36636	1.97	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11179	23585	36637	1.97	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11785	24800		2.04	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12573	24555		1.33	1.4E+00	7857624	NT	Homo sapiens staufen (Drosophila, RNA-binding protein) homolog 2 (STAU2), mRNA
587	13157		1.46	1.3E+00	Z73840.1	NT	M.mucedo gene encoding 4-Dihydroxyethyl-trisporate dehydrogenase
925	13479	25928	2.54	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1156	13699		24.84	1.3E+00	Y19213.1	NT	Homo sapiens putative psithHba pseudogene for hair keratin, exons 2 to 7
1329	13865	26315	16.11	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (ZFP157) mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1329	13865	26316	16.11	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 167 (ZNF167) (ZNF167) mRNA
1386	13921		1.48	1.3E+00	U61730.2	NT	Cox lacyrna-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1925	14156		2.15	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2461	14963		1.65	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916945 3'
2893	16447	27870	5.92	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythrocyte (Sptn1), mRNA
3591	16133	28546	1.12	1.3E+00	AF018494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P65), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5140	17644	30007	1.61	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5140	17644	30008	1.51	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5776	18357	30817	0.94	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOXYGENASE P3 COMPONENT)
5980	18556	31240	0.43	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6251	18815	31529	0.8	1.3E+00	BF663825.1	EST_HUMAN	602145264F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309085 5'
6322	18882	31510	8.23	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-708 CT0289 Homo sapiens cDNA
6322	18882	31610	8.23	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-708 CT0289 Homo sapiens cDNA
6756	19299	32084	1.28	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
7131	19884		0.86	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
7174	19897		0.84	1.3E+00	P49940	SWISSPROT	SPORE GERMINATION PROTEIN KB
7232	19844	32682	1.02	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7348	24626	32566	0.84	1.3E+00	AW821580.1	EST_HUMAN	IL2-ST0311-020200-040-G12 ST0311 Homo sapiens cDNA
7364	19821	32635	1.07	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447865 5'
7639	19989	32628	1.03	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7943	20380	33247	0.68	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8849	21283	34195	1.48	1.3E+00	AJ008912.1	NT	Sus scrofa plp gene
8861	21394	34306	1.76	1.3E+00	BE963379.2	EST_HUMAN	601657149R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866195 3'
9044	21476	34389	0.99	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
9142	21574		1.61	1.3E+00	9910247	NT	Homo sapiens GL004 protein (GL004), mRNA
9208	21638	34547	0.91	1.3E+00	A1927629.1	EST_HUMAN	wo86a07.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9703	22126		6.32	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9711	22134	35059	2.75	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9711	22134	35060	2.75	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9780	22183	35118	1.05	1.3E+00	AF059250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9811	22214	35150	1.8	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9865	22208	35207	1.59	1.3E+00	A1827629.1	EST_HUMAN	wo85a07.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9943	22345	35294	3.69	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3868195 3'
10187	22588	35564	1.43	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10198	22599	35585	1.78	1.3E+00	M29893.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10420	22820		1.03	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10481	22931		6.42	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
10886	23128	36106	2.17	1.3E+00	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA16
11085	23519		3.28	1.3E+00	AW274791.1	EST_HUMAN	xp08e03.x1 NCL CGAP_HN9 Homo sapiens cDNA clone IMAGE:2738868 3'
11294	23659	36705	3.91	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11373	23735	36793	3.45	1.3E+00	Z96932.1	NT	Bacillus subtilis genomic DNA 23.9kb fragment
11537	23894	36977	1.93	1.3E+00	P03719	SWISSPROT	TYPE I RESTRICTION ENZYME ECK1 SPECIFICITY PROTEIN (S PROTEIN)
11931	24146		2.53	1.3E+00	BF348043.1	EST_HUMAN	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12120	24281	30930	4.58	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCL CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158452 5'
12133	24686		2.13	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12234	24342		1.2	1.3E+00	AF187035.1	NT	Sturnira lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
689	13234	25646	10.66	1.2E+00	AA676246.1	EST_HUMAN	z22d08.e1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
846	13403	25844	1.2	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
848	13403	25845	1.2	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
846	13403	25846	1.2	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (PRO3077) (PRO3077), mRNA
801	13455		0.87	1.2E+00	8924234	NT	Homo sapiens hypodermal protein PRO3077 (PRO3077), complete cds
1197	13732	26175	5.72	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete genome
1236	13774	26221	1.07	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1236	13774	26222	1.07	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2370	14875	27394	8.56	1.2E+00	BE063338.1	EST_HUMAN	PMO-BT0274-211089-001-e04 BT0274 Homo sapiens cDNA
3071	16826	28031	1.06	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3124	16877	28091	5.04	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3124	16877	28092	5.04	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3248	16769		3.21	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3329	15876	28299	0.7	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3709	16249	28653	9.7	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4000	16534	28636	1.81	1.2E+00	BF373570.1	EST_HUMAN	MRO-F010175-050300-203-g06_1 FT0175 Homo sapiens cDNA
4317	16876	28289	1.02	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4505	17023		2.28	1.2E+00	M87080.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4569	17076	29481	1.03	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, conlig fragment No. 21
4597	17113	29501	1.54	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4827	17143		5.98	1.2E+00	Y09200.1	NT	T. pinatum chloroplast rbcL gene, partial
5694	18279	30702	1.12	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5819	18399	31063	1.3	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6080	18651		0.6	1.2E+00	X81879.1	NT	Callicivirus cDNA for orf1, orf2 and orf3
6162	18730	31434	1	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6465	19021	31754	2.2	1.2E+00	X74895.1	NT	D. hydei eyf1 repeat cluster DNA, fragment D
6530	19082	31823	4.21	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0080-270400-190-a03 BN0080 Homo sapiens cDNA
6618	19168	31918	1.63	1.2E+00	X89084.1	NT	C. glutamicum pta gene and ackA gene
6616	19166	31919	1.63	1.2E+00	X89084.1	NT	C. glutamicum pta gene and ackA gene
6663	19211	31959	40.66	1.2E+00	AA759254.1	EST_HUMAN	an84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374.3'
6775	19318	32084	0.66	1.2E+00	N33295.1	EST_HUMAN	W59b12.s1 Soares_melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:273599.3' similar to gb J87935 HUMAAALU472 Homo carcinoma cell-derived Alu RNA transcript, (rRNA); gb:J04970
6851	19392	32167	0.58	1.2E+00	P17871	SWISSPROT	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6855	19395	32171	1.04	1.2E+00	AW813276.1	EST_HUMAN	ECDOYSONE-INDUCIBLE PROTEIN E75-A
7323	19735	32538	1.33	1.2E+00	AB029010.1	NT	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7337	19749	32552	2.9	1.2E+00	AJ002141.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7484	19866	32800	0.63	1.2E+00	AA167810.1	EST_HUMAN	Mus musculus DGPP gene
7703	20148		0.77	1.2E+00	AJ271735.1	NT	z38f05.r1 Stratagene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:632001.5' similar to gb D10522 Homo sapiens mRNA for 80K-L protein, complete cds. (HUMAN);
7858	24638	33163	1.62	1.2E+00	AV734585.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
8181	20603	33490	2.81	1.2E+00	X74207.1	NT	AV734585 cda Homo sapiens cDNA clone cDAAFH03.5'
8247	20664	33553	0.42	1.2E+00	J05218.1	NT	L. lactis pyrD and pyrF genes
8427	20841	33740	0.58	1.2E+00	BE787648.1	EST_HUMAN	Chicken muscarinic acetylcholine receptor (cm4 mAChR) gene, complete cds
							601481761F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3884270.5'
							Chicken muscarinic acetylcholine receptor (cm4 mAChR) gene, complete cds
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1; Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds: Sacm21 gene, partial>
							Homo sapiens mRNA for KIAA1204 protein, partial cds
8434	20848	33749	0.53	1.2E+00	AF110520.1	NT	Homo sapiens cDNA
8049	21481	34993	2.71	1.2E+00	AB030303.1	NT	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
9359	21791	34700	2.12	1.2E+00	AW377210.1	EST_HUMAN	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9618	22033	34963	2.7	1.2E+00	Z32850.1	NT	HUMH-IM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hmo1e01
9768	22171	35103	1.96	1.2E+00	D11745.1	EST_HUMAN	

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9990	22392	35343	3.7	1.2E+00	X56832.1	NT	H.sapiens ENO3 gene for muscle specific enolase
10259	22690		0.86	1.2E+00	AB008668.1	NT	Homo sapiens Ildho gene, exon 1
11105	23558	36599	2.38	1.2E+00	AW817817.1	EST_HUMAN	PMO-ST0284-181198-001-d01 ST0284 Homo sapiens cDNA
11137	23688		12.04	1.2E+00	BE160781.1	EST_HUMAN	PM1-HT0422-180200-007-g10 HT0422 Homo sapiens cDNA
11207	22859	35833	2.7	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
11899	24789	30880	20.86	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11918	24138		1.85	1.2E+00	AP001515.1	NT	Homo sapiens chromosome 21 segment HS21C014
481	13055	25472	1.45	1.1E+00	D86880.1	NT	Bacillus halodurans genomic DNA, section 8/14
1750	14277	26761	1.04	1.1E+00	AW965393.1	EST_HUMAN	Human mRNA for KIAA0227 gene, partial cds
2501	15002	27514	6.8	1.1E+00	AF067124.1	NT	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
3300	15849	28287	9.29	1.1E+00	AL163213.2	NT	Wheat yellow mosaic virus RNA1 270 kDa precursor protein gene, complete cds
3300	15849	28288	9.29	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3462	16006	28427	0.83	1.1E+00		NT	Homo sapiens chromosome 21 segment HS21C013
3543	16095		1.87	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3570	16112	28527	1.18	1.1E+00	AI808360.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3718	16256	28659	1.37	1.1E+00	AE003888.1	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3716	16256	28660	1.37	1.1E+00	AE003888.1	NT	wf64h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P631_HUMAN Q12888 P63-BINDING PROTEIN 63BP1 ;
3825	16362		0.88	1.1E+00	X65374.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3957	16492	28901	1.06	1.1E+00	8922841	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
4230	16755		7.57	1.1E+00	8633331	NT	H. parahemolyticus hphIM(A), hphIM(C), hphIR and menB genes
5092	17602	29987	3.24	1.1E+00	U18466.1	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
						NT	R.unicornis complete mitochondrial genome
						NT	African swine fever virus, complete genome
						NT	Emericella nidulans sterigmatocystin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcD), (stcE), (stcF), (stcG), (stcH), (stcI), (stcJ), (stcK), (stcL), (stcM), (stcN), (stcO), (stcP), (stcQ), (stcR), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds
5156	17660	30021	7.13	1.1E+00	U34740.1	NT	GALACTOSE TRANSPORTER (GALACTOSE PERMEASE)
5517	18107	30361	0.57	1.1E+00	P13181	SWISSPROT	GALACTOSE TRANSPORTER (GALACTOSE PERMEASE)
5590	18149	30511	1.37	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5881	18480	31134	14.95	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
6900	18478	31159	1.4	1.1E+00	AI138582.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:1736260 3'
						NT	q885c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6400	18957	31691	1.07	1.1E+00	11418739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6598	18149	31898	0.72	1.1E+00	AF197861.1	NT	Macrogorgia pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6745	19289	32050	0.8	1.1E+00	RO6037.1	EST_HUMAN	ye89g03.r1 Soares fetal liver spleen 1NFLS.Homo sapiens cDNA clone IMAGE:124924 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptr
7090	19624	32420	0.58	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7242	19853	32873	0.51	1.1E+00	AF287747.1	NT	Mus musculus p47-phox gene, complete cds
7706	20151		0.69	1.1E+00	AF101091.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7754	20198	33060	0.81	1.1E+00	X55981.1	NT	Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
7961	20397	33266	0.48	1.1E+00	BF983714.1	EST_HUMAN	602136978F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301322 5'
7993	20427	33293	1.85	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7993	20427	33294	1.85	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
8017	20449	33320	6.7	1.1E+00	AL161888.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8098	24844	33404	0.84	1.1E+00	11987960	NT	Mus musculus silent mating type Information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8724	21159	34065	3.29	1.1E+00	BF683998.1	EST_HUMAN	602082592F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
9164	21598	34505	0.85	1.1E+00	AB003088.1	NT	Acetabularia calliculus mitochondrial COXI-like gene
9225	21657	34566	0.85	1.1E+00	S80750.1	NT	VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
9820	22223		0.93	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9917	22319	35285	1.54	1.1E+00	AB20151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
9994	22396	35348	5.33	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10032	22434	35380	22.47	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10376	22776	35744	1.13	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10443	22894	35870	1.75	1.1E+00	11067364	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
10493	22943		4.44	1.1E+00	AF068942.1	NT	Klebsiellidium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
10869	23302	36296	5.97	1.1E+00	L16877.1	NT	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
10884	16085		4.44	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
10887	23319	36317	4.26	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
10937	23319	36318	4.26	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11113	23596	36508	6.27	1.1E+00	AB090899.1	EST_HUMAN	wf76e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11869	24112		3.1	1.1E+00	P07863	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
11973	24168	36978	2.48	1.1E+00	AF216696.1	NT	Teaena sodium immunoglobulin protein Ts78 mRNA, partial cds
12110	24765		1.88	1.1E+00	AF234169.1	NT	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (Dipl) mRNA, complete cds
102	12719		1.57	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
117	12729	25142	1.95	1.0E+00	D98425.1	NT	Gavia cobaya mRNA for serine/threonine kinase, complete cds

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435	13009		2.87	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
593	13163	25566	1.66	1.0E+00	AJ251660.1	NT	Girardia ligurina mRNA for homeodomain transcription factor (so gene)
598	13258	25676	7.84	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
698	13260		1.09	1.0E+00	AF125984.1	NT	Aedes aegypti much-like protein MUC1 mRNA, complete cds
1418	15309		1.2	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
2628	15123	27636	7.19	1.0E+00	AF131205.1	NT	Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Snm), neuronal apoptosis inhibitory protein-rs6 (Naip-rs6), and neuronal apoptosis inhibitory protein-rs3 (Naip-rs3) genes, complete cds
2830	15386	27798	4.35	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2830	15386	27799	4.35	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2920	15475		1.16	1.0E+00	O14228	SWISSPROT	HYPOTHETICAL 679 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3155	15708	28129	1.22	1.0E+00	AA628453.1	EST_HUMAN	af2608.st Scars_total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP-C42D8.3 OE4204; contains element MER22 MER22 repetitive element;
3350	15886		0.7	1.0E+00	AF222761.1	NT	Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6
3593	12719		0.87	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3680	16220	28628	1.52	1.0E+00	AJ23816.1	NT	Agaricus bisporus mRNA for tyrosinase
4084	16815	29003	0.87	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4862	17374	29752	1.19	1.0E+00	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5395	17892	30249	1.91	1.0E+00	AF162436.1	NT	Raja erinacea peripherin/rds mRNA, complete cds
5405	17901		1.78	1.0E+00	AJ245481.2	NT	Human immunodeficiency virus type 1 proviral complete genome, isolate 95ML84
5533	18123	30478	2.9	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
6138	18705	31401	5.9	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6138	18705	31402	5.9	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6255	18819	31534	1.62	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6426	18982	31715	4.65	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6433	18988	31720	1.29	1.0E+00	AW452782.1	EST_HUMAN	UI-H-B13-ax-d-09-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6838	19379	32155	2.05	1.0E+00	U75602.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6892	19432	32208	0.89	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6902	19529		1.11	1.0E+00	P46506	SWISSPROT	SRB-11 PROTEIN

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7022	19558	32344	0.8	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
7022	10558	32345	0.8	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
7161	19874	32697	1.07	1.0E+00	Y11204.1	NT	V. carteri gene encoding valoxopsh
7253	18027	30410	0.6	1.0E+00	U63721.1	NT	Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds
7578	20028	32873	1.07	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt] B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE)
7978	20414		9.25	1.0E+00	P20273	SWISSPROT	(BL-CAM)
8256	20873	33563	1.37	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
8274	20891	33583	7.32	1.0E+00	AA775191.1	EST_HUMAN	ac70b08.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:888781 3'
8503	20915		0.84	1.0E+00	BF679213.1	EST_HUMAN	602153792F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'
8603	21038	33942	1.82	1.0E+00	BE868287.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3948005 5'
8603	21038	33943	1.82	1.0E+00	BE868287.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3948005 5'
8731	18010		1.54	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase II, complete cds
8890	21324	34235	2.62	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
8890	21324	34238	2.62	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
8985	21418		0.88	1.0E+00	P51764	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
9027	24651		1.95	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0228-181089-011-e06 HT0229 Homo sapiens cDNA
9055	21487	34399	1.05	1.0E+00	U42720.2	NT	Simian Immunodeficiency Virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
9153	21585	34493	1.73	1.0E+00	M38427.1	NT	Human Immunodeficiency virus type 1 (HIV-1), isolate SF33,
9528	21943	34865	2.04	1.0E+00	BE907692.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9680	22092	35021	1.82	1.0E+00	6753423	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9680	22092	35022	1.82	1.0E+00	6753423	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9773	22176	35109	2.19	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKCC Homo sapiens cDNA clone GKCCYA11 5'
9778	22178	35113	1.41	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
9778	22179	35114	1.41	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
10260	22661	35623	3.98	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW C04 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10361	22761	35728	19.76	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10361	22761	35729	19.76	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10382	22782	35750	1.29	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11480	18123	30478	1.66	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
11752	24034		2.9	1.0E+00	P16308	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12098	24247		2.5	1.0E+00	AW976184.1	EST_HUMAN	EST388283 MAGE resequences, MAGN Homo sapiens cDNA
1589	14121	26588	1.16	9.8E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
1589	14121	26589	1.16	9.8E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
3599	18140	31162	1.28	9.8E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5902	18480	31162	8.99	9.8E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
6157	18726	31428	0.94	9.8E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1280.5 IN CHROMOSOME II
8922	21937		1.9	9.8E-01	Q65667.1	NT	Lycopodium obscurum putative M1 copy 1 nematode-resistance gene
9735	22062		2.63	9.8E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10500	22950	35931	2.13	9.8E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
541	13113	25522	1.63	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
3804	16341	28742	2.22	9.8E-01	Q67551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEASE IV)
3807	16344	28745	0.61	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838481 3'
3807	16344	28746	0.61	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838481 3'
7644	20091	32943	4.46	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7644	20091	32944	4.46	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
8176	20598	33483	1.11	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3860049 5'
8176	20598	33484	1.11	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3860049 5'
9149	21581	34497	0.89	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
11280	23645		1.83	9.8E-01	AE002110.1	NT	Ureaplasma urealyticum section 11 of 59 of the complete genome
11979	24173		1.51	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
7600	20049	32899	2.27	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
9005	21438	34348	2.13	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
9008	21441	34361	1.61	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
10945	23376		4.31	9.7E-01	BF811209.1	EST_HUMAN	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12603	24576		1.55	9.7E-01	AL114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4466	16086	29369	0.63	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4468	16986	29370	0.63	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4489	17008	29393	1.58	9.6E-01	AF197925.1	EST_HUMAN	PM2-UM0063-240300-006-f12 UM0063 Homo sapiens cDNA
6032	18606	31294	4.12	9.6E-01	AF197925.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6032	18606	31294	4.12	9.6E-01	AF197925.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
7127	18606	32455	0.51	9.6E-01	AF197925.1	NT	Arabidopsis thaliana DNA chromosome 4, ESSA FCA contig fragment No. 6
7828	20269	33130	0.51	9.6E-01	AF197925.1	NT	Helix lucorum presenilin (PS) mRNA, complete cds
8926	21360	36889	1.19	9.6E-01	AF197925.1	NT	P. falciparum complete gene map of plasmodium-like DNA (IR-A)
11272	23638	36889	2.98	9.6E-01	AF197925.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11272	23638	36889	2.98	9.6E-01	AF197925.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11645	23968		2.19	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12322	24851	30569	1.76	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
3784	16321	28720	1.96	9.5E-01	BE002340.1	EST_HUMAN	601676639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3784	16321	28721	1.98	9.6E-01	BE002340.1	EST_HUMAN	601676639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
9414	21848	34760	1.32	9.5E-01	AF165990.1	EST_HUMAN	RC1-CT0295-241199-011-502 CT0295 Homo sapiens cDNA
11012	23439	36457	2.17	9.6E-01	BF21877.1	NT	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
3157	15710		3.44	9.4E-01	AF165990.1	NT	Bartonella claridigeae RNA polymerase beta subunit (rpoB) gene, partial cds
3176	15729		2.03	9.4E-01	AF080593.1	EST_HUMAN	Pimpla brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
11922	24141		1.63	9.4E-01	BE781251.1	EST_HUMAN	601468703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3689929 5'
12321	24759		1.27	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
2669	15067	27583	2.7	9.3E-01	BE071172.1	EST_HUMAN	RC6-BT0503-271199-011-501 BT0503 Homo sapiens cDNA
4048	16580	28968	0.81	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4048	16580	28968	0.81	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5859	18438	31113	1.28	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5947	18524	31207	4.11	9.3E-01	L36189.1	NT	Spodoptera frugiperda methyltetrahydrofolate dehydrogenase mRNA, complete cds
7798	20240		0.7	9.3E-01	AF270948.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8683	21118	34020	2.23	9.3E-01	AA847040.1	EST_HUMAN	oe09b03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
9224	21656		0.87	9.3E-01	AF061881.1	NT	Xenopus laevis COCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
12442	24472	30874	1.25	9.3E-01	11440298	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (ITPR2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12454	24477		1.97	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3198	15750	28171	4.32	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918184 3'
4936	17447		0.99	9.2E-01	BF129973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5320	17820		0.82	9.2E-01	4557702	NT	Human keratin keratin 2A (epidermal ichthyosis bullosa of Siemens) (KRT2A) mRNA
5992	18568		2.84	9.2E-01	7108410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
5289	18851	31572	4.91	9.2E-01	BF037588.1	EST_HUMAN	601481163F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3864661 5'
9998	19532	32315	0.55	9.2E-01	M64703.1	NT	N.cressa valy-IRNA synthetase (cyl-20/un-3) gene
9804	22207	35146	0.97	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
10220	22621	35598	3.68	9.2E-01	11430963	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
10313	22713	36678	1.71	9.2E-01	BF593251.1	EST_HUMAN	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
11444	23804	36882	2.05	9.2E-01	BF132402.1	EST_HUMAN	7058606X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NIUSM_TRYBB
2492	14993	27508	3.92	9.1E-01	AF062919.1	NT	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5:
3162	15715	28134	1.12	9.1E-01	T26418.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
3162	15715	28135	1.12	9.1E-01	T26418.1	EST_HUMAN	Pseudomonas fluorescens DNA polymerase III (dnaE) gene, complete cds
4467	16987	30042	1.07	9.1E-01	D17428.1	NT	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
5178	17682	30042	1.96	9.1E-01	4885228	NT	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6481	18038	31776	1.51	9.1E-01	L36033.1	NT	Corynebacterium glutamicum secA gene for SecA protein, complete cds
6856	19398	32172	3.85	9.1E-01	Q61704	SWISSPROT	Homo sapiens FAT tumor suppressor (Drosophila) homolog (FAT) mRNA
8092	20519	33398	18.93	9.1E-01	AA808623.1	EST_HUMAN	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
8289	20705	33597	1.84	9.1E-01	U72895.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
8478	20891		0.46	9.1E-01	AB025540.1	NT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
12017	24844		12.97	9.1E-01	AF050113.1	NT	cb71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'
3164	15717	28138	0.63	9.0E-01	AL161515.2	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
3331	16878	28308	0.59	9.0E-01	AF099810.1	NT	Epiplatys burgeri mRNA for EphA2, partial cds
4401	16923	33177	1.78	9.0E-01	L42547.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
7871	20310		0.86	9.0E-01	D38621.1	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
7903	20342		1.37	9.0E-01	D38621.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
							Homo sapiens neuroligin III-alpha gene, partial cds
							Homo sapiens neuroligin III-alpha gene, partial cds
							Danio rerio LIM class homeodomain protein (lim6) mRNA, complete cds
							Xenopus laevis gene for aldolase, complete cds
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1
							(PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
5987	18543	31227	2.8	8.9E-01	AF026198.1	NT	Rabbit MHC fragment RL4-DF DNA
6570	19121		1.2	8.9E-01	X60986.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6808	24815	32120	0.6	8.9E-01	BF217839.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085216 5'
6809	24816	32121	0.6	8.9E-01	BF217839.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085216 5'
7648	20092		0.59	8.9E-01	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruoylserahydropterin synthase, complete cds
8951	21384	34298	1.59	8.9E-01	AF259697.1	NT	Oithona nana cytochrome-c oxidase subunit I (cox) gene, partial cds; mitochondrial gene for mitochondrial product
11484	23842	36910	2.72	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
11850	24088		3.38	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 84 of the complete genome
4578	17094	29482	3.18	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5629	18216	30618	0.87	8.9E-01	AF510817.1	NT	Pseudorabies virus Eα glycoprotein M gene, complete cds
8040	20472	33348	0.56	8.9E-01	M81182.1	NT	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10864	23287	36291	2.11	8.8E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
11882	24939		2.13	8.8E-01	D90911.1	NT	Synochocystis sp. PCC68803 complete genome, 13/27, 1576583-1719843
482	13056	25473	1.41	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2301	14808	27326	1.59	8.7E-01	5801893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2828	15394	27798	5.69	8.7E-01	AA505863.1	EST_HUMAN	nm00611.s1 NCL_CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
5109	17617		3.27	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put>
9858	22261	35199	1.89	8.7E-01	AE004993.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
10242	22643	35607	0.95	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309808 3'
10242	22643	35608	0.95	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309808 3'
10612	23055	36042	7.31	8.7E-01	BF563970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
11458	23815	36878	3.46	8.7E-01	BF107694.1	EST_HUMAN	601823884R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11458	23815	36877	3.46	8.7E-01	BF107694.1	EST_HUMAN	601823884R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12070	24725		2.28	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3'
492	13065		2.01	8.6E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
881	13438	25885	5.61	8.6E-01	W69089.1	EST_HUMAN	zd44e03.r1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:343518 5'
3616	18156	28595	0.92	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3805	16342	28743	1.38	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
6189	18755	31457	8.11	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6189	18755	31458	8.11	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6712	24613	32014	0.63	8.6E-01	S78772.1	NT	polyprotein [Coxsackie B4 virus CB4, host-mbo, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
7081	19816	32409	1.8	8.6E-01	AF143732.1	NT	Gru. canadensis recombination activating protein 1 (RAG-1) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7081	19615	32410	1.8	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
8034	20466		0.71	8.6E-01	AE000601.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
8592	21017		1.93	8.6E-01	AF001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
12269	24672		1.21	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2339	14844		1.05	8.5E-01	AJ011624.1	NT	Arabidopsis thaliana (ecotype Columbia) sp12 gene, exons 1-5
4528	17046	28427	0.7	8.5E-01	AJ701029.1	EST_HUMAN	we09h02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340827 3'
7102	19635	32429	1.07	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
8032	20464	33338	2.69	8.5E-01	BE542612.1	EST_HUMAN	601087107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8945	21378	34290	1.15	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8845	21378	34291	1.15	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
12002	24846		2.78	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12008	24188		2.4	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4488	17007	28392	1.05	8.4E-01	AF158600.2	NT	Streptococcus thermophilus bacteriophage Sfi11, complete genome
4804	17318	28698	0.6	8.4E-01	AF083976.2	NT	Fowl adenovirus 8, complete genome
5754	24592	30789	2.97	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5754	24592	30790	2.97	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
8409	20823	33720	0.56	8.4E-01	AF051142.1	NT	Manesra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
10002	22404		3.65	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
762	13322	28751	3.58	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3056	15610	28019	3.16	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3818	16355	28765	0.93	8.3E-01	AB010878.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4025	16556	28954	3.1	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5406	17902	30256	2.34	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5520	18110	30354	2.39	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9810	22213		4.32	8.3E-01	AJ761952.1	EST_HUMAN	nm01112.5 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1078495 5' similar to contains THR.L1 THR repetitive element:
10124	22525	35492	1.48	8.3E-01	AF098070.1	NT	Drosophila melanogaster List1 homolog mRNA, complete cds
10191	22592	35558	4.17	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10464	22914	35893	3.29	8.3E-01	AE000803.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10479	22929		1.88	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11072	23497	36525	2.71	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
1979	14485	27004	3.57	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds

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2014	14530		1.28	8.2E-01	AF145589.1	NT	Mus musculus trophoblast (Tm) gene, complete cds
2621	15116		1.21	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0218-161199-031-C08 CT0219 Homo sapiens cDNA
3911	16446	28853	0.6	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4147	16875	29062	0.69	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
4147	16875	29063	0.69	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
5255	17756	30125	1.1	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
7007	19543	32327	0.5	8.2E-01	X95283.1	NT	G. gallus mRNA for C-Serrate-1 protein
7007	19543	32328	0.6	8.2E-01	X95283.1	NT	G. gallus mRNA for C-Serrate-1 protein
7158	19871	32694	0.95	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SCIII25 protein
7304	19808	32620	3.19	8.2E-01	AW379433.1	EST_HUMAN	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7723	24635	33026	4.82	8.2E-01	Z12126.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
10083	22484	35441	1.62	8.2E-01	AF052659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
10283	22694	35659	3.39	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10283	22694	35660	3.39	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11450	23809	36868	2.9	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11457	23816	36878	5.33	8.2E-01	H87398.1	EST_HUMAN	yw14d02.r1 Scarsa_placenta_8to9weeks_2NbhP8c9w Homo sapiens cDNA clone IMAGE:262165 5'
12028	24200	30953	1.88	8.2E-01	AJ001261.1	NT	similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
2717	15207		1.32	8.1E-01	AF191839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3435	15979	28393	3.36	8.1E-01	AF055096.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3435	15979	28394	3.36	8.1E-01	AF055096.1	NT	Homo sapiens MHC class I region
4648	17164	29543	7.73	8.1E-01	4506290	NT	Homo sapiens MHC class I region
4897	17507		0.79	8.1E-01	AF202634.1	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2) mRNA
5978	18554	31239	0.66	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR)
6843	19191	31942	0.89	8.1E-01	U16790.1	NT	(MELANOCORTIN-1 RECEPTOR) (MC1-R)
6883	19520	32301	2.36	8.1E-01	Q13481	SWISSPROT	Mus musculus putative collagen alpha-2 (X) chain (COL11A2) gene, partial cds
6883	19520	32302	2.36	8.1E-01	Q13481	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7784	20236	33096	0.49	8.1E-01	AB007877.1	NT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
8018	20450	33321	0.49	8.1E-01	O47477	SWISSPROT	Homo sapiens KIAA0417 mRNA, complete cds
							CYTOSCHROME B
8570	21005	33904	1.05	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pico) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative sorine-enriched protein (gprs) gene, partial cd>

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8570	21005	33905	1.05	8.1E-01	AF022743.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pico) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
9191	21623	34533	1.33	8.1E-01	AW242847.1	EST_HUMAN	Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, contains MER22.b1 PTR5 repetitive element
11237	23605	36849	3.83	8.1E-01	BE938568.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11237	23605	36850	3.83	8.1E-01	BE938568.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11724	24016	31010	1.78	8.1E-01	AE001711.1	NT	Thermoboga maritima section 23 of 136 of the complete genome
181	12784		3.51	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pta gene for phosphate acetyltransferase allele 15
302	12888	25317	8.78	8.0E-01	AJ132772.1	NT	Bos taurus tub and rlf genes
1969	14487		1.19	8.0E-01	BF53062.1	EST_HUMAN	602072473F1 NCL CGAP Bm87 Homo sapiens cDNA clone IMAGE:4215091 5'
3039	15594	28006	1.4	8.0E-01	AF127897.1	NT	Salimiri bolivensis olfactory receptor (SBO27) gene, partial cds
3277	15826	28244	1.32	8.0E-01	AF127897.1	NT	Mus musculus gene for olfactory glycoprotein, complete cds
4569	17089	29473	5.62	8.0E-01	X83739.2	NT	Mus musculus gene for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5077	17587	29855	1.02	8.0E-01	7657362	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) mRNA
8627	21062		2.56	8.0E-01	AW901489.1	EST_HUMAN	Mus musculus myosin IXb (Myo9b) mRNA
8015	21448	34358	1.18	8.0E-01	Y11095.1	NT	RCO-NN1012-270300-021-h08 NN1012 Homo sapiens cDNA
10735	23173	36158	1.97	8.0E-01	Q92783	SWISSPROT	Rice stripe virus RNA 3
471	13045	25468	0.91	7.9E-01	D11476.1	NT	CREB-BINDING PROTEIN
735	13286		3.14	7.9E-01	AE002130.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
1621	14152		7.03	7.9E-01	AB040885.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1657	14188		0.96	7.9E-01	U32739.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
2168	14678	27203	5.09	7.9E-01	AB004816.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
2187	14679	27204	1.56	7.9E-01	AF130459.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
3496	16039	28480	2.84	7.9E-01	AF228684.1	NT	Oryctolagus cuniculus mRNA for mitogen-activated protein kinase 28, complete cds
4319	16842		0.87	7.9E-01	BE263612.1	EST_HUMAN	Danio rerio Tnp4-associated protein Tnp1A (tp1A) mRNA, complete cds
4653	17169	29550	1.08	7.9E-01	6753745	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4653	17169	29551	1.08	7.9E-01	6753745	NT	6071192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
5242	17743	30164	0.63	7.9E-01	Z47210.1	NT	Mus musculus embigin (Emb), mRNA
5269	17789	30165	8.59	7.9E-01	Z47210.1	NT	Mus musculus embigin (Emb), mRNA
5269	17789	30165	8.59	7.9E-01	AF139718.1	NT	Mus musculus enabled homolog (Drosophila) (Enah), mRNA
5342	17841		0.61	7.9E-01	D38145.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
6675	18223	31971	0.94	7.9E-01	D38145.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8710	21145	34048	2.73	7.9E-01	X90998.1	NT	P. salivum GR gene
9728	22150	35081	4.68	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3MB (vspG3MB) mRNA, partial cds
10076	22477	35435	5.07	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10108	22509	35472	1.05	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKODRE12 3'
10383	22783	35751	0.93	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-thiamine reductase, complete cds
10787	23225		2.7	7.9E-01	766247.1	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
899	13453		1.94	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2176	14688	27210	2.11	7.8E-01	AW989587.1	EST_HUMAN	EST1371637 MAGE resequences, MAGF Homo sapiens cDNA
4751	17265	29846	1.01	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc6H1 mRNA, complete cds
6375	18933	31671	2.31	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
6536	18088	31830	0.98	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6807	19348	32122	0.82	7.8E-01	AL445066.1	NT	BETA-2 (HYBRIDOMA GROWTH FACTOR)
8245	20682	33552	0.47	7.8E-01	Q09908	SWISSPROT	Thermoplasma acidophilum complete genome, segment 4/5
8996	21429	34338	1.63	7.8E-01	BF108927.1	EST_HUMAN	HYPOTHETICAL 60.7 KD PROTEIN C30D11.08C IN CHROMOSOME 1
9500	21931	34855	1.65	7.8E-01	Y10159.1	NT	7164d06.x1 Soares NSF F8 9W OT PA P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
10133	22534		1.46	7.8E-01	Q25452	SWISSPROT	7164d06.x1 Soares NSF F8 9W OT PA P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
11996	24622		2.11	7.8E-01	L29260.1	NT	D.discoideum racGAP gene
148	12753	25171	6.45	7.7E-01	AF184345.1	NT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
748	13308						MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
2684	15157	27669	1.81	7.7E-01	AF050157.1	NT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
3330	15877		0.81	7.7E-01	8393408	NT	Arabidopsis thaliana 1-aminocyclopropane carboxylate synthase (ACS5) gene, complete cds
3594	16135	28548	4.25	7.7E-01	AF18085.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
4420	16941	29332	3.36	7.7E-01	AF199488.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds;
4420	16941	29333	3.36	7.7E-01	AF199488.1	NT	butyrophilin-like (NCG), butyrophilin-II
5825	18405	31070	1.36	7.7E-01	P16553	SWISSPROT	CITRATE SYNTHASE
5825	18405	31071	1.36	7.7E-01	P16553	SWISSPROT	Homo sapiens UDP-N-acetyl-alpha-D-galactoseamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNAC-T7), mRNA
6254	18818	31533	0.91	7.7E-01	R08600.1	EST_HUMAN	Homo sapiens PRO1975 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11773	12753	25171	1.21	7.7E-01	AF184345.1	NT	Lycopodium hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
11879	24118		6.73	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
6407	18984	31699	4.56	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6407	18984	31700	4.56	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6888	19408	32182	0.62	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
7249	18023	30406	0.91	7.6E-01	AI253399.1	EST_HUMAN	ec14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7249	18023	30439	0.91	7.6E-01	AI253399.1	EST_HUMAN	ec14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7482	18686	32483	0.88	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-tetrotxin receptor mRNA, complete cds
8881	21116	34019	1.49	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; pPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and HsAR (HsAR) gene, complete cds
8721	21156	34062	2.58	7.6E-01	6857752	NT	Mus musculus advinin (Advin-pending), mRNA
8721	21158	34063	2.58	7.6E-01	6857762	NT	Mus musculus advinin (Advin-pending), mRNA
9318	21750	34659	1.49	7.6E-01	6753577	NT	Mus musculus cyclochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9536	21951	34874	3.73	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9536	21951	34875	3.73	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11115	23568	36610	1.9	7.6E-01	X86347.1	NT	H.aspersa mRNA for neurofilament NF70
11115	23568	36611	1.9	7.6E-01	X86347.1	NT	H.aspersa mRNA for neurofilament NF70
11433	23794		2.04	7.6E-01	AL161692.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11623	23951		4.09	7.6E-01	AB020702.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
531	13103		1.55	7.5E-01	AL163301.2	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
601	13170	28574	1.08	7.5E-01	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C101
4717	17253	33335	1.13	7.5E-01	U48498.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
8028	20460	33336	0.83	7.5E-01	AF052730.1	NT	Human skeletal muscle tyrosine kinase receptor gene (RYR1), exon 92
10980	23419	36436	5.59	7.5E-01	AB047819.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
11948	24152		5.71	7.5E-01	AF163151.2	NT	Homo sapiens GCM1 gene for chorion-specific transcription factor GCM1, complete cds
12462	24482	30879	1.73	7.5E-01	D90907.1	NT	Homo sapiens dentin sialoprotein precursor (DSPP) gene, complete cds
12526	24523	30859	1.4	7.5E-01	AE000823.1	NT	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885
							Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 28 of 148) of the complete genome

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1157	13700	26139	1.42	7.4E-01	AI598146.1	EST_HUMAN	int14b09.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
3725	16265	28669	0.71	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
3912	16447	28854	0.65	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-e (rsR-e) and Calcutta-rsR-b (rsR-b) genes, complete cds
4331	16853	29239	7.05	7.4E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C046
8525	20960	33861	1.14	7.4E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8525	20960	33862	1.14	7.4E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8525	20960	33862	1.14	7.4E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
9092	21524	34431	1.07	7.4E-01	BF346286.1	EST_HUMAN	602018466F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154340 5'
9406	21838	34752	7.98	7.4E-01	BE747503.1	EST_HUMAN	601573028F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9443	21874	34792	1.36	7.4E-01	AA187986.1	EST_HUMAN	601573028F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
10305	22705	35670	0.84	7.4E-01	11424933	NT	2p87h01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO_MOUSE P42832 T-COMPLEX PROTEIN 1, THETA SUBUNIT;
11549	23908	36991	1.64	7.4E-01	AL112699.1	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
11590	23927		4.61	7.4E-01	6753217	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
11708	24008		1.95	7.4E-01	AI472641.1	EST_HUMAN	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
2955	16510	27930	0.59	7.3E-01	P09710	SWISSPROT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
3988	16522		0.78	7.3E-01	AF000062.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4653	17175	29555	0.95	7.3E-01	AE001166.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4760	17284	29845	2.12	7.3E-01	AF228421.1	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
5448	17943	30293	1.5	7.3E-01	8051618	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
5448	17943	30294	1.5	7.3E-01	8051619	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
6964	19501	32278	5.96	7.3E-01	L35772.1	NT	HYPOTHETICAL PROTEIN HKLF1 (IRL-1) (TRL-1)
6964	19501	32279	5.96	7.3E-01	L35772.1	NT	HYPOTHETICAL PROTEIN HKLF1 (IRL-1) (TRL-1)
7633	24632	32818	0.84	7.3E-01	AJ011418.1	NT	Aeropyrum pernix genomic DNA, section 5/7
7944	20381	33248	0.52	7.3E-01	Z14133.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
8060	20491	33367	7.99	7.3E-01	M26511.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
8060	20491	33368	7.99	7.3E-01	M26511.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
8418	20832	33729	0.54	7.3E-01	U34631.1	EST_HUMAN	Homo sapiens HT017 mRNA, complete cds
11181	23597	36639	3.19	7.3E-01	AA678019.1	EST_HUMAN	Homo sapiens LIM domain kinase 2 (LMK2), transcript variant 2a, mRNA
11181	23597	36640	3.19	7.3E-01	AA678019.1	EST_HUMAN	Homo sapiens LIM domain kinase 2 (LMK2), transcript variant 2a, mRNA
854	13410	26922	2.92	7.2E-01	L29281.1	NT	Homo sapiens LIM domain kinase 2 (LMK2), transcript variant 2a, mRNA
1806	14425	26922	3.16	7.2E-01	X76140.1	NT	Mus musculus antigen (CD72) gene
3027	16582	27992	1.4	7.2E-01	AF198100.1	NT	Mus musculus antigen (CD72) gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3430	15974	28387	3.01	7.2E-01	AF066606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-8) gene, vsp417-6(A-I) allele, complete cds
3608	16148	28556	1.08	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
3879	16414	28818	1.06	7.2E-01	BF338350.1	EST_HUMAN	602035589f1 NCI CGAP Br64 Homo sapiens cDNA clone IMAGE:4183222 5'
4077	16608		0.62	7.2E-01	AF108083.1	NT	Homo sapiens IA-2 gene, intron 18
4124	16663	28038	0.59	7.2E-01	U02568.1	NT	Diclyocaulus viviparus nematode polyprotein antigen precursor (DvA) mRNA, complete cds
4821	17333	29712	2.81	7.2E-01	D80314.1	NT	L. mesenteroides gene for sucrose phosphorylase [EC 2.4.1.7]
5276	17777	30143	8.97	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
5276	17777	30144	8.97	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
5336	17836	30183	2.23	7.2E-01	AF158600.2	NT	Streptococcus thermophilus bacteriophage St11, complete genome
7659	20105	32957	0.89	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8129	20552		0.43	7.2E-01	8625876	NT	Human herpesvirus 3, complete genome
8987	21400	34312	1.34	7.2E-01	AF236081.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
10268	22869	35632	2.16	7.2E-01	BF670081.1	EST_HUMAN	602118331F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
10522	22869	35649	2.93	7.2E-01	U82823.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12160	24286		3.05	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
712	13273	25693	14.86	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RYR1), complete cds
3023	15578	27989	16.27	7.1E-01	AJ270777.1	NT	Homo sapiens partial TGF-4 gene for T-cell transcription factor-4, exons 15-16
4223	16748	28138	3.61	7.1E-01	7305360	NT	Mus musculus obogelin (Obog), mRNA
4223	16748	28139	3.61	7.1E-01	7305360	NT	Mus musculus obogelin (Obog), mRNA
6246	18810	31524	1.83	7.1E-01	BF681034.1	EST_HUMAN	602155439F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6246	18810	31525	1.83	7.1E-01	BF681034.1	EST_HUMAN	602155439F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
7360	19817	32651	7.41	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyl-tetrahydropterin synthase (pt) gene, complete cds
9163	21596	34503	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-309 BT0567 Homo sapiens cDNA
9163	21595	34504	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-309 BT0567 Homo sapiens cDNA
9934	22336	35285	1.54	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3698495 5'
10310	22710	35676	1.11	7.1E-01	M12961.1	NT	Human T-cell receptor gamma-gamma-chain J2 gene
11932	24743		1.78	7.1E-01	AA421492.1	EST_HUMAN	z008111.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1262	13799	26247	1.14	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1262	13789	26248	1.14	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
6173	17677		1.85	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5350	17849	30206	0.63	7.0E-01	AE003921.1	NT	Xylella fastidiosa, section 67 of 228 of the complete genome
6250	18814		0.94	7.0E-01	AB021318.1	NT	Xylella fastidiosa, section 67 of 228 of the complete genome
8914	21348		6.51	7.0E-01	AE000253.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
10900	23332	36334	1.8	7.0E-01	AV763842.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
10900	23332	36335	1.8	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
12534	24783	30686	1.72	7.0E-01	9830464	NT	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
994	13546	25989	14.67	6.9E-01	U69674.1	NT	Bacteriophage N15 virion, complete genome
994	13546	25990	14.67	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1342	13878	26331	2.03	6.9E-01	AA593530.1	EST_HUMAN	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
3178	15731	28150	1.73	6.9E-01	AE002271.2	NT	nr28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
6084	18636	31575	0.71	6.9E-01	AB035662.1	NT	Chlamydia muridarum, section 3 of 65 of the complete genome
8292	18854	31575	0.68	6.9E-01	Y18278.1	NT	Branchiostoma belcheri BbNA3 mRNA for notochord actin, complete cds
6703	19250	32001	1.51	6.9E-01	BE298188.1	EST_HUMAN	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
8375	20789	33688	0.47	6.9E-01	AF248663.1	NT	801177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
8617	21052	33957	3.11	6.9E-01	AL161573.2	NT	Strongylocentrotus purpuratus myosin V, complete cds
8617	21052	33958	3.11	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
11025	23452	36472	1.78	6.9E-01	D88013.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
11025	23452	36473	1.78	6.9E-01	D88013.1	NT	Homo sapiens DAN gene, complete cds
11384	23726	36786	1.97	6.9E-01	11559024	NT	Homo sapiens DAN gene, complete cds
11585	24736		3.07	6.9E-01	Q98958	SWISSPROT	Homo sapiens DAN gene, complete cds
981	13534	25977	1.3	6.8E-01	AF017784.1	NT	Homo sapiens hypothetical protein LOC63928 (LOC63928), mRNA
2613	15108		9.23	6.8E-01	D60917.1	NT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
2787	14150	26630	1.13	6.8E-01	AA854475.1	EST_HUMAN	HEAD PROTEIN 1 (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
4608	17125	29510	1.15	6.8E-01	J00762.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
4814	17425	29797	0.65	6.8E-01	4758521	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
9789	22192	35129	1.77	6.8E-01	AB037786.1	NT	aj78a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402286 3' similar to gb:X58411.maf1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
312	12807	25327	30.59	6.7E-01	AF213884.1	NT	Rat(hooded) prolactin gene: exon III and flanks Homo sapiens hevin (HEVIN) mRNA Homo sapiens mRNA for KIAA1345 protein, partial cds Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
353	12943	25357	32.74	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2059	14574	27090	1.14	6.7E-01	AA451884.1	EST_HUMAN	z12g12.s1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2074	15328	27108	2.34	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mel85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2950	15505	27925	4.42	6.7E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4483	17002	29388	0.84	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5771	18352	30811	0.83	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5771	18352	30812	0.83	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6262	18928	31540	0.83	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6652	19200	31850	1.38	6.7E-01	9635035	NT	Galid herpesvirus 2, complete genome
6652	19200	31851	1.38	6.7E-01	9635035	NT	Galid herpesvirus 2, complete genome
6978	19515	32286	0.48	6.7E-01	BE966241.2	EST_HUMAN	601680177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
6978	19515	32287	0.48	6.7E-01	BE966241.2	EST_HUMAN	601680177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
7779	20221	32297	4.72	6.7E-01	AE004508.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7807	20249	33109	1.18	6.7E-01	AE001488.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10147	22548	36153	0.94	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
10732	23170	36153	1.84	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010800-197-c03 HT0769 Homo sapiens cDNA
11210	22882	35838	2.95	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYL INOSITOL BIOSYNTHETIC PROTEIN GPI1
2649	15142	27653	1.01	6.6E-01	AF199339.1	NT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYL INOSITOL BIOSYNTHETIC PROTEIN GPI1
3465	16009	28430	1.16	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3657	16197	28604	3.89	6.6E-01	Y07669.1	NT	C.albicans random DNA marker, 282bp
4126	16655	31958	0.78	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6692	19210	31958	4.82	6.6E-01	6680577	NT	(HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7562	20012	32855	0.61	6.6E-01	AE004458.1	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7562	20012	32856	0.61	6.6E-01	AE004458.1	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7562	20012	32856	0.61	6.6E-01	AE004458.1	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
8223	20642	33532	4.02	6.6E-01	AF163278.2	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
9807	22210	30956	1.98	6.6E-01	AF10001.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
12043	24212	30956	1.45	6.6E-01	AF10001.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12214	24329	30921	1.41	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
642	13208	25613	1.48	6.5E-01	M76140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
642	13208	25614	1.48	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3410	15955	28368	5.52	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4050	16582	28971	1.33	6.5E-01	4504632	NT	Homo sapiens Interleukin 10 receptor, alpha (IL10RA) mRNA
4299	16824	29210	4.73	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4334	16856	29241	0.9	6.5E-01	AL161639.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39.
4635	17181	29532	1.33	6.5E-01	D00584.1	NT	Oryza sativa gene for prepro-glutelin, exons 1, 2, 3, 4, complete cds
5184	17698	30048	2.52	6.5E-01	U28021.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5700	24591	30709	2.08	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SW/SNF COMPLEX COMPONENT SNF5)
5988	18564	31250	0.57	6.5E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
7101	18634	32428	1.48	6.5E-01	D98348.1	NT	Chicken mRNA for 116-kDa melanosomal matrix protein, complete cds
8107	20533	33410	0.64	6.5E-01	X04769.1	NT	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
8202	20623	33510	0.78	6.5E-01	A1798882.1	EST_HUMAN	wc46a02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321642 3'
9621	22323	35628	0.87	6.5E-01	T78904.1	EST_HUMAN	yd21b04.s1 Soares fetal liver epigen 1NPLS Homo sapiens cDNA clone IMAGE:108847 3'
10264	22665	35628	1.32	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10432	22884	35861	4.65	6.5E-01	H87683.1	EST_HUMAN	yw17f06.r1 Soares placenta_8t60weeks_2Nblp8t60W Homo sapiens cDNA clone IMAGE:252516 5'
10477	22927	35907	2.24	6.5E-01	AA601287.1	EST_HUMAN	no18c07.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100748 3'
10572	23019		3.91	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11348	23712	36769	2	6.5E-01	AF014115.1	NT	Plasmidium berghal cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
11991	24182		2.78	6.5E-01	BE465050.1	EST_HUMAN	hw74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12255	24677		2.19	6.5E-01	Z74145.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL097c
265	12863	26281	12.3	6.4E-01	U48848.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL097c
3433	15977	28391	4.37	6.4E-01	U48854.2	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3897	16403	28807	1.53	6.4E-01	AB046827.1	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
4527	17045	29425	0.77	6.4E-01	Y12488.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4527	17045	29426	0.77	6.4E-01	Y12488.1	NT	M. musculus win gene
5317	17817	30180	1.4	6.4E-01	H85337.1	EST_HUMAN	M. musculus win gene
5398	17896	30252	2.97	6.4E-01	AE002551.2	NT	ys90e08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222088 5'
8079	21611	34420	1.74	6.4E-01	AE001247.1	NT	Neisseria meningitidis serogroup B strain MC58 section 193 of 208 of the complete genome
							Treponema pallidum section 63 of 87 of the complete genome

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10108	22507	35471	7.64	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10120	22521	35488	1.32	6.4E-01	BF670405.1	EST_HUMAN	602150288F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281128 5'
12116	24257		6.8	6.4E-01	AV769212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCC08 5'
451	13026	25451	5.63	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
553	13125	25534	3.44	6.3E-01	U32888.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2071	14588	27104	2.14	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2497	14998	27512	2.81	6.3E-01	U76331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2497	14998	27513	2.81	6.3E-01	U76331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2975	15530		0.79	6.3E-01	Y12726.1	NT	Lycopodium obscurum p66a gene, complete CDS
5282	17783	30149	4.16	6.3E-01	AE001257.1	NT	Treponema pallidum section 73 of 87 of the complete genome
6473	17968	31663	0.99	6.3E-01	AF176377.1	EST_HUMAN	Caenorhabditis briggsae CES-1 (ces-1) gene, complete cds; and CPN-1 (cpn-1) gene, partial cds
6370	18928	32272	0.96	6.3E-01	L27798.1	NT	PMO-BT0767-010500-002-e05 BT0767 Homo sapiens cDNA
6955	18492	32273	0.96	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6955	18492	32273	0.96	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
8014	21447		3.61	6.3E-01	BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
9634	22049	34980	3.26	6.3E-01	8627521	NT	Varicella virus, complete genome
9634	22049	34981	3.26	6.3E-01	8627521	NT	Varicella virus, complete genome
10322	22722	35690	1.5	6.3E-01	Z73003.1	NT	S.cerevisiae chromosome VII reading frame ORF YGR218w
10392	22792	35763	0.92	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10843	23277	36267	1.97	6.3E-01	AA87715.1	EST_HUMAN	m09h06.s1 NC1_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002816 002816
11096	23520	36557	4.05	6.3E-01	AI604180.1	EST_HUMAN	HLARK.1
11177	23593	36634	1.82	6.3E-01	P47003	SWISSPROT	CM-BT043-060289-046 BT043 Homo sapiens cDNA
11337	23701	36755	2.11	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11883	24613	30455	12.22	6.3E-01	9910293	NT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11784	24054		1.75	6.3E-01	AF105227.1	NT	Mus musculus keratin complex 2, gene 5g (Kf2-5g), mRNA
12007	24818		2.4	6.3E-01	X83528.1	NT	Mus musculus 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
6158	18726	31429	2.11	6.2E-01	Q10135	SWISSPROT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
7999	20433		2.87	6.2E-01	AF022253.1	NT	C.limicola pscD gene
8056	24843	33363	1.32	6.2E-01	AL021127.2	NT	HYPOTHETICAL 142.5 KD PROTEIN C3E2.02 IN CHROMOSOME 1
8852	21288	34197	5.7	6.2E-01	HT2255.1	EST_HUMAN	Mus musculus calcium-sensing receptor related protein 4 (CaSR-r4) mRNA, partial cds
9653	20944	33844	1.82	6.2E-01	BE562687.1	EST_HUMAN	Mus musculus calcitonin receptor-related protein 4 (CaSR-r4) mRNA, partial cds
9699	22111		2.81	6.2E-01	M24461.1	NT	Mus musculus chromosome X contig; putative Magea9 gene, Callitricin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
						EST_HUMAN	Y901608.s1 Soares fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:213542 3'
						EST_HUMAN	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
						NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds

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10098	22469	35461	7.21	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10396	22768	35769	6.08	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN)
10398	22769	35770	6.08	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN)
2292	14799		6.06	6.1E-01	6878076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5102	17611	28972	4.03	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds
5102	17611	28973	4.03	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds
5798	18379	31038	1.3	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CehlyoD (hly-1) alternatively spliced genes, complete cds
7273	19778	32686	4.19	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7273	19778	32687	4.19	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7443	19946	32780	0.7	6.1E-01	AW105653.1	EST_HUMAN	xd50h03.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gbX12871_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7544	19994	32834	0.63	6.1E-01	Q63769	SWISSPROT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8804	21238	34145	3.6	6.1E-01	AF033635.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9211	21843	34550	1.24	6.1E-01	11431066	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9211	21843	34551	1.24	6.1E-01	11431066	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9632	22047	34977	24	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9632	22047	34978	24	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9928	22328	35275	1.08	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 529 of the complete genome
10073	22474	35431	1.38	6.1E-01	AF118117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11453	23812	36871	1.97	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11453	23812	36872	1.97	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11780	24695	30777	1.92	6.1E-01	AB041350.1	NT	Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds
12472	24489		1.67	6.1E-01	X95287.1	NT	M.mazei orfA, orfB, and orfC of archaeal ABC-transporter system
512	13085	25499	1.34	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
578	13149		3.28	6.0E-01	5802599	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1394	13928	26386	2.83	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3822	16359	28759	0.89	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
5532	18122	30477	2.34	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5598	18281	30705	2.48	6.0E-01	AW139713.1	EST_HUMAN	UH-B11-aeb-e-10-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719619 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6890	19430	32205	2.21	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
7027	19583	32350	0.75	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-ROX)
7208	19917	32746	0.72	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7208	19917	32746	0.72	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7823	20264	33125	8.61	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8719	21154	34080	5.43	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8719	21154	34081	5.43	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8910	22312	35257	1.93	6.0E-01	AB008183.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10227	22628		1.78	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
11305	23070	36719	5.28	6.0E-01	A1420623.1	EST_HUMAN	HO0107.X1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2035621 3'
12083	24234	30981	1.68	6.0E-01	11421683	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3) mRNA
12197	24316		1.36	6.0E-01	AA706087.1	EST_HUMAN	386905.a1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12408	24747	30678	3.08	6.0E-01	9059303	NT	Mus musculus cGMP-Inhibited phosphodiesterase (Pde3a) mRNA
12436	24670		3.11	6.0E-01	BE167617.1	EST_HUMAN	RC1-HT0376-030500-015-c03 HT0376 Homo sapiens cDNA
1027	13678	26019	1.2	6.0E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
1434	13868	28422	1.41	5.9E-01	6680232	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl) mRNA
3232	15784	28201	5.39	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3232	15784	28202	5.39	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3821	16358	28758	0.66	5.8E-01	U74341.1	NT	Pterodroma neglecta cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
4237	16762		4.28	5.9E-01	AF162756.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
6810	19351	32126	1.47	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7720	20185	33022	1.17	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7876	20315		0.55	5.9E-01	X68801.1	NT	G.gallus gene for skeletal alpha-actinin, exon EF2
10189	22870	35536	1.21	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-6)
10741	23179	36163	3.08	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-R03 DT0041 Homo sapiens cDNA
10987	23396	36408	3.61	5.9E-01	AF084626.1	NT	Mus spectus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds
11231	23600	36843	1.7	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN
11231	23600	36844	1.7	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN
11723	24015	81009	1.43	5.8E-01	L42320.1	NT	Oryzopsis curvicaulis alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11976	24168		2.67	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
12207	24323		5.87	5.9E-01	P34028	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
2478	14979	27493	8.71	5.8E-01	7305230	NT	Mus musculus low density lipoprotein B (Ldlb), mRNA
3998	16532	28834	1.2	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076131 5'
4551	17068	29460	3.46	5.8E-01	AB006077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4851	17363		1.67	5.8E-01	AF110846.1	NT	Megascalia scalaris sex-lethal homolog (Megaxl) gene, partial cds, alternatively spliced products
5830	18217		1.02	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5793	18374	31032	0.89	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6488	19052	31782	1.5	5.8E-01	D78659.1	EST_HUMAN	HUM600E06B Human placenta polyA+ (Tfujwara) Homo sapiens cDNA clone GEN-500E06 5'
6840	19189	31939	2.64	5.8E-01	D50501.1	NT	Shigella sonnei DNA for 26 ORFs, complete cds
7203	19914		2.27	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8552	20987		2.41	5.8E-01	H41571.1	EST_HUMAN	yn91b03.at Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175767 3' similar to gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8768	21202	34103	3.07	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP88
8768	21202	34104	3.07	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP88
9271	21703	34614	12.36	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
9322	21754	34662	1.1	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
10772	23210	38182	3.87	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10813	23249		3.32	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 6'
10813	23249		3.32	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 6'
10919	23351		2.38	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 6'
3003	15558		0.71	5.7E-01	6755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3182	15735	28154	1.5	5.7E-01	Q9WTJ2	SWISSPROT	POTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3483	18029		2.72	5.7E-01	AB035603.1	NT	Populus eurameritana peacs-2 mRNA for 1-antihydroxypropane-1-carboxylate synthase, complete cds
3914	19449	28856	0.88	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S772-BJ1S1) mRNA, partial cds
5425	17920	30272	2.7	5.7E-01	L41887.1	NT	Drosophila extra sex combis gene, exon 1-4, complete cds
6888	19234	31984	5.14	5.7E-01	BF035413.1	EST_HUMAN	601454982F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
7083	19517	32412	0.7	5.7E-01	AA194201.1	EST_HUMAN	z38c08.r1 Soares NHMPu_S1 Homo sapiens cDNA clone IMAGE:685874 5'
7261	18035	30419	1.62	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8320	20735	33629	2.2	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8480	20883	33789	0.46	5.7E-01	AL161590.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 86
8918	21350		3.48	5.7E-01	AI055051.1	EST_HUMAN	HA0895 Human fetal liver cDNA library Homo sapiens cDNA
9895	22287	35238	1.1	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9895	22287	35238	1.1	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10416	22815	35789	1.11	5.7E-01	BF54082.1	EST_HUMAN	602087712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068610 5'
11677	23986		1.35	5.7E-01	BE715051.1	EST_HUMAN	MR3-HTD736-180700-003-e02 HT0736 Homo sapiens cDNA
12428	24463		1.24	5.7E-01	BE959722.2	EST_HUMAN	601654814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839763 3'
3341	15888	28308	1.2	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3341	15888	28310	1.2	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3882	16427	28833	0.87	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
8244	20681	33551	0.47	5.6E-01	L44513.1	EST_HUMAN	HUMEST4B9 Human thymus NSTH II Homo sapiens cDNA
9217	21649	34560	4.89	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 6'
9217	21649	34561	4.89	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9603	22063	35010	1.06	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11572	23917		2.72	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3816467 6'
11693	23999	36561	1.9	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:940874 similar to contains element PTR7 repetitive element:
12081	16427	28833	1.79	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12111	24255		2.45	5.6E-01	P06505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12565	24547		4.13	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
12610	24580		1.34	5.6E-01	AA663881.1	EST_HUMAN	ae74b04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969871 3'
1242	13780	26227	3.21	5.6E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2650	15143	27654	2.1	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2650	15143	27655	2.1	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2872	15427	27846	0.74	5.5E-01	5902085	NT	Homo sapiens superkiller viralidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3026	16581		1.5	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b51HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3183	15748	28167	2.95	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3690	16230	28639	1.34	5.5E-01	P48765	SWISSPROT	FOS-RELATED ANTIGEN-1
7705	20150	33007	0.6	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7705	20150	33008	0.6	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7744	20188		0.7	5.5E-01	AB015596.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
10280	22691	35655	0.89	5.5E-01	T05047.1	EST_HUMAN	EST02935 Fetal brain, Stratagene (cat#939206) Homo sapiens cDNA clone HFBCQ35

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10918	23350	36359	2.34	5.5E-01	BF128507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
149	12754	25172	7.64	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
149	12734	25173	7.64	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
602	13171	25575	0.96	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds; and unknown genes
602	13171	25576	0.96	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds; and unknown genes
1304	13839	26288	2.44	5.4E-01	AW89087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2027	14543		2.65	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome
2160	14873	27196	1.93	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
3925	16460	28868	0.59	5.4E-01	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5236	17738		6.71	5.4E-01	AW747972.1	EST_HUMAN	QV0-BT0041-061099-033-c02 BT0041 Homo sapiens cDNA
5413	17809		1.35	5.4E-01	X85973.1	NT	A. thaliana mRNA for phosphatidyl-specific phospholipase C
5926	18504	31187	0.78	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6505	19059	31802	1.02	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7454	19957	32791	0.8	5.4E-01	BE986592.2	EST_HUMAN	601660276RT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906080 3'
7802	20244	33102	0.82	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7802	20244	33103	0.82	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7804	20248	33108	1.7	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
10026	22428		2.01	5.4E-01	BF572536.1	EST_HUMAN	602076545FT NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243660 5'
10801	23294	36289	2.48	5.4E-01	P39858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11367	23728	36787	2.44	5.4E-01	Q60075	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11367	23728	36788	2.44	5.4E-01	Q60075	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11637	23982		2.82	5.4E-01	A1858398.1	EST_HUMAN	w37g04.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2427128 3' similar to gb:M13452 LAMIN A (HUMAN);
534	13106	25517	2.11	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
2741	15231	27743	6.05	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA

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2741	15231	27744	6.05	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3202	15754	29172	3.41	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LIS1CL) gene, complete cds
4228	16751		1.35	5.3E-01	U39687.1	NT	Myoplasma genitalium section 9 of 61 of the complete genome
5715	18298	30727	1.74	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5715	18298	30728	1.74	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5818	18398	31081	0.98	5.3E-01	AA193872.1	EST_HUMAN	zu42g09.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5818	18398	31082	0.98	5.3E-01	AA193872.1	EST_HUMAN	zu42g09.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5914	18492	31175	2.19	5.3E-01	BE845620.1	EST_HUMAN	7e73c12.x1 NCJ CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5914	18492	31176	2.19	5.3E-01	BE845620.1	EST_HUMAN	7e73c12.x1 NCJ CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
8509	20921	33817	0.52	5.3E-01	BF381837.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9281	21713		1.61	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for
11312	23676	36727	7.5	5.3E-01	BE566291.1	EST_HUMAN	601339897.F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
11564	24744		3.64	5.3E-01	AA916053.1	EST_HUMAN	qg30e05.s1 NCJ CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441378 3' similar to gb:J02811
12807	24781	30885	1.27	5.3E-01	AF278706.1	NT	APOLIPOPROTEIN D PRECURSOR (HUMAN);
839	13396	25834	12.8	5.2E-01	L20770.1	NT	Pseudocitronomas haloplanktis peckate lyase A (pslA) gene, complete cds
1194	13735	26178	9.19	5.2E-01	Q9WV30	SWISSPROT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1222	13762	26206	2.23	5.2E-01	AF224492.1	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1851	14373		2.69	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2058	14573	27069	1.86	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
2404	14908	27427	4.1	5.2E-01	AF198339.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
2404	14908	27428	4.1	5.2E-01	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2449	14950	27456	4.19	5.2E-01	U77717.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2449	14950	27467	4.19	5.2E-01	U77717.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3080	15634	28040	1.78	5.2E-01	U65942.1	NT	Bos taurus desmosome associated protein p19n mRNA, complete cds
3188	15748		0.8	5.2E-01	D73443.1	NT	Bos taurus desmosome associated protein p19n mRNA, complete cds
3382	15928		1.79	5.2E-01	AL116780.1	NT	Chlamydomonas reinhardtii lcd gene for isocitrate dehydrogenase, complete cds
3422	15966	28379	2.16	5.2E-01	AA984165.1	EST_HUMAN	Azobacter vinelandii lcd gene for isocitrate dehydrogenase, complete cds
3630	16170		0.88	5.2E-01	AF020269.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
							am77g05.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
							Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3832	18172	28582	0.61	5.2E-01	U82674.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cellitracin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
4647	17163	28542	0.59	5.2E-01	6752947	NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
5118	17625		1.05	5.2E-01	7106444	NT	Mus musculus vanilloid receptor-like protein 1 (Vrl1), mRNA
5308	17808		0.98	5.2E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5922	18500	31181	1.12	5.2E-01	AA284281.1	EST_HUMAN	z04409.17 Soares, senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:325169 3'
10058	22456	35406	1.28	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12630	24526		4.11	6.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
638	13200	25608	2.04	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
667	13232	25643	4.58	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt) 16S rRNA gene
667	13232	25644	4.58	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt) 16S rRNA gene
4091	18822	28011	5.21	5.1E-01	A1858495.1	EST_HUMAN	w93612.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2427263 3'
4203	16728	28116	3.42	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5198	17989		0.59	5.1E-01	BE081788.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6540	18092	31833	0.57	5.1E-01	BE541068.1	EST_HUMAN	601063608F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6600	19151		0.83	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAUJ07 5'
7328	19738	32542	1.25	5.1E-01	R80873.1	EST_HUMAN	y94409.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148872 3'
8823	22226	35182	5.08	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
8825	22228	35185	3.78	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp509-cleaved sublibrary Homo sapiens cDNA not directional
10155	22558	35524	1.09	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
11795	24662		5.8	5.1E-01	BF030207.1	EST_HUMAN	601558883F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828787 5'
12054	24220		2.5	5.1E-01	BF439982.1	EST_HUMAN	ncs51f10.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element
2051	14567	27081	0.85	5.0E-01	4885552	NT	TAR1 repetitive element
2051	14567	27082	0.85	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation Increased 2-like 9 (PMS2L9), mRNA
3747	18286	28680	0.7	5.0E-01	U55574.1	NT	Homo sapiens postmitotic segregation Increased 2-like 9 (PMS2L9), mRNA
3981	18416	28819	3.29	5.0E-01	AB033010.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 383p.138, partial cds
5849	18428	31099	0.47	5.0E-01	U30320.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
5849	18428	31100	0.47	5.0E-01	U30320.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
7008	19544		0.68	5.0E-01	BF576189.1	EST_HUMAN	Sparus aurata gonadotropin-releasing hormone (sbGnRH) precursor mRNA, complete cds
7104	19637	32432	0.41	5.0E-01	AF042848.1	NT	602132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271839 5'
8198	20519	33504	0.75	5.0E-01	AL161549.2	NT	Homo sapiens EMMPRIN gene, promoter and exon 1
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8198	20819	33505	0.76	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8463	20878		0.47	5.0E-01	Z71560.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL284c
9019	21452		1.94	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
9661	20952	33850	3.58	5.0E-01	BF317212.1	EST_HUMAN	60190387F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
9781	22184	35119	1.53	5.0E-01	P35573	SWISSPROT	GLYCOCEN DEBRANCHING ENZYME (GLYCOCEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYL-O-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9781	22184	35120	1.53	5.0E-01	P35573	SWISSPROT	GLYCOCEN DEBRANCHING ENZYME (GLYCOCEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYL-O-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10297	22898		1.3	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
11728	24020		2.87	5.0E-01	AF029216.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
12496	24503		2.65	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12509	24510		4.52	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN GUT11
812	13370	25807	1.88	4.9E-01	BF671462.1	EST_HUMAN	602078649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243660 5'
4720	17236		2.71	4.9E-01	AW988780.1	EST_HUMAN	EST380868 IMAGE resequences, MAG.J Homo sapiens cDNA
5662	18247	30847	1.32	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6341	18899	31630	2.83	4.9E-01	AF020831.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6341	18899	31631	2.83	4.9E-01	AF020831.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7837	20374	33241	1.61	4.9E-01	AB040051.1	NT	Oryza sativa subsp. Japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
8249	20868	33556	0.77	4.9E-01	Q10608	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
8249	20868	33556	0.77	4.9E-01	Q10608	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
6334	21768		1.99	4.9E-01	BF209791.1	EST_HUMAN	601874864F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:41025603 5'
9468	21897	34819	1.1	4.9E-01	AW339905.1	EST_HUMAN	hc80c02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR-O95714
9548	24989		2.42	4.9E-01	10946983	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10263	22854	36616	0.98	4.9E-01	AF053980.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
11817	23948		1.39	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
12489	24950		4.91	4.9E-01	AA613562.1	EST_HUMAN	mq22e11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
12497	24504	30854	1.25	4.9E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4355	16877		0.71	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5478	17973	30318	3.45	4.9E-01	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5769	18350	30809	9.57	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) genes required for meiotic recombination, complete cds
7048	18582	32377	0.61	4.8E-01	U02882.1	NT	Mus musculus slow skeletal muscle tropomyosin T (Tnni1) gene, complete cds
7058	18592		4.19	4.8E-01	AA659878.1	EST_HUMAN	hu85109.s1 NCJ_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7780	20222		2.06	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (DRS2298E) mRNA
8201	20622	33509	1.03	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8316	20731	33624	3.8	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8318	20731	33625	3.6	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8565	21000	33897	1.14	4.8E-01	A1820744.1	EST_HUMAN	y77110.y6 Soares breast 2NblH8t Homo sapiens cDNA clone IMAGE:164795 5' similar to cortisone element
9508	21971		1.04	4.8E-01	BE165148.1	EST_HUMAN	MIER6 repetitive element
10513	22862		1.83	4.8E-01	X83502.1	NT	PM1-HT0350-201289-004-b04 HT0350 Homo sapiens cDNA
11534	23891	36974	3.19	4.8E-01	BE700327.1	EST_HUMAN	S.cerevisiae ORFs from chromosome X
11700	24003		1.55	4.8E-01	AL163227.2	NT	PM4-NN0091-010600-002-009 NN0091 Homo sapiens cDNA
11937	24701		3.31	4.8E-01	AF227565.1	NT	Homo sapiens chromosome 21 segment HS21C027
6885	19405	32179	6.59	4.7E-01	BF217173.1	EST_HUMAN	Trypanosoma cruzi transposon VIP II SIRE repeat region
7470	19874	32470	0.64	4.7E-01	A1204374.1	EST_HUMAN	601883880F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4086387 5'
10823	23065		6.25	4.7E-01	AF102673.1	NT	qt7(2a)09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
10867	23300	38294	2.17	4.7E-01	U41069.1	NT	Influenza A Virus isolate HK51697 hemagglutinin (HA) gene, partial cds
11053	23479	36505	3.7	4.7E-01	BF529658.1	EST_HUMAN	Human collagen alpha2(X) (COL11A2) gene, exons 8 through 16, and partial cds
11958	24158		1.74	4.7E-01	AW341581.1	EST_HUMAN	602043889F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181303 5'
12613	24583		1.19	4.7E-01	AF227607.1	NT	hd11c08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909188 3'
3742	16282	28685	1.54	4.6E-01	BF693300.1	EST_HUMAN	Rattus norvegicus intestinal alkaline phosphatase-1 (IAP-1) gene, complete cds
3742	16282	28686	1.54	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5261	17762	30131	0.89	4.6E-01	AF129074.1	NT	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5315	17816		8.29	4.6E-01	M11287.1	NT	Prunus persica 1-aminocyclopropane-1-carboxylate oxidase (ACO2) gene, complete cds
5975	18260	30659	1.03	4.6E-01	BF313593.1	EST_HUMAN	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
5975	18260	30660	1.03	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5731	18313	30745	3.98	4.6E-01	Q90643	SWISSPROT	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5731	18313	30746	3.98	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5810	18390	31051	1.91	4.6E-01	BE734781.1	EST_HUMAN	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5824	18404	31068	3.56	4.6E-01	A1247679.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
							qh59h02.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
							TR:O15338 O15338 BUTYROPHILIN;

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5824	18404	31069	3.58	4.6E-01	A1247679.1	EST_HUMAN	q159h02.x1 Scores_fetal_liver_apleer_infls_s1 Homo sapiens cDNA clone IMAGE:1848011 3' similar to
5832	18412	31080	1.75	4.6E-01	P20050	SWISSPROT	TR:O15338 O15338 BUTYROPHILIN.;
5916	18493		0.68	4.6E-01	AF212124.1	NT	MEIOSIS SPECIFIC PROTEIN HOP1
6007	18581		0.81	4.6E-01	BE817247.1	EST_HUMAN	Anolis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
6190	18756	31459	0.56	4.6E-01	D28215.1	NT	PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6578	18130	31876	1.19	4.6E-01	AE000894.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
7065	19628	32425	0.55	4.6E-01	AF115340.1	NT	Methanobacterium thermoautotrophicum from bases 1165761 to 1176238 (section 100 of 148) of the complete genome
7149	19892	32680	2.88	4.6E-01	U62332.1	NT	Bacillus subtilis Bbma (bbma) gene, complete cds
7149	19892	32681	2.88	4.6E-01	U62332.1	NT	Emeticella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7878	24634	32877	0.71	4.6E-01	L07320.1	NT	Emeticella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
8278	20605	33586	0.82	4.6E-01	AA493577.1	EST_HUMAN	Murine cytomagalovirus e1 protein gene, complete cds
8313	20728		0.54	4.6E-01	Q90069	SWISSPROT	nh04h05.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element ;
8386	20800		0.54	4.6E-01	AE004031.1	NT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3; 6 KD PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 8 KD PROTEIN 2 (8K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NI>
8868	21300	34210	11.32	4.6E-01	BF697399.1	EST_HUMAN	Xyella fastidiosa, section 177 of 229 of the complete genome
9552	21966	34889	1.75	4.6E-01	P56202	SWISSPROT	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
9552	21966	34890	1.75	4.6E-01	P56202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
10015	22417	35365	1.77	4.6E-01	A1915634.1	EST_HUMAN	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
10016	22417	35366	1.77	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
11224	22876	35851	7.41	4.6E-01	AF019369.1	NT	wg73e12.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
11224	22876	35852	7.41	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11881	24117		1.37	4.6E-01	D58318.1	EST_HUMAN	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
1967	14369	26880	0.89	4.5E-01	AE001931.1	NT	HUM105F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03 5'
1967	14369	26881	0.89	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1967	14369	26881	0.89	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2823	15379	27793	5.66	4.5E-01	AA877086.1	EST_HUMAN	z55d02.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3270	15821	28237	0.68	4.5E-01	AW083761.1	EST_HUMAN	xc25c08.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-4 (HUMAN);
3270	15821	28238	0.68	4.5E-01	AW083761.1	EST_HUMAN	xc25c08.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3284	15833	28251	5.64	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3355	15901	28321	1.14	4.5E-01	AF128378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4042	16574		1.23	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4089	16820	28008	0.93	4.5E-01	AI708908.1	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
4193	17995		5.11	4.5E-01	AW873495.1	EST_HUMAN	as96c09.x1 Barstead acrlia HPLRB8 Homo sapiens cDNA clone IMAGE:2353480 3'
5025	17535	29907	1	4.5E-01	BE963445.2	EST_HUMAN	ho80q02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5813	18393	31056	1.33	4.5E-01	AW608814.1	EST_HUMAN	801657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
8963	19500		1.6	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
7894	20333	33200	0.99	4.5E-01	M37036.1	NT	COAT PROTEIN
8136	20559	33435	2.71	4.5E-01	AI858849.1	EST_HUMAN	Rat nuclear proteins B23.1 and B23.2
8857	21291		1.06	4.5E-01	M32861.1	NT	w92e02.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425618 3' similar to TR:Q82923 Q82923 SW/SNF COMPLEX 170 KDA SUBUNIT. ;
8935	21369	34282	3.1	4.5E-01	AI848598.1	EST_HUMAN	D.melanogaster Shaw2 protein mRNA, complete cds
9043	21475	34388	0.83	4.5E-01	Q52728	SWISSPROT	tb56g11.x1 NCI_CGAP_Oy35 Homo sapiens cDNA clone IMAGE:2282844 3'
9200	21632		1.78	4.5E-01	11444786	NT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
9986	22398		0.95	4.5E-01	0630818	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
10370	22770	35739	25.32	4.5E-01	M86006.1	EST_HUMAN	Bombix mori nuclear polyhedrosis virus, complete genome
10370	22770	35739	25.32	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBCY17
10645	23085	36070	4.04	4.5E-01	AW591271.1	EST_HUMAN	EST02531 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBCY17
11584	24941		3.15	4.5E-01	BE87461.1	EST_HUMAN	xc14h01.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT9 MOUSE Q64252 VIRAL INTEGRATION SITE PROTEIN INT-9 [1];
11884	24120		1.46	4.5E-01	AJ132045.1	NT	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852861 5'
12303	24383		1.33	4.5E-01	BF337531.1	EST_HUMAN	Theileria annulata shaT2 gene
12379	24423		4.96	4.5E-01	11422099	NT	60203275F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183280 5' Homo sapiens testis-specific kinase 2 (TESK2), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2287	14784	27313	7.21	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3281	16830	28248	1.55	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3281	16830	28249	1.55	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3286	16835	28253	2.37	4.4E-01	BF056728.1	EST_HUMAN	791d02.y1 NCL_CGAP_Brt16 Homo sapiens cDNA clone IMAGE:3363795 5'
4251	16776		1.45	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608393 5'
5676	18261	30681	0.89	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5676	18261	30682	0.89	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
6959	18534	31218	5.67	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5976	18552	31237	1.91	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLO Homo sapiens cDNA clone GLCCSC12 5'
6252	18816	31530	1.18	4.4E-01	AI168413.1	EST_HUMAN	q82h11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN
6252	18816	31531	1.18	4.4E-01	AI168413.1	EST_HUMAN	q82h11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN
6561	19112	31857	1.88	4.4E-01	AW080785.1	EST_HUMAN	xc27e08.x1 NCL_CGAP_C018 Homo sapiens cDNA clone IMAGE:2885510 3' similar to TR:O95154 O95154 AFLATOXIN B1-ALDEHYDE REDUCTASE ;
6658	19206		1.31	4.4E-01	AA776132.1	EST_HUMAN	ae85d11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970985 3' similar to gb:AI16038
7877	20316	33181	1.01	4.4E-01	AE000571.1	NT	TYROSINE-PROTEIN KINASE LYN (HUMAN);
8463	24049		0.82	4.4E-01	AE001198.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
8524	20859		13.46	4.4E-01	Z11679.1	NT	Treponema pallidum section 4 of 87 of the complete genome
9185	21871	34528	0.97	4.4E-01	AA056427.1	EST_HUMAN	S.tuberosum mRNA for induced stolon tip protein (partial)
9440	21871	34789	0.87	4.4E-01	AF112540.1	EST_HUMAN	z69a03.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509835 3'
9543	21958	34881	1.27	4.4E-01	O62836	SWISSPROT	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
10004	22406	36356	2.19	4.4E-01	AI268650.1	EST_HUMAN	ZINC FINGER X-CHROMOSOMAL PROTEIN
10005	22407		2.28	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10114	22516	35480	5.42	4.4E-01	P35590	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10288	22689	35652	1.66	4.4E-01	S76404.1	NT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10288	22689	35653	1.66	4.4E-01	S76404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
11863	24108	30897	4.88	4.4E-01	6677874	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
11874	24899		7.53	4.4E-01	AL183282.2	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12346	24408	30890	3.58	4.4E-01	9627742	NT	Homo sapiens chromosome 21 segment HS21C082
12456	24478		2.1	4.4E-01	P54725	SWISSPROT	Autographa californica nucleopolydnavirus, complete genome
428	13002	25428	2.69	4.3E-01	AF155218.1	NT	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A)
							Callithrix jacchus MW/LW opsin gene, upstream flanking region

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
428	13002	25429	2.69	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1620	14151	26822	0.92	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2826	16381		1.27	4.3E-01	AW936289.1	EST_HUMAN	CM2-DT0003-010200-077-501 DT0003 Homo sapiens cDNA
3021	15576	27987	0.9	4.3E-01	AW989477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4431	13002	25428	1.27	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4431	13002	25429	1.27	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5044	17554		1.07	4.3E-01	AL101502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5269	17770		0.93	4.3E-01	9635250	NT	Xestia c-nigrum granulovirus, complete genome
5620	18207	30605	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5620	18207	30606	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6178	18746	31447	1.22	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
6198	18764	31467	1.83	4.3E-01	AF170825.1	NT	Salinix sclerous olfactory receptor (SSC188) gene, partial cds
7080	19814	32408	4.3	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica lincG gene
7171	19884	32709	0.58	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
7269	19774		1.03	4.3E-01	O33387	SWISSPROT	DNA GYRASE SUBUNIT B
7913	20352		1.64	4.3E-01	BF349001.1	EST_HUMAN	602023134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158298 5'
8419	20833		0.51	4.3E-01	M58643.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
8952	21385		2.96	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds
9516	21979	34805	1	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9852	22255	35191	2.37	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
9852	22255	35192	2.37	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
12562	24545		2.22	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1390	15308	26382	1.31	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FISH HOMOLOG PRECURSOR
3603	16143	28552	4.48	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 83 of 228 of the complete genome
3637	16177	28585	1.01	4.2E-01	A1280338.1	EST_HUMAN	q94601.x1 Soares_NHMPU_ST1 Homo sapiens cDNA clone IMAGE:1879945 3'
3708	17894		0.79	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
3887	18422	28827	0.65	4.2E-01	AW835527.1	EST_HUMAN	QV0-LT0015-180200-127-h01 LT0015 Homo sapiens cDNA
3986	16530	28933	1	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4690	17206		2.54	4.2E-01	BE073574.1	EST_HUMAN	RC5-BT0559-020300-013-E08 BT0559 Homo sapiens cDNA
4747	17281	28641	3.19	4.2E-01	AA534093.1	EST_HUMAN	q99h01.st1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4833	17345	29728	4.4	4.2E-01	R13497.1	EST_HUMAN	yf77e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5200	17703		5.65	4.2E-01	U08071.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
5987	18563	31249	1.77	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6062	18634	31328	2.89	4.2E-01	AW854182.1	EST_HUMAN	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA
6919	19072	31816	1.03	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7362	19819	32633	11.36	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7362	19819	32634	11.36	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7432	24630	32769	2.69	4.2E-01	S82504.1	NT	Breast-1 breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7632	19983	32817	6.91	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
8088	20515	33394	0.61	4.2E-01	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21C062
8029	21084	33972	4.4	4.2E-01	AW857448.1	EST_HUMAN	EST369413 MAGe resequences, MAGe Homo sapiens cDNA
8929	21084	33973	4.4	4.2E-01	AW857448.1	EST_HUMAN	EST369413 MAGe resequences, MAGe Homo sapiens cDNA
10371	22771	35740	1.75	4.2E-01	AW893666.1	EST_HUMAN	MR3-SN0010-280300-103-H07 SN0010 Homo sapiens cDNA
10823	23259	36244	1.79	4.2E-01	AB023489.1	NT	Oryza latipes OIG7 mRNA for membrane guanylyl cyclase, complete cds
12596	24572		1.67	4.2E-01	AI392837.1	EST_HUMAN	IG10c05x1 NCL CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2108360 3'
1121	13665	26104	1.71	4.1E-01	AI805481.1	EST_HUMAN	RC-BT091-210189-142 BT091 Homo sapiens cDNA
1130	13674	26113	1.27	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1130	13674	26114	1.27	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 6'
2662	15155	27687	4.7	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2894	15448	27871	2.32	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2894	15448	27872	2.32	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3772	16310	28710	0.65	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGe resequences, MAGe Homo sapiens cDNA
3772	16310	28711	0.65	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGe resequences, MAGe Homo sapiens cDNA
4291	16816	29200	3.1	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 IsoG, IsoH, IsoI, IsoJ, IsoK, IsoL and IsoF genes
4324	16847		1.09	4.1E-01	AA090257.1	EST_HUMAN	om33402.s1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4710	17226	29610	1.19	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
5338	17837	30195	0.65	4.1E-01	6995993	NT	Homo sapiens aggrecan 1 (chondroin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA
5338	17837	30196	0.65	4.1E-01	6995993	NT	Homo sapiens aggrecan 1 (chondroin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA
6291	18863	31574	5.19	4.1E-01	BF681393.1	EST_HUMAN	60215680F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
7091	19826	32421	0.84	4.1E-01	U02298.1	NT	Mus musculus NIH 3T3 chemokine rantes (Scys6) gene, complete cds
7917	20355	33222	2.59	4.1E-01	U07536.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
8399	20813	33711	0.41	4.1E-01	U67278.1	NT	Bos taurus osteocalcin mRNA, complete cds
8477	20890		0.46	4.1E-01	M84694.1	NT	Homo sapiens aromatic decarboxylase gene, exon 4
8657	21092	33998	1.64	4.1E-01	BF674604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4286238 5'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9401	21833	34747	1.83	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Slitpec-pending), mRNA
10218	22819		1.24	4.1E-01	AL193076.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 316
10311	22711	35677	1.2	4.1E-01	AV649579.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLCBVD12.3'
10417	22817		1.24	4.1E-01	BF349382.1	EST_HUMAN	CM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA
10618	23061	36048	50.18	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
11144	22834	35804	1.7	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12218	24918		2.43	4.1E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1084	13609	26049	1.06	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1371	13906	26362	1.19	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1513	14045		3.72	4.0E-01	6879256	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgrfb), mRNA
2763	12751	25170	1.71	4.0E-01	6878480	NT	Mus musculus ubiquitin-protein ligase e3 component h-recogntn (Ubr1), mRNA
2821	15476	27898	1.36	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2921	15476	27899	1.35	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3692	16232	28842	2.22	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (Y1C), Y1D (Y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3837	16374	28774	3.32	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3837	16374	28776	3.32	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4874	17386		8.94	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
6203	18769	31473	1.15	4.0E-01	AW970810.1	EST_HUMAN	EST382691 MAGE resequences, MACK Homo sapiens cDNA
6416	18973	31707	0.49	4.0E-01	BF243741.1	EST_HUMAN	601877853F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106221 5'
6778	19321	32087	0.85	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 8 KD PEPTIDE]
9344	21776	34682	1.06	4.0E-01	AA323289.1	EST_HUMAN	EST26088 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11319	23693		1.75	4.0E-01	BF030282.1	EST_HUMAN	601558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
11443	23803		1.88	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
11880	24762		2.41	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12430	24898		1.18	4.0E-01	Z46301.1	NT	S. cerevisiae chromosome X reading frame ORF YJL026W
12457	24479		1.33	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
12554	24541		1.34	4.0E-01	AL19075.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 216
1410	13944	26401	3.08	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2578	15074	27592	4.5	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1183 protein, partial cds
2655	15148	27658	2.83	3.9E-01	X82032.1	NT	H. sapiens B-myb gene

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2655	15148	27659	2.83	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3058	15812	28021	4.16	3.9E-01	AJ225896.1	NT	Shorhizobium meliloti egl, eysB2, eys3 genes and orf3
4095	16826	28018	1.81	3.9E-01	BF592811.1	EST_HUMAN	7161d01.x1 NCI CGAP Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
6091	17601	29866	1.88	3.9E-01	BE726887.1	EST_HUMAN	601663948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
6230	18785	31503	2.33	3.9E-01	BF208036.1	EST_HUMAN	601882362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
8604	19155	31803	0.87	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8999	21034	33936	0.89	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
9261	21693	34604	1.17	3.9E-01	AW177011.1	EST_HUMAN	GM3-CT0105-170899-004-b08 CT0105 Homo sapiens cDNA
9501	21932	34858	1.68	3.9E-01	AW185888.1	EST_HUMAN	nr86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821
9727	22149	35080	1.65	3.9E-01	A1937337.1	EST_HUMAN	wp76a02.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to
9951	22363	35302	2.9	3.9E-01	M19878.1	NT	SW:RFX5 HUMAN P48382 BINDING REGULATORY FACTOR, ;
10602	23046	36928	8.71	3.9E-01	AV695974.1	EST_HUMAN	Human clabardin 27 gene, exons 10 and 11, and L1 and Alu repeats
11497	23855	36928	2.19	3.9E-01	AW981155.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBCQ11 5'
11497	23855	36928	2.19	3.9E-01	AW961155.1	EST_HUMAN	EST373227 MAGC resequences, MAGF Homo sapiens cDNA
11641	24845		4.08	3.9E-01	AF304354.1	NT	EST373227 MAGC resequences, MAGF Homo sapiens cDNA
11770	24048		1.65	3.9E-01	Q61670	SWISSPROT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
11854	24102	30896	1.41	3.9E-01	AE001811.1	NT	HOMEOBOX PROTEIN HLX1
12323	24394		1.28	3.9E-01	11433335	NT	Thermotoga maritima section 123 of 136 of the complete genome
164	12769		8.83	3.9E-01	7019488	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
523	13085		2.41	3.9E-01	AB072821.1	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1840	14362		0.91	3.9E-01	AE003870.1	NT	Mus musculus pcn-1 mRNA for pericentriolar material-1, complete cds
2487	14888	27601	5.38	3.9E-01	AF214117.1	NT	Xyella fastidiosa, section 10 of 229 of the complete genome
2565	15341	27577	3.07	3.9E-01	6878002	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2958	15513		0.97	3.9E-01	AJ251057.1	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3008	15563	27977	1.94	3.9E-01	AF043383.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3459	16003	28422	10.64	3.9E-01	AL161618.2	NT	Pleurocetes americanus antihopitidase N (arnpN) gene, partial cds
3621	16084		0.62	3.9E-01	A1807219.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3539	16084		0.7	3.9E-01	A1807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357865 3'
3571	16113	28528	2.01	3.9E-01	AF109372.1	NT	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357865 3'
3571	16113	28528	2.01	3.9E-01	AF109372.1	NT	Danio rerio blue-sensitive opsin (bluops) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3930	18466	28873	0.59	3.8E-01	6754095	NT	Mus musculus general transcription factor II I (GTF2), mRNA
5257	17758	30127	4.76	3.8E-01	BE544653.1	EST_HUMAN	601074110F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5'
5877	18456	31130	0.82	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
8869	19217		0.58	3.8E-01	S48825.1	NT	p10n protein [mink, Ganonic, 2448 nt]
6885	18522	32304	6.2	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271289-049-e02 BT0537 Homo sapiens cDNA
7141	19854	32874	4.75	3.8E-01	A1374601.1	EST_HUMAN	taS4f11.x1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047817 3' similar to contains Alu repetitive element;
7350	19761	32568	1.51	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
8005	20438	33306	0.55	3.8E-01	AA626274.1	EST_HUMAN	zu88c05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745084 3'
8022	20454		4.64	3.8E-01	X61697.1	NT	M. musculus gene for kallikrein-binding protein
8275	20692	33584	0.57	3.8E-01	V00883.1	NT	Yeast mitochondrial gene for ATPase (genes oii-2 and oii-4)
9041	21473	34385	2	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
9087	21519	34428	0.89	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9227	21659	34598	1.44	3.8E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
9741	22068		4.32	3.8E-01	T85413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element;
11289	23654		3.78	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11421	23782	36842	3.28	3.8E-01	R42550.1	EST_HUMAN	y82h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11421	23782	36843	3.28	3.8E-01	R42550.1	EST_HUMAN	y82h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11884	24109		3.38	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
11994	24867		2.04	3.8E-01	U94788.1	NT	Human p63 (TP63) gene, complete cds
12117	24259		1.94	3.8E-01	BE828258.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
12563	24841		1.19	3.8E-01	AF291483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1re4) gene, complete cds
2381	14885	27405	8.68	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3437	15981	28396	12.83	3.7E-01	AF056338.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3878	16413	28817	0.66	3.7E-01	AA319482.1	EST_HUMAN	EST121715 Adrenal gland tumor Homo sapiens cDNA 6' end
4245	16770	29157	10.71	3.7E-01	A1218707.1	EST_HUMAN	ck39c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4342	16884	29247	1.28	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4412	16933	29324	3.17	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
6043	18616	31304	1.27	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6248	18812	31527	0.93	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6415	18972		0.71	3.7E-01	6754833	NT	Mus musculus nuclear factor, erythroid derived 2, like 3 (Nfe2l3), mRNA
6860	19400	32176	0.6	3.7E-01	M10809.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
8881	19421		0.81	3.7E-01	L10353.1	NT	Mus saxicola haemoglobin mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7583	20032	32879	3.48	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7609	20348	33216	3.96	3.7E-01	BE873743.1	EST_HUMAN	607483887F1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3886652 5'
7809	20348	33216	3.96	3.7E-01	BE873743.1	EST_HUMAN	607483887F1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3886652 5'
8350	20765	33681	0.88	3.7E-01	T68802.1	EST_HUMAN	ya50a07.03 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66324 5'
8439	20852	33763	0.44	3.7E-01	AW511328.1	EST_HUMAN	hd45d05.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2812467 3' similar to contains Alu repetitive element; contains L1/L2 L1 repetitive element;
8874	21308	34220	1.8	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8874	21308	34221	1.8	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8903	21337	34281	0.86	3.7E-01	AA802912.1	EST_HUMAN	ck43b11.s1 NCL_CGAP_Lel2 Homo sapiens cDNA clone IMAGE:1516701 3'
9478	21907		2.34	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10185	22886	35551	4.62	3.7E-01	A1336411.1	EST_HUMAN	q146b07.x1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:1950997 3'
10837	23078	36082	3.78	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
10807	23243	36225	2.2	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
10807	23243	36228	2.2	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
10811	23247	36232	2.64	3.7E-01	AF149766.1	NT	Erythrocytic pallas isolate #B289 decay-accelerating factor (CD55) gene, partial cds
11218	22870	35844	2.97	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
11475	23833		3.13	3.7E-01	6877678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
11564	24445		2.04	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
11735	24024		3.67	3.7E-01	AJ243526.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
11836	24088		2.39	3.7E-01	D88976.1	NT	Human mRNA for KIAA0223 gene, partial cds
12233	24341		2.21	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
12311	24389	30884	2.77	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
274	12871	25288	0.93	3.6E-01	AJ009603.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1022	13573		9.49	3.6E-01	U89241.1	NT	Human mlbp gene, partial cds
1346	13881	26336	4.67	3.6E-01	T80255.1	EST_HUMAN	yd03a05.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:24443 5'
1346	13881	26337	4.67	3.6E-01	T80255.1	EST_HUMAN	yd03a05.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:24443 5'
1871	14393	26885	4.6	3.6E-01	AW590184.1	EST_HUMAN	hg33002.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2847419 3'
1871	14393	26886	4.6	3.6E-01	AW590184.1	EST_HUMAN	hg33002.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2847419 3'
1902	14421	26920	3.72	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2288	14795		1.12	3.6E-01	X78725.1	NT	P. Irregularis (P3804) gene for actin
2389	14893	27412	1.32	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2582	15061	27675	12.19	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2862	17992		9.63	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3445	15989	28407	2.08	3.6E-01	X78758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
3445	15989	28408	2.08	3.6E-01	X78758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
4433	16953	28341	1.15	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4792	17308	28688	0.63	3.6E-01	AJ009608.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4808	17320	28689	0.68	3.6E-01	Y11528.1	NT	Z.mays mRNA for casein kinase II alpha subunit
5111	17619	29982	2.87	3.6E-01	AW339393.1	EST_HUMAN	ha02g04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872568 3'
5241	17742	30111	0.73	3.6E-01	BE087698.1	EST_HUMAN	MR4-BT0356-270300-005-c10 BT0358 Homo sapiens cDNA
5409	17905	30258	1.3	3.6E-01	AE001187.1	NT	Treponema pallidum section 3 of 87 of the complete genome
5428	17923	30274	2.78	3.6E-01	X15577.1	NT	Bacillus brevis DNA for grsT, grsA and grsB gene fragment
5438	17931		3.41	3.6E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07879, Z40498
5638	18225	30825	0.66	3.6E-01	AJ006565.1	NT	Homo sapiens lipo gene intron 5
6394	18951	31688	0.94	3.6E-01	P18431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6824	19365	32141	1.68	3.6E-01	Y10188.1	NT	Homo sapiens PHEX gene
7688	20037		3.95	3.6E-01	R84080.1	EST_HUMAN	y74e08.1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:276987 5'
7740	20184	33046	1.81	3.6E-01	AW027174.1	EST_HUMAN	w72c10.x1 Scores thymus NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
8358	20773	33670	0.44	3.6E-01	AW079100.1	EST_HUMAN	O15117 FYN BINDING PROTEIN. [1];
8838	21270	34178	10.86	3.6E-01	AL161583.2	NT	MER5 repetitive element
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
9342	21774	34679	2.82	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9342	21774	34680	2.82	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9469	21900	34823	1.15	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9819	22034	34904	1.03	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9819	22034	34985	1.03	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9941	22343	35292	18.01	3.6E-01	Q63184	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
10724	23162	36146	5.55	3.6E-01	BE902390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3688897 5'
10891	23323	36322	4.06	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
10981	23380	36401	6.03	3.6E-01	L41687.1	NT	Mus musculus T-cell receptor V region delta 1 chain gene, 5' region
						NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11193	22645	35818	7.4	3.6E-01	AE000856.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor:
11522	23880	36963	5.05	3.6E-01	AW088510.1	EST_HUMAN	xd10b05.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2683329 3'
11593	24979		2.39	3.6E-01	Y19210.1	NT	Homo sapiens hHb6 gene for hair keratin, exons 1 to 9
11682	23991		4.48	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
11846	24095		2.89	3.6E-01	U68888.1	NT	Mus musculus Emr1 mRNA, complete cds
12240	24345		1.69	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) (Drosophila) homolog); translocated to, 10 (AF10), mRNA
12532	24920		1.73	3.6E-01	AW190229.1	EST_HUMAN	xd0a11.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879116 3' similar to gb:K00568 TUBULIN ALPHA-1 CHAIN (HUMAN);
119	12731	26144	1.97	3.6E-01	AL161638.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
215	12818	25234	2.28	3.6E-01	06789333	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
697	13259	25676	4.48	3.6E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
745	13305	26730	1.8	3.6E-01	7706133	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
745	13305	26731	1.8	3.6E-01	7706139	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
802	13361	25798	3.86	3.6E-01	BF129786.1	EST_HUMAN	601811060R1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4053051 3'
2180	14691	27215	0.9	3.6E-01	P06798	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2533	15340	27547	16.84	3.6E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:660872 3'
2854	15147		3.28	3.6E-01	U05897.1	NT	Fibroblast succinogenes S85 endoglycanase E (celE) and endoglycanase D (celD) gene, complete cds
2954	15509	27928	0.61	3.6E-01	AA057691.1	EST_HUMAN	294103.r1 Stragene corneal stroma (#837222) Homo sapiens cDNA clone IMAGE:512285 5'
3702	16242		0.6	3.6E-01	BF214381.1	EST_HUMAN	601845470F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4076680 5'
3812	16349		0.82	3.6E-01	AA642138.1	EST_HUMAN	mf60d03.s1 NCL_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4279	16804	29187	2.39	3.6E-01	AF071253.1	NT	Danio rerio homeobox protein (hox5b) gene, complete cds
4513	17031	29410	0.75	3.6E-01	BE146585.1	EST_HUMAN	RC5-HT0218-181089-011-g02 HT0218 Homo sapiens cDNA
4719	17235	26816	2.07	3.6E-01	Y18477.1	NT	Mus musculus Alox12B gene 5' flanking region
4952	17463	29839	0.85	3.6E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07876, Z40498
5012	17522	29897	5.26	3.6E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5587	18175	30539	1.03	3.6E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5587	18175	30540	1.03	3.6E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5814	18394	31057	1.31	3.6E-01	D42045.1	NT	Human mRNA for KIAA0086 gene, complete cds
6558	19110		1.03	3.6E-01	AW683916.1	EST_HUMAN	PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA
6746	19290	32051	0.77	3.6E-01	AA431833.1	EST_HUMAN	zw7903.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066936
6793	19336	32107	0.84	3.6E-01	U37150.1	NT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds

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Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7030	19568	32353	0.7	3.5E-01	Q24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7487	19591		3.62	3.5E-01	X98505.1	NT	S scrofa mRNA for CD31 protein (PECAM-1)
8054	20488	33381	0.45	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8054	20488	33382	0.45	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8301	20716	33511	0.43	3.5E-01	X06091.1	NT	E. coli L-arabinose transport operon with genes araG and araH
8688	21121		2.06	3.5E-01	11448042	NT	Homo sapiens tumor protein p63-binding protein, 2 (TP63BP2), mRNA
8298	21728	34638	1.46	3.5E-01	4507810	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9858	22259	35197	2.05	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BII)
9959	22361	35311	6.62	3.5E-01	Z28825.1	NT	X laevis gene for albumin including HP1 enhancer
10009	22411	35360	1.15	3.5E-01	BE174784.1	EST_HUMAN	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10518	22868	35945	2.28	3.5E-01	X61084.1	NT	C. griseus rhodopsin gene for opsin protein
10800	23237	36220	3.43	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
10800	23237	36221	3.43	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11368	23728		3.4	3.5E-01	M82885.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
11767	24045		2.44	3.5E-01	X64565.1	NT	B. taurus alpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12138	24271		3.02	3.5E-01	AE001691.1	NT	Thermoboga maritima section 3 of 138 of the complete genome
12590	24814	30584	2.41	3.5E-01	H80814.1	EST_HUMAN	ys84f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5'
12590	24814	30585	2.41	3.5E-01	H80814.1	EST_HUMAN	ys84f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5'
727	13288		1.73	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1000	13551	25995	5.98	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene
1002	13553	25997	1.04	3.4E-01	AW380120.1	EST_HUMAN	QV3-HT0261-241199-019-g10 HT0261 Homo sapiens cDNA
1358	13893	26348	2.12	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2300	14807	27325	2.43	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2816	15111	27827	6.27	3.4E-01	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
2957	15512	27832	0.82	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2957	15512	27933	0.82	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3120	15673	28086	7.03	3.4E-01	U63905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3316	15884	28282	0.92	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3513	16056	28478	6.61	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GpE (gpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds

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3792	16328		1.29	3.4E-01	BF449010.1	EST_HUMAN	7n94a01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
4063	16594		1.44	3.4E-01	AA584198.1	EST_HUMAN	Q9UJ15 DJ18C8.1;
4689	17205	29584	2	3.4E-01	BE069912.1	EST_HUMAN	nc11b10.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4886	17496	29873	1.02	3.4E-01	BE463761.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
							hy17d08.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197585 3' similar to contains L1.13 L1
							repetitive element;
5038	17548		4.85	3.4E-01	AI240973.1	EST_HUMAN	qj95c05.x1 NCL_CGAP_Kt43 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element;
5237	17739	30109	1.8	3.4E-01	U67578.1	NT	Methanococcus jannaschii section 121 of 150 of the complete genome
5393	17890	30248	13.82	3.4E-01	AW002545.1	EST_HUMAN	wu10d12.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516567 3' similar to TR:Q13537 Q13537
5459	17954		1.78	3.4E-01	BE906919.1	EST_HUMAN	SIMILAR TO POGO ELEMENT.;
5954	18550	31213	2.72	3.4E-01	AL161594.2	NT	G01500717F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902477 5'
6095	18664		5.24	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
							zn12d11.s1 Strategene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
6310	18871		1.84	3.4E-01	L02971.1	NT	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6334	18892	31624	0.94	3.4E-01	BE748912.1	EST_HUMAN	G01571811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838828 3'
6419	18976	31709	1.78	3.4E-01	AW204505.1	EST_HUMAN	U1H-B11-aet-e-12-Q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718582 3'
6555	19107	31851	1.59	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249 J1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
7123	19666		1.39	3.4E-01	N95226.1	EST_HUMAN	zb53e12.e1 Soares_fetal_lung_NbhL10W Homo sapiens cDNA clone IMAGE:307342 3'
							Im83g05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
7358	19815	32629	1.27	3.4E-01	AM68082.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7491	19695	32491	0.58	3.4E-01	BF678702.1	EST_HUMAN	G02085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
7966	20402	33272	0.84	3.4E-01	BE971698.1	EST_HUMAN	G01651613R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934947 3'
8993	21426		2.01	3.4E-01	AA337083.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' and
9255	21697	34598	1.81	3.4E-01	9633624	NT	Bovine enterovirus strain K2577, complete genome
9485	21916	34839	4.07	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9485	21916	34840	4.07	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9851	20942	33941	5.63	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9851	20942	33942	5.63	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9831	22234	35170	0.85	3.4E-01	U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scof-1) mRNA, complete cds
9862	22384	35315	1.51	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10795	23233		4.78	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome

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10834	23289	36256	8.18	3.4E-01	P08925	SWISSPROT	PROBABLE E4 PROTEIN
10874	23307	36303	2.02	3.4E-01	AF045981.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11283	23648	36695	2.99	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11569	23914		1.95	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
11886	23693		1.36	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
11784	24697		1.46	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwf8p (Gwf8) gene, complete cds
11918	24137		7.04	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
11944	24730		2	3.4E-01	BE218652.1	EST_HUMAN	h42h08.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12004	24842		1.78	3.4E-01	8838361	NT	PTR5 repetitive element
12125	24263	30831	2.1	3.4E-01	AJ287131.1	NT	Beta vulgaris mitochondrion, complete genome
12463	24483		2.06	3.4E-01	AF019413.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
14	12634	25021	9.51	3.3E-01	X07990.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
109	12634	25021	4.62	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
465	13039	25463	0.92	3.3E-01	AL161545.2	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
662	13217	26628	2.08	3.3E-01	7662485	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
1231	13770	26218	3.02	3.3E-01	Q12446	SWISSPROT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1339	13875	26328	3.59	3.3E-01	BF568880.1	EST_HUMAN	PROLINE-RICH PROTEIN LAS17
1389	13924	26381	1.4	3.3E-01	U43626.1	NT	802184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1622	14153	26623	0.93	3.3E-01	6753685	NT	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster
2304	14811		3.23	3.3E-01	4507834	NT	Mus musculus disintegrin 5 (Dign5), mRNA
2803	15458	27894	1.81	3.3E-01	AJ261805.1	NT	Homo sapiens uridine monophosphate synthetase (uracil phosphate transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2974	15529		0.73	3.3E-01	O02743	SWISSPROT	Bacteriophage phi-Ye03-12 complete genome
3016	15571	27983	0.91	3.3E-01	AJ007832.2	NT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3471	16015	28438	1.17	3.3E-01	AB012922.1	NT	Streptomyces argillaceus mithramycin biosynthesis genes
3817	16354	28754	2.75	3.3E-01	O84645	SWISSPROT	Homo sapiens MTA1-L1 gene, complete cds
3826	16363	28762	0.8	3.3E-01	P22602	SWISSPROT	EXODEOXRIBONUCLEASE V BETA CHAIN
							GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]

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3978	16514	28920	1.76	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4015	16548	28945	1.85	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4389	16911		2.45	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4738	17252		1.62	3.3E-01	AI539114.1	EST_HUMAN	tp78b12.x1 NCI_CGAP_UK3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gpX57622 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4896	17407	29779	1.2	3.3E-01	D64003.1	NT	Synechocystis sp. PCC6803 complete genome, 22127, 2755703-2868766
5440	17935	30287	7.73	3.3E-01	AJ277046.1	NT	Mus musculus processed Psm44 pseudogene for a-type of proteasome subunit C9
5577	18165	30529	2.76	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5577	18165	30530	2.76	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5650	18429	31101	0.76	3.3E-01	P39055	SWISSPROT	DYNAMIN
5650	18429	31102	0.76	3.3E-01	P39055	SWISSPROT	DYNAMIN
6070	18642	31338	0.71	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6244	18808	31521	1.63	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6244	18808	31522	1.63	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6342	18900	31632	1.3	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
7178	18991	32714	0.7	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7178	18991	32715	0.7	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7284	19799	32609	4.9	3.3E-01	AI628131.1	EST_HUMAN	ly64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element
7284	19799	32610	4.9	3.3E-01	AI628131.1	EST_HUMAN	ly64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element
7755	20199	33081	0.48	3.3E-01	P32018	SWISSPROT	COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN)
8343	20758	33653	2.01	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8353	20768	33664	0.53	3.3E-01	AJ231163.1	NT	Citocarcinoma paracentesis mitochondrial 16S rRNA gene, partial
9045	21477	34390	24.16	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
9605	22085	35012	1.11	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9605	22085	35013	1.11	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9700	22112	35039	3.17	3.3E-01	N69666.1	EST_HUMAN	z667h01.a1 Sceres_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:287649 3'
9732	22059	34868	2.78	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10027	22429		1.77	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
10507	22956	35936	3.17	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10507	22956	35937	3.17	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10803	23239		2.51	3.3E-01	BF526499.1	EST_HUMAN	602070802F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4213585 6'

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10999	23428	36446	5.63	3.3E-01	BE218351.1	EST_HUMAN	hvf1g02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11104	23557	36598	5.39	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAG-2 ANTIGEN) (IGE-BINDING PROTEIN) (95 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
11440	23800		2.88	3.3E-01	AA808621.1	EST_HUMAN	cb71g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
11872	23984	36555	1.65	3.3E-01			Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12447	24474		12.58	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
474	13048		2.34	3.2E-01	AF018281.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
738	13299		1.38	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1192	13733	26176	25.28	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1315	13860	26301	1.75	3.2E-01	Z50202.1	NT	P. vulgaris arcs-1 gene
1422	13955	26411	11.36	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1765	14292	26775	4.07	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAG2 resequences, MAGD Homo sapiens cDNA
1765	14292	26776	4.07	3.2E-01	AW957194.1	EST_HUMAN	EST368264 MAG2 resequences, MAGD Homo sapiens cDNA
2059	14584	27102	8.18	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111612 5'
2432	14953		1.64	3.2E-01	7710078	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxk1), mRNA
2659	15152	27684	1.52	3.2E-01	AF080583.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3802	16142		0.77	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arginine N-acetyltransferase
3953	16496		0.98	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4417	16938	29329	1.53	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4509	17027	29406	0.72	3.2E-01	AF111187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4536	17054	29437	1.12	3.2E-01	Q10288	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4787	17301		7.59	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4940	17451	29827	0.88	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
5132	17637	29999	0.61	3.2E-01	BE782748.1	EST_HUMAN	601465591F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3888799 5'
5523	18113	30470	2.99	3.2E-01	BE173984.1	EST_HUMAN	GM0-110569-060300-289-f10 HT0569 Homo sapiens cDNA
6256	18820	31535	1.39	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6550	19102	31845	0.59	3.2E-01	BE383518.1	EST_HUMAN	601297331F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3827462 5'
6550	19102	31846	0.59	3.2E-01	BE383518.1	EST_HUMAN	601297331F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3827462 5'

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Single Exon Probes Expressed In Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6831	19180	31632	0.6	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6951	19488	32298	0.72	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FH7A Homo sapiens cDNA clone FH7AABH01 5'
7112	19845		1.31	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8756	21180	34082	1.41	3.2E-01	M60268.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8905	21339	34253	16.13	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8908	21342	34258	16.01	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8974	21407		1.57	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
9002	21435	34344	1.1	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
9002	21435	34345	1.1	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
9052	21484	34395	1.61	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
9117	21549	34463	0.87	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
9117	21549	34464	0.87	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
9393	21825		2.88	3.2E-01	M89511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
10029	22431	35377	4.03	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10247	22848		3.85	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
10461	22911	35891	6.01	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stratiogene (cist936206) Homo sapiens cDNA clone HFBZ21
11710	24868		2.38	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12126	24931		1.35	3.2E-01	BE886846.1	EST_HUMAN	601507820F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3609532 5'
12278	24368		3.84	3.2E-01	O63217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12378	24878		1.48	3.2E-01	AF157025.1	NT	Bos taurus inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds
12424	24460		2.04	3.2E-01	L39874.1	NT	Homo sapiens deoxyribidylate deaminase gene, complete cds
12493	24912	30454	1.43	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2910	15105	27624	12.38	3.1E-01	R18051.1	EST_HUMAN	yes0106.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2946	15272	27649	8.31	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2946	15272	27650	8.31	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2912	15368		1.27	3.1E-01	AW629036.1	EST_HUMAN	h146f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3132	15885		3.27	3.1E-01	AB028069.1	NT	Mus musculus gene for Ser/Thr kinase KKLAMPRE, exon 6
3918	18454	28861	0.82	3.1E-01	AJ251888.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5002	17512	29886	0.74	3.1E-01	S69245.1	NT	carbonic anhydrase IV [rats, Sprague-Dawley, lung, mRNA, 1205 nt]
5053	17563	29931	0.85	3.1E-01	AE003984.1	NT	Xyella fastidiosa, section 130 of 229 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5161	17665	30027	1.04	3.1E-01	AL181503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
5321	17821	30182	0.96	3.1E-01	AL117210.1	NT	S. pombe chromosome I p1 p8A3
5738	18320	30755	10.61	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5887	18448	31121	0.6	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN HI1238
5888	18447	31122	0.9	3.1E-01	Z74883.1	NT	S. cerevisiae chromosome XV reading frame ORF YOL141w
5879	18458		1	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
6052	18624	31314	2.55	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6009	24012	31909	0.57	3.1E-01	R94322.1	EST_HUMAN	Yq41f04.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:198307 5'
6811	18352	32127	1.26	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-504 HN0001 Homo sapiens cDNA
6884	19424	32198	0.98	3.1E-01	AI284458.1	EST_HUMAN	q19d01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874689 3'
7052	19586	32381	0.66	3.1E-01	X71887.1	NT	H. sapiens gene for immunoglobulin kappa light chain variable region A9 and A9
7147	19660		0.8	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-281099-005-H03 CT0222 Homo sapiens cDNA
7385	24585	30363	2.72	3.1E-01	BE737392.1	EST_HUMAN	601308121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
8217	20637	33527	0.68	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8317	20732	33626	0.63	3.1E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nai6) gene, complete cds; and Nai6 gene, exons 2-9 and 11-16
8504	20918	33811	0.57	3.1E-01	AW850168.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
8504	20916	33812	0.57	3.1E-01	AW850168.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
9101	21533	34442	1.2	3.1E-01	R45318.1	EST_HUMAN	Yg46f01.s1 Soares infant brain T1NB Homo sapiens cDNA clone IMAGE:35639 3'
10087	22488	35445	0.92	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10087	22488	35446	0.92	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10136	22637	35505	1.47	3.1E-01	A1244001.1	EST_HUMAN	q181e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S65700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10725	23163	36147	8.09	3.1E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magéa9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
11291	23656	36702	3.35	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11844	24094		1.23	3.1E-01	AF284308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11883	24119		1.78	3.1E-01	AF304162.1	NT	Silvestrodon vitreum 40S ribosomal protein S11 mRNA, partial cds
12033	24205		2.81	3.1E-01	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12432	24466		4.14	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor GCM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
12477	24905		1.19	3.1E-01	10948623	NT	Mus musculus peptidoglycan recognition protein-like (Pglypl-pending), mRNA

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75	15252	25105	1.9	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkoa), mRNA
267	12865	25283	12.35	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1256	13794	26240	2.68	3.0E-01	AW300400.1	EST_HUMAN	xs6308.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1535	14067	26527	4.73	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2447	14948		5.69	3.0E-01	AJ250194.1	NT	Listeria monocytogenes spl gene for secreted protein P45
2982	15517		0.84	3.0E-01	AB008677.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3161	15714		1.1	3.0E-01	X63615.1	NT	S. pombe plc1 gene
3170	15723		1.38	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 atYPG gene for polygluturonate lyase, complete cds
3871	16407	28811	1.41	3.0E-01	AW617785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4550	17067	29449	2.16	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
4779	17293		1.05	3.0E-01	AF157835.1	NT	Bacteriophage APSE-1, complete genome
5325	15919	28337	0.69	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
5607	18195	30560	5.3	3.0E-01	BE741628.1	EST_HUMAN	601594860F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5688	18273	30694	0.69	3.0E-01	AF224693.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5692	18277	30699	0.88	3.0E-01	AF229247.1	NT	Centigalo orthopoxvirus hemagglutinin gene, complete cds
5766	18347	30803	4.77	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5768	18347	30804	4.77	3.0E-01	BE693576.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5804	18384	31045	4.72	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
7224	19836	32653	3.34	3.0E-01	D16313.1	NT	Mouse cytokeratin 15 gene, complete cds
7260	18034	30418	0.71	3.0E-01	U02369.1	NT	Streptococcus pyogenes 34/67 kDa laminin-binding protein mRNA, partial cds
7335	19747	32550	1	3.0E-01	AF229247.1	NT	Centigalo orthopoxvirus hemagglutinin gene, complete cds
7420	18925	32767	0.59	3.0E-01	X63941.1	NT	S. cerevisiae GAC1
7560	20010	32853	0.69	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7792	20234	33094	2.32	3.0E-01	10947007	NT	Mus musculus midkolin (Midk-pending), mRNA
8006	20439	33307	1.66	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
8581	21016	33916	1.32	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 138 of the complete genome
8911	21345		4.28	3.0E-01	8910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec9f), mRNA
8983	21416	34329	2.64	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681694 5'
9490	21921	34846	0.84	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmmB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
10301	22701	35666	2.33	3.0E-01	AB030231.1	NT	Aspergillus oryzae btpA gene for ER chaperone BiP, complete cds
11476	23834	36901	2.92	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'

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11476	23834	36902	2.92	3.0E-01	H51028.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12155	24852		2.04	3.0E-01	AJ287631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12471	24902		4.56	3.0E-01		NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1959	14477	26984	1.19	2.8E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2384	14888		2.08	2.8E-01	M93290.1	NT	Mouse apolipoprotein A-II (Apo-2) gene, complete cds
3141	15894	28113	1.1	2.9E-01	AF076111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3211	15763	28182	2.76	2.9E-01	AW764239.1	EST_HUMAN	PM1-CT0326-171289-001-f12 CT0326 Homo sapiens cDNA
3211	15763	28183	2.76	2.9E-01	AW764239.1	EST_HUMAN	PM1-CT0326-171289-001-f12 CT0326 Homo sapiens cDNA
3906	16441	28947	0.93	2.9E-01	AI010836.1	EST_HUMAN	tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gbD16050 NIL-2-A
4101	16832		0.88	2.9E-01	AW002802.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element ;
4521	17039	29417	0.99	2.9E-01	AA284488.1	EST_HUMAN	wr0210.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4731	17247		0.6	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4892	17404	29775	0.84	2.8E-01	AB018028.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5271	17772		1.12	2.8E-01	AI670899.1	EST_HUMAN	wad0603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287309 3' similar to contains L1.12 L1 repetitive element ;
5401	17404	29775	0.6	2.9E-01	AB018028.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5508	18099		1.93	2.9E-01	R37485.1	EST_HUMAN	yf77e12.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:28291 3'
5651	19767	32575	0.92	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
6044	18617	31305	5.8	2.9E-01	X56098.1	NT	B. subtilis levansase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levansase
6044	18617	31308	5.8	2.9E-01	X56098.1	NT	B. subtilis levansase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levansase
6057	18629	31321	5.71	2.9E-01	6879662	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
6362	18920	31655	1.55	2.9E-01	AA418145.1	EST_HUMAN	z67b12.r1 Soares_NH/MMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6605	19156	31904	0.98	2.9E-01	A1797128.1	EST_HUMAN	wz27c06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.11 L1 repetitive element ;
6655	19203	31954	2.8	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6800	19343	32114	0.48	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6800	19343	32115	0.48	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
7097	19630		0.9	2.9E-01	Z50156.1	NT	D. discoidium gene for 34 kD actin binding protein
7262	19767	32575	0.55	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
7404	18073	30366	1.8	2.9E-01	AF142329.1	NT	Mus musculus Filin protein (Filin) gene, complete cds; and Ligh protein (Ligh) gene, partial cds

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7535	19985	32820	3.44	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR508C
7601	20060	32900	1.9	2.9E-01	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
8575	21010	33909	1.73	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8575	21010	33910	1.73	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8747	21181	34408	1.01	2.9E-01	BF217743.1	EST_HUMAN	601065830F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085113 5'
9065	21497	34894	0.88	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
9509	21972	34894	1.28	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9509	21972	34895	1.28	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10676	23116	36092	2.17	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
10940	23372	36381	17.94	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
10940	23372	36382	17.94	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11333	23697	36750	4.24	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
11349	23713	36770	2.05	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11349	23713	36771	2.05	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12099	24248	30825	1.44	2.9E-01	AW005871.1	EST_HUMAN	w288105.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2865921 3' similar to contains element MIER29 repetitive element;
12194	24313	30912	3.28	2.9E-01	AF092453.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
12245	24349	30912	1.28	2.9E-01	BE788169.1	EST_HUMAN	601482059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5'
12625	24522	30857	1.47	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
12525	24522	30858	1.47	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
585	13155		1.62	2.8E-01	U87136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP160 mRNA, complete cds
690	13160		0.92	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1110	13654	26087	3.09	2.8E-01	AF168050.1	NT	Gulra gulra oocyte maturation factor Mos (c-mos) gene, partial cds
1310	13845	26285	1.1	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1310	13845	26286	1.1	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1323	13858	26307	1.35	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1724	14252	26737	1.13	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0364-120200-085-505 CT0364 Homo sapiens cDNA
1951	14470	26974	0.94	2.8E-01	AL047620.1	EST_HUMAN	DKFZp588i232t_11 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp588i232t
2367	14872	27392	4.76	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2367	14872	27393	4.76	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2458	14960		1.51	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2602	15098	27613	3.58	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2924	15479		1.43	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP60) mRNA, partial cds
2925	15480	27902	2.3	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
2925	15480	27903	2.3	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3356	15902	28322	1.07	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
4010	16543	28940	1.79	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4214	16739		1.81	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4485	17004	29390	1	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4482	17010	29395	2.23	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4835	17347	29730	1.46	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4835	17347	29731	1.46	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4885	17397	29768	3.11	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4919	17430	29803	1.38	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4180129 5'
4949	17460	29836	3.87	2.8E-01	AI272669.1	EST_HUMAN	q159c11.x1 Soares_NhrHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
5411	17907		1.48	2.8E-01	S60150.1	NT	ORF1...ORF8 (3' terminal region) [chrysantherum virus B CVB, Genomic RNA, 6 genes, 3428 nt]
5564	24588	30514	26.39	2.8E-01	AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5873	18452	31127	80.15	2.8E-01	AB016825.1	NT	Homo sapiens OCTN2 gene, complete cds
6101	18670		0.78	2.8E-01	AW992583.1	EST_HUMAN	GM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
6216	18762	31487	0.70	2.8E-01	AA765286.1	EST_HUMAN	aa01408.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK500-BINDING PROTEIN (HUMAN);
6238	18800		0.69	2.8E-01	AA404576.1	EST_HUMAN	z41f01.r1 Soares ovary tumor Nk-HOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element
6490	24984		0.83	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1,723 satellite DNA
6535	19087	31828	1.54	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6535	19087	31829	1.54	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
7110	19843	32439	8.78	2.8E-01	BF511215.1	EST_HUMAN	U1H-B14-act-f04-0-U1.st NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7426	19931	32763	0.63	2.8E-01	U65300.1	NT	Orthogomys helarodius cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7828	20267	33128	0.44	2.8E-01	BE881455.1	EST_HUMAN	601490157F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3892142 5'
7928	20363		1.02	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7983	20418	33285	0.43	2.8E-01	X59980.1	NT	L.esculentum yp42 mRNA for GTP-binding protein

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8393	20807	33706	0.44	2.8E-01	BE537151.1	EST_HUMAN	601063105F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449569 5'
8697	21132	34033	1.48	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cd51 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8697	21132	34034	1.46	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cd51 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8784	21218	34123	2.31	2.8E-01	U51688.1	NT	(Homo sapiens) lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8061	21493		8.31	2.8E-01	BF547847.1	EST_HUMAN	602022987F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4168526 5'
9689	22015	34945	1.17	2.8E-01	U17261.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scn-2) gene, complete cds
9844	22247		0.98	2.8E-01	L13654.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
9981	22363	35313	1.02	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9981	22363	35314	1.02	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10084	22485	35442	3.35	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10248	22649		0.94	2.8E-01	9626154	NT	Fujinami sarcoma virus, complete genome
10527	22974	35954	3.27	2.8E-01	BF241062.1	EST_HUMAN	601880784F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10527	22974	35955	3.27	2.8E-01	BF241062.1	EST_HUMAN	601880784F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10556	23002	35987	3.42	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076028 5'
11048	23474		4.44	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
12143	24274		11.72	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12281	24358	30802	4.83	2.8E-01	BE178699.1	EST_HUMAN	PM4-HIT0606-030400-001-a07 HT0606 Homo sapiens cDNA
12458	24856		2.32	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
12606	24964		1.46	2.8E-01	AW025400.1	EST_HUMAN	wu9805.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2527928 3'
494	13097	25486	3.48	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
632	13196	25602	4.29	2.7E-01	AA450061.1	EST_HUMAN	z39b10.s1 Scores_total_fetus_Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1294	13829	26278	1.78	2.7E-01	AB004908.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1632	14164		1.68	2.7E-01	X79815.1	NT	G. lambia SR2 gene
1726	14254	26738	2.47	2.7E-01	W56067.1	EST_HUMAN	zid22h10.1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1759	14286	26769	0.98	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2052	15327		2.08	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monamine transporter type 2, promoter region and exon 1
2262	14770	27289	4.88	2.7E-01	Y13668.1	NT	Feline immunodeficiency virus env gene, isolate ITT008P1U (M85), partial
2353	14858	27378	2.6	2.7E-01	A1310968.1	EST_HUMAN	ta49c1.1.x2 NCL_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2048836 3' similar to contains element L1 repetitive element;
2639	15494		0.89	2.7E-01	BF088294.1	EST_HUMAN	CM1-HIT0875-060900-385-e05 HT0875 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3251	15802	28219	0.67	2.7E-01	8393620	NT	Rattus norvegicus Insulin receptor (Insr), mRNA
4024	16557	28953	2.03	2.7E-01	A1928015.1	EST_HUMAN	wo92e11.x1 NCL_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2462828 3'
4035	16668	28960	0.75	2.7E-01	AF218214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4036	16566	28961	0.75	2.7E-01	AF218214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4043	16575	28966	2.57	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4958	17499	29846	0.7	2.7E-01	L27516.1	NT	Trilium esilvum (Wcs66) gene, complete cds
5148	17652		3.53	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-a03 CT0286 Homo sapiens cDNA
5481	17976	30320	0.94	2.7E-01	AV761450.1	EST_HUMAN	AV761450 MDS Homo sapiens cDNA clone MDSBZA02 5'
5518	18108	30352	2.77	2.7E-01	P17277	SWISSPROT	HOMEBOX PROTEIN HOXA4 (CHOX-1.4)
5750	18332		1	2.7E-01	AB033171.1	NT	Aaleopora myriophthalma mitochondrial cyb gene for cytochrome b, partial cds
6872	18220	31968	0.8	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6872	18220	31967	0.8	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6968	19505	32284	1.1	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6968	19505	32285	1.1	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
7163	19876	32700	2.04	2.7E-01	Q81584	SWISSPROT	FIBRILLIN 1 PRECURSOR
7438	19942	32776	0.5	2.7E-01	U16967.1	NT	Drosophila melanogaster rfc40 protein, Rep protein (Rep), and small GTP binding protein (DRas2) genes, complete cds
7483	19697		1.13	2.7E-01	A1540070.1	EST_HUMAN	td08h08.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2075103 3'
7827	20268	33129	0.78	2.7E-01	Q11078	SWISSPROT	HYPOPHYSICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
8077	20505	33383	0.76	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
8077	20505	33384	0.76	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
8226	20845	33536	2.34	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8226	20845	33537	2.34	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8290	20706	33598	0.85	2.7E-01	AA351121.1	EST_HUMAN	EST68740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
8290	20706	33599	0.85	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
8371	20786	33686	0.58	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8536	20971	33873	0.88	2.7E-01	AA013147.1	EST_HUMAN	z835b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9182	21614	34524	0.92	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9573	21996	34926	10.97	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9573	21996	34927	10.97	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9574	21997		2.69	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
10129	22630	35498	1.48	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10212	22613	35579	1.93	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10212	22613	35580	1.93	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10584	23039	36022	1.72	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBC0005 5'
10584	23039	36023	1.72	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBC0005 5'
10604	23048	36033	1.86	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12226	24728		1.27	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12335	24403		1.21	2.7E-01	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
12438	24470		2.86	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
487	15284	25479	1.98	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
488	13072		1.62	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1425	13958	26414	2.08	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1465	13998	26462	1.1	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1859	14381	26871	4.91	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1859	14381	26872	4.91	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
2017	14533		7.88	2.6E-01	AW733152.1	EST_HUMAN	bb04d10x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14989_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE)
2084	14579	27087	1.12	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2368	14873		10.78	2.6E-01	Y12596.1	NT	B. maritimus rbl gene
2457	14959		7.89	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
3054	15608		1.07	2.6E-01	AW974631.1	EST_HUMAN	EST386635 MAGe resequences, MAGM Homo sapiens cDNA
3572	16114	28530	1.15	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3642	16182	28591	2.08	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4116	16646	29031	0.88	2.6E-01	AW895510.1	EST_HUMAN	EST371580 MAGe resequences, MAGF Homo sapiens cDNA
4171	18898	29088	19.46	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0830-040400-132-603 BT0830 Homo sapiens cDNA
4378	16900	29284	1.14	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4531	17049	29431	1.05	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4531	17049	29432	1.05	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4584	17100	29490	1.32	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Stratogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838477 5'
4693	17209	29587	1.53	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhcas3*) mRNA, complete cds
4766	17280	29663	1.32	2.6E-01	AF142703.1	NT	Ophresita radicea maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5060	17570	29938	0.95	2.6E-01	AF153350.1	NT	Mus musculus metalloproteinase disintegrin (Adam28) mRNA, complete cds
5087	17577	29946	3.84	2.6E-01	H04858.1	EST_HUMAN	y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5150	17654		0.84	2.6E-01	AA884625.1	EST_HUMAN	am33b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 3'
5472	17987		1.08	2.6E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
5595	18183		1.12	2.6E-01	AB035972.1	NT	Paramecium caudatum gene for PAP, complete cds
5706	18290	30716	1.11	2.6E-01	M98060.1	NT	Acetabacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CopAx genes, complete cds
5838	18416		0.89	2.6E-01	AB62398.1	EST_HUMAN	td16a03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element
6055	18627	31318	0.71	2.6E-01	AF207550.1	NT	MER35 repetitive element ;
6377	24883		2.64	2.6E-01	AE001811.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, plm-2 protooncogene homolog plm-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g>
							Thermotoga maritima section 123 of 136 of the complete genome
6515	19068	31811	2.09	2.6E-01	AI592557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6515	19068	31812	2.09	2.6E-01	AI592557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6761	19304	32069	0.78	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
7036	19571	32361	0.68	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936166 5'
7036	19571	32362	0.68	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936166 5'
7467	19969	32803	0.92	2.6E-01	AI914380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7767	20201	33063	0.42	2.6E-01	U22971.1	NT	Pisum sativum glutamine synthetase (GS2) gene, nuclear gene encoding chloroplast protein, partial cds
7868	20307	33173	0.68	2.6E-01	BE148961.1	EST_HUMAN	CMO-HT0245-031199-085-104 HT0245 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7914	24639		1.63	2.6E-01	AL139077.2	NT	Camphylacter jejuni NCTC11168 complete genome, segment 4/6
7955	20392		0.78	2.6E-01	AA198149.1	EST_HUMAN	z092a01.r1 Stragene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:627672 5'
8291	20707	33600	1.9	2.6E-01	R10365.1	EST_HUMAN	y037a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8352	20767	33663	0.71	2.6E-01	Q09855	SWISSPROT	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C29E8.01 IN CHROMOSOME I
8435	20849		0.53	2.6E-01	AF314149.1	NT	Mus musculus telokin mRNA, complete cds
8528	20863	33864	1.32	2.6E-01	R02411.1	EST_HUMAN	ye82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
8564	20889	33896	1.48	2.6E-01	BE144331.1	EST_HUMAN	MRO-HT0166-181199-003-412 HT0166 Homo sapiens cDNA
8878	21312	34224	2.99	2.6E-01	BF34388.1	EST_HUMAN	60201442F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150396 5'
8938	21372	34285	2.32	2.6E-01	Q10169	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
9131	21563	34467	3.91	2.6E-01	BE830339.1	EST_HUMAN	RCS-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9131	21563	34468	3.91	2.6E-01	BE830339.1	EST_HUMAN	RCS-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9869	22018	34946	0.97	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9859	22262		0.97	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9944	22346	35295	1.21	2.6E-01	P87368	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
9944	22346	35298	1.21	2.6E-01	P87368	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
11281	23646		51.91	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11682	23998		1.99	2.6E-01	10190655	NT	Mus musculus jerky (Jrk), mRNA
11897	24860		3	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
11961	24162	30977	2.37	2.6E-01	AF316998.1	NT	Homo sapiens Naik-A-TPase gamma subunit (FXD2) gene, complete cds, alternatively spliced
12329	24398		1.73	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
12414	24455		1.19	2.6E-01	AE001713.1	NT	Thermoboga maritima section 25 of 136 of the complete genome
12467	24486		1.29	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
12505	24509		1.21	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
254	12854	25271	2.09	2.6E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
255	12854	25271	1.89	2.6E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
268	12868		3.82	2.6E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
855	13411	25855	1.49	2.6E-01	U09884.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1086	13632		1.11	2.6E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1148	13692	26133	5.16	2.6E-01	T80837.1	EST_HUMAN	ye11g07.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1725	14253		4.47	2.5E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2306	14813		7.18	2.6E-01	AE000876.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2397	14901	27420	4.21	2.5E-01	6978216	NT	Mus musculus protein-L-isopartate (D-aspartate) O-methyltransferase 1 (Pomt1), mRNA
2401	14905		4.3	2.5E-01	AA261087.1	EST_HUMAN	z31a12.1 NCLCGAP_GCB1 Homo sapiens cDNA clone IMAGE:694882 5'
2572	15059	27595	2.61	2.5E-01	X96310.1	NT	B.taurus mRNA for D-aspartate oxidase
3390	15936		3.97	2.5E-01	AW973471.1	EST_HUMAN	EST385484 MAGE resequences, MAGM Homo sapiens cDNA
3517	16060	28482	0.77	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3534	16077	28493	7.8	2.5E-01	AL161617.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
4083	16814		1.42	2.5E-01	P32923	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4340	16892		0.87	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4658	17174	29554	0.65	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naiip6) gene, complete cds; and Naiip3 gene, exons 2-9 and 11-16
4802	17316		0.96	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4810	17322	29701	5.8	2.5E-01	AF007768.1	NT	Charobacterium funiformans diapause associated protein 2 (DAP2) mRNA, complete cds
4834	17346	29728	2.7	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4880	17372		3.22	2.5E-01	AJ230113.1	NT	Mus musculus anneal V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4899	17401	29772	0.66	2.5E-01	BE896785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922800 5'
4915	17426	29798	0.65	2.5E-01	AB011070.1	NT	Mus musculus gene for uncoupling protein 3, 5'-flanking region and partial 5'UTR WP:Y71F9A_294.D CE22858;
5157	17681	30022	0.61	2.5E-01	AW873588.1	EST_HUMAN	h62f11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2179269 3'
5455	17850		2.18	2.5E-01	AJ565615.1	EST_HUMAN	h62f11.x1 NCLCGAP_U12 Homo sapiens cDNA clone IMAGE:2179269 3'
5463	17958		1.54	2.5E-01	BE084165.1	EST_HUMAN	PMO-BT0651-110500-004-409 BT0651 Homo sapiens cDNA
5579	18187	30532	13.35	2.5E-01	S83390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6258	18822	31537	0.67	2.5E-01	AJ008345.1	NT	Homo sapiens KVLQ11 gene
6259	18823		1	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6722	19288	32028	0.47	2.5E-01	P22219	SWISSPROT	PROTEIN KINASE VPS15
6966	19523	32305	0.96	2.5E-01	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
7474	19678	32474	0.71	2.5E-01	8394138	NT	Rattus norvegicus rabin 3 (RABIN3), mRNA
7821	20262	33123	0.78	2.5E-01	U13992.1	NT	Feline calicivirus CF/108 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7852	20282		2.11	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
8119	20544	33421	0.74	2.5E-01	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8187	20389	33470	4.88	2.5E-01	AL103282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8449	20863	33765	0.44	2.5E-01	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 92
8528	20981	33863	1.91	2.6E-01	BF109040.1	EST_HUMAN	7157a03.x1 Soares NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8797	21231	34138	1.92	2.5E-01	BF038595.1	EST_HUMAN	60146238F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862809 5'
9095	21527	34434	3.91	2.5E-01	H53236.1	EST_HUMAN	W84f07.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:202501 5'
9268	21698	34609	0.84	2.5E-01	M88626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9704	22127	35052	18.55	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Ras1-1 gene, promoter region
9704	22127	35053	18.55	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Ras1-1 gene, promoter region
9748	22116	35044	1.98	2.5E-01	AF085184.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9748	22116	35045	1.98	2.5E-01	AF085184.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10115	22516	36481	1.26	2.5E-01	AW681987.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10401	22801	35777	1.7	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
10402	22802	35778	1.57	2.5E-01	X88491.1	NT	Mouse L1Md LINE DNA
10858	23291	36284	4.33	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
11624	23952	37009	4.91	2.5E-01	AF200526.1	NT	Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds
11853	24945		5.1	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
12193	24693		1.47	2.5E-01	AV692543.1	EST_HUMAN	AV692543 GKC Homo sapiens cDNA clone GKCGZF10 5'
570	13141	25549	1.21	2.4E-01	AA836316.1	EST_HUMAN	on70d04.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
871	13426	25875	2.82	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1336	13872	26323	18.22	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1336	13872	26324	18.22	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1416	13950	26405	1.42	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1823	14345		10.12	2.4E-01	AF287763.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
2165	14677	27202	1.84	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2281	14799	27309	0.93	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2444	14946	27463	2.12	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A;
2721	15211	27127	2.35	2.4E-01	X17183.1	NT	D.discoideum (Ax3-K) ponA gene
2744	15234	27147	3.45	2.4E-01	AF030164.1	NT	S.pombe swi6 gene
						NT	Bovine adenovirus 3 complete genome
3083	15647		3.06	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pd) genes, complete cds
3108	15661	28073	1.54	2.4E-01	X74208.1	NT	Hi.sapiens AGT gene, Pail fragment of intron 4
3761	16300	28701	0.81	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4044	16578		0.74	2.4E-01	D29960.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4977	17488	29866	0.98	2.4E-01	BE160080.1	EST_HUMAN	QV1-HT0412-020400-138-b10 HT0412 Homo sapiens cDNA
5185	17689	30049	1.79	2.4E-01	BE737692.1	EST_HUMAN	601572882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839776 5'
5197	17700	30094	0.63	2.4E-01	AW076596.1	EST_HUMAN	xb18a02.x1 NCL_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:2576618 3'
5197	17700	30095	0.63	2.4E-01	AW076596.1	EST_HUMAN	xb18a02.x1 NCL_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:2576618 3'
5285	17768	30135	2.1	2.4E-01	AI277899.1	EST_HUMAN	qnt50d10.x1 Soares_placenta_8to9weeks_2NbhP8to9W Homo sapiens cDNA clone IMAGE:1892179 3'
5407	17903		3.52	2.4E-01	Q10158	SWISSPROT	similar to gb:L12693 CELLULAR NUCLEIC ACID BINDING PROTEIN (HUMAN);
5720	18302	30733	0.85	2.4E-01	AI825707.1	EST_HUMAN	PROBABLE SERINE/THREONINE-PROTEIN KINASE C1D4.11C
5720	18302	30734	0.85	2.4E-01	AI825707.1	EST_HUMAN	wo33405.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5745	18327	30794	0.77	2.4E-01	D50871.1	NT	wo33405.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5824	18502	31184	9.21	2.4E-01	AF091216.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5824	18502	31185	9.21	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5952	18528		0.72	2.4E-01	M83377.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
6179	24801		1.17	2.4E-01	AJ133836.2	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
							Branchiostoma floridae mRNA for calmodulin 2 (calM2) gene
							7B4d04.x1 NCL_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
							Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4, contains element TAR1 TAR1 repetitive element
6186	18753	31453	2.59	2.4E-01	BF692338.1	EST_HUMAN	
8288	18848	31588	2.5	2.4E-01	AF035548.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6398	18955	31699	2.48	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6454	19010	31744	1.19	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cda Homo sapiens cDNA clone cdaADE11 5'
6720	19268	32023	0.67	2.4E-01	AA398872.1	EST_HUMAN	zf70d02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727683 3'
							we82c11.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03484
6886	19428	32201	1.25	2.4E-01	AI698889.1	EST_HUMAN	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7074	19608	32403	0.51	2.4E-01	AA661832.1	EST_HUMAN	nv05c01.s1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:1219296 3'
7476	19860	32476	0.44	2.4E-01	AF163863.1	NT	Mustela vison tyrosine aminotransferase gene, complete cds
7810	20252	33113	9.71	2.4E-01	L43001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
8010	20442	33311	0.57	2.4E-01	N48732.1	EST_HUMAN	yf56c11.1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:277460 5'
8271	20688		0.47	2.4E-01	U06013.1	NT	Rattus norvegicus Sprague-Dawley heme oxygenase-2 non-reducing isoform gene, complete cds
8273	20990	33582	0.86	2.4E-01	AF228944.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8775	21209	34111	1.28	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae rro8 and hko8 genes; two component system 08
8775	21209	34112	1.28	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae rro8 and hko8 genes; two component system 08
8889	21323	34234	1.68	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9069	21501	34410	1.32	2.4E-01	BF242794.1	EST_HUMAN	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
9743	22070	34995	7.9	2.4E-01	AI693515.1	EST_HUMAN	wd43602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330806 3' similar to contains
9837	22240	35176	0.92	2.4E-01	AF220067.1	NT	MER22 b1 TAR1 repetitive element:
9837	22240	35176	0.92	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10330	22730	35998	1.88	2.4E-01	Q03692	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
10550	22997	35980	2.68	2.4E-01	AL161494.2	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11720	24717		2.76	2.4E-01	AF004213.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11786	24055		2.11	2.4E-01	AJ278191.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12554	24933		1.26	2.4E-01	BF228975.1	EST_HUMAN	Mus musculus mRNA for putative me7 protein (me7 gene)
12501	24506		4.61	2.4E-01	AL163281.2	NT	RC3-CT0413-100800-023-b08 CT0413 Homo sapiens cDNA
404	12880	25402	1.07	2.3E-01	S75898.1	NT	Homo sapiens chromosome 21 segment HS21C081
656	13221		12.53	2.3E-01	U39713.1	NT	aromatase [Poephilia guttata=zebra finches, ovary, mRNA; 3188 nt]
686	13250	25965	26.3	2.3E-01	U87598.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
958	13510	25951	3.38	2.3E-01	BE311893.1	EST_HUMAN	Methanococcus jannaschii section 138 of 150 of the complete genome
1538	14069	26629	0.91	2.3E-01	Y10887.2	NT	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1640	14171	26841	2.81	2.3E-01	Y10887.2	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
2344	14850	27368	1.17	2.3E-01	BE297718.1	EST_HUMAN	Mus musculus cdh5 gene, exon 1, partial
2483	14984	27497	4.62	2.3E-01	AF113897.1	NT	601175662F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2483	14984	27498	4.62	2.3E-01	AF113597.1	NT	Escherichia coli translocated intimin co-receptor (tir) and OrlU (oriU) genes, complete cds; and intimin (eae) gene, partial cds
2587	15083	27597	3.16	2.3E-01	M11319.1	NT	Escherichia coli translocated intimin co-receptor (tir) and OrlU (oriU) genes, complete cds; and intimin (eae) gene, partial cds
2816	16471	27894	1.21	2.3E-01	AA601379.1	EST_HUMAN	Human erythropoietin gene, complete cds
3046	16600		7.67	2.3E-01	R21732.1	EST_HUMAN	no16d08.s1 NCI_CGAP_Pho1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu
3347	16893	28316	0.94	2.3E-01	H69836.1	EST_HUMAN	repetitive element; contains element THR repetitive element:
3848	16483		5.54	2.3E-01	7662133	NT	y21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
4372	16894	29276	1.07	2.3E-01	R82252.1	EST_HUMAN	y97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
4424	16945		2.3	2.3E-01	L76789.1	NT	Homo sapiens KIAA0460 gene product (KIAA0460), mRNA
4481	17000	29385	1.12	2.3E-01	D90899.1	NT	y1701.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4524	17042	29422	2.57	2.3E-01	AF092535.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4590	17106	29496	5.3	2.3E-01	6031984	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4945	17456	29893	0.82	2.3E-01	J03280.1	NT	Homo sapiens milogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
							Homo sapiens nuclear transport factor 2 (placental protein 16) (PP16) mRNA
							Human phenylethanolamine N-methyltransferase gene, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5135	17458	29833	0.61	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5168	17692	30023	0.71	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5273	17774		0.94	2.3E-01	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
5328	17827	30186	0.61	2.3E-01	BF574804.1	EST_HUMAN	802132210F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271647 5'
5557	18146	30508	2.39	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5685	18270	30690	2.62	2.3E-01	BF098381.1	EST_HUMAN	730506.x1 NC1 CGAP_OY18 Homo sapiens cDNA clone IMAGE:3476689 3' similar to SW:GAG_SMSAV P03330 GAG POLYPEPTIDE [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].
5792	18373	31031	5.39	2.3E-01	X96587.1	NT	C.familiaris rom1 gene
5918	18496		0.96	2.3E-01	L39112.1	NT	Vittiforma cornuini small subunit ribosomal RNA gene
6030	18604	31291	0.61	2.3E-01	S60371.1	NT	293 RNA [Leucostoc carnosum, Genomic, 2866 nt]
6239	18803	31614	2.15	2.3E-01	AI708940.1	EST_HUMAN	as27612.x1 Barslead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6239	18803	31515	2.15	2.3E-01	AI708940.1	EST_HUMAN	as27612.x1 Barslead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7021	19557	32343	0.78	2.3E-01	AF198088.1	NT	Oryctolagus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for mitochondrial product
7282	19787	32598	4.41	2.3E-01	AI718148.1	EST_HUMAN	as4212.x1 Barslead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
7550	20000	32842	0.88	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7745	20188	33050	0.86	2.3E-01	AF000227.1	NT	Secale cereale omega secalin gene, complete cds
7897	20336	33204	2.68	2.3E-01	AF175389.1	NT	Glycine max resistance protein LMT7 precursor RNA, partial cds
7900	20339	33206	0.8	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDGB08 5'
7900	20339	33207	0.8	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDGB08 5'
8135	20558		3.83	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
8140	20563	33440	1.56	2.3E-01	BE888071.1	EST_HUMAN	601611673F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
8308	20721		2.95	2.3E-01	N80983.1	EST_HUMAN	za12608.r1 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:292358 5'
8355	20770	33666	0.71	2.3E-01	11416821	NT	Homo sapiens protocadherin alpha cluster (LOC83960), mRNA
8355	20770	33667	0.71	2.3E-01	11416821	NT	Homo sapiens protocadherin alpha cluster (LOC83960), mRNA
8630	21085	33974	1.78	2.3E-01	M68931.1	NT	Oxyficha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8916	22318	35264	1.33	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9991	22393	36344	2.89	2.3E-01	BE173060.1	EST_HUMAN	MR0-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10028	22430	36376	2.71	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10334	22734	35701	0.98	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10343	22743		6	2.3E-01	BF133577.1	EST_HUMAN	601846155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
11109	23562	36603	3.8	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 84 of the complete genome
11702	24009		3.6	2.3E-01	U45428.1	NT	Borrelia burgdorferi 2.9-8 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
11797	24082		32.01	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT28M6 Homo sapiens cDNA clone HCOE44 5'
11822	24661		1.8	2.3E-01	AA089819.1	EST_HUMAN	chr1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
11830	24082		1.81	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
11893	24871	30570	3.24	2.3E-01	AW303623.1	EST_HUMAN	xc21d07.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q8Z175
11927	24924	30462	8.26	2.3E-01	BE882464.1	EST_HUMAN	Q8Z175 LYSYL OXIDASE-RELATED PROTEIN 2; contains PTR5.b2 TAR1 repetitive element;
11978	24172		3.19	2.3E-01	BF663319.1	EST_HUMAN	601807202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
12032	24204		2.07	2.3E-01	AJ008519.1	NT	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12134	24267		1.54	2.3E-01	U49845.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12140	24204		1.36	2.3E-01	AJ008519.1	NT	Plautodes walt distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12415	24458		3.42	2.3E-01	BF475611.1	EST_HUMAN	Rattus norvegicus mRNA for acid gated ion channel
12588	24830	30595	1.19	2.3E-01	M60675.1	NT	rac38h12.x1 Lupskl_sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
12612	24582		1.88	2.3E-01	AL161535.2	NT	MER38 repetitive element;
92	12709	25123	0.78	2.2E-01	A052180.1	EST_HUMAN	Human von Willebrand factor gene, exons 23 through 34
1595	14117	26584	2.24	2.2E-01	AF187850.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2013	14529	27044	1.96	2.2E-01	M34840.1	NT	oz14a10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1676280 3' similar to
2302	14809	27327	8.83	2.2E-01	BF677638.1	EST_HUMAN	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
2508	15009	27620	0.89	2.2E-01	BE581258.1	EST_HUMAN	Homo sapiens PPAR delta gene, promoter region
2508	15009	27521	0.89	2.2E-01	BE581258.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2619	15114		1.95	2.2E-01	AL163218.2	NT	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
2836	15392	27805	3.94	2.2E-01	BE155625.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3886190 5'
2836	15392	27806	3.94	2.2E-01	BE155625.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3886190 5'
2875	15430		1.66	2.2E-01	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C018
3370	15916		2.56	2.2E-01	AL161562.2	NT	PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA
							PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4227	16752		1.27	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4234	16759	29145	7.84	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K ⁺ channel subunit (Kcnk6) genes, complete cds
4280	16805	29188	2.23	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekkt1) mRNA, complete cds
4280	16805	29189	2.23	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekkt1) mRNA, complete cds
4377	16899	29282	1.04	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4377	16899	29283	1.04	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4454	16974	29361	0.72	2.2E-01	AW361098.1	EST_HUMAN	RC1-C10249-141189-021-g04 CT0249 Homo sapiens cDNA
4882	17394		1.46	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4887	17399	29770	2.82	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.r1 Stratagene NNT neuron (#937233) Homo sapiens cDNA clone IMAGE:848988 6'
5063	17573	29942	1	2.2E-01	M86524.1	NT	Human dystrophin gene
5151	17655		1.87	2.2E-01	L13289.1	NT	Mus musculus vinculin gene, exon 3
5281	17782	30148	1.23	2.2E-01	BE141035.1	EST_HUMAN	MRO-HT0067-207089-002-g10 HT0067 Homo sapiens cDNA
5307	17807	30172	0.93	2.2E-01	H60548.1	EST_HUMAN	y42h09.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:208001 5' similar to gb:Z14116_ma1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
5380	17877	30238	0.62	2.2E-01	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
5380	17877	30239	0.62	2.2E-01	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
6023	18597	31284	1.48	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
6034	18608		4.23	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6302	18663	31588	0.8	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6302	18663	31589	0.8	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
7078	19812	32405	0.65	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
7182	18895	32720	0.42	2.2E-01	AA490106.1	EST_HUMAN	ab02909.s1 Stratagene fetal retina B37202 Homo sapiens cDNA clone IMAGE:839656 3'
7182	18895	32721	0.42	2.2E-01	AA490106.1	EST_HUMAN	ab02909.s1 Stratagene fetal retina B37202 Homo sapiens cDNA clone IMAGE:839656 3'
7450	19853	32787	10.1	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC08 5'
7569	20019	32862	1.48	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spA) genes, complete cds; and unknown genes
7569	20019	32863	1.48	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spA) genes, complete cds; and unknown genes
7749	20193	33094	2.08	2.2E-01	M24736.1	NT	Human glycoprotein B gene, exon 4
7749	20193	33055	2.08	2.2E-01	M24736.1	NT	Human glycoprotein B gene, exon 4
7987	20422	33289	0.73	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
8240	20657	33548	0.69	2.2E-01	AF287967.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8277	20694	33585	0.69	2.2E-01	AB024553.1	NT	Bacillus halodurens DNA, complete and partial cds, strain C-125
8847	21082		2.6	2.2E-01	AF165143.1	NT	Mus musculus nm23-M1 gene, promoter region
8895	21130	34031	0.97	2.2E-01	Z49833.1	NT	E.coli sepA and sepB genes
9274	21706	34618	4.76	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 138 of the complete genome
9357	21789		3.13	2.2E-01	AW865039.1	EST_HUMAN	PM3-CT0268-241289-009-b07 CT0263 Homo sapiens cDNA
9419	21851	34765	1.84	2.2E-01	8383247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9473	21804	34828	1.48	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0046-110900-008-c02 TN0045 Homo sapiens cDNA
9542	21857	34880	1.77	2.2E-01	W02888.1	EST_HUMAN	zao408.r1 Soares melanocyte 2NHM Homo sapiens cDNA clone IMAGE:297591 5'
9557	22120	35048	13.54	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9594	22074	34989	0.92	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9804	22084	35011	4.93	2.2E-01	M89843.1	NT	Brachydanio rerio apendymin beta and gamma chains (Epo) gene, complete cds
9804	22306	35249	4.17	2.2E-01	AF197841.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds; nuclear gene for chloroplast product
10000	22402	35352	1.58	2.2E-01	BF206507.1	EST_HUMAN	601868724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10181	22562	35530	0.98	2.2E-01	9625671	NT	Human herpesvirus 5, complete genome
11174	22554	35595	3.21	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11212	22864	35838	3.84	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
11627	23955		2.53	2.2E-01	BE870959.1	EST_HUMAN	601448957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850870 6'
11742	24937		3.98	2.2E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CAL-T), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
11833	24085		3.5	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
11845	16974	28361	3.18	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141189-021-g04 CT0249 Homo sapiens cDNA
11948	24151		1.21	2.2E-01	AW661922.1	EST_HUMAN	h117502.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
12511	24929		3.26	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAH02 5'
995	13547	25991	1.74	2.1E-01	AA569289.1	EST_HUMAN	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
998	13548	25993	0.93	2.1E-01	AL161604.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1151	13694		2.87	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1229	13768	26214	1	2.1E-01	6754298	NT	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1229	13768	26215	1	2.1E-01	6754299	NT	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1869	14391	26883	1.15	2.1E-01	AA086824.1	EST_HUMAN	ok73e02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1618910 3' similar to gb:K02765
2066	14581	27099	2.4	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2242	14751	27271	4.98	2.1E-01	6753235	NT	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
							Mus musculus calcium channel, voltage dependent, alpha2/delta subunit 3 (Caen2d3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2380	16336	27403	1.71	2.1E-01	H73988.1	EST_HUMAN	y0407.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2380	16336	27404	1.71	2.1E-01	H73988.1	EST_HUMAN	y0407.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2484	14965	27478	5.16	2.1E-01	AF022814.1	NT	Fugu rubripes transcription factor (SLP-1) and heme-oxygenase genes, complete cds
2879	15434	27852	1.98	2.1E-01		NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3813	16350		6.82	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
4066	16597	28988	1.15	2.1E-01	P11075	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4066	16597	28989	1.15	2.1E-01	P11075	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4266	16791		0.88	2.1E-01	AF124526.1	NT	Orchestria caviniana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4398	16920		1.78	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4615	17131	29516	2.61	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
4678	17194	29570	0.65	2.1E-01	X93161.1	NT	P. falciparum mRNA for small GTPase reb11
5339	17838	30197	2.95	2.1E-01	AF173401.1	EST_HUMAN	q23003.x5 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028413 3'
5477	17872	30317	12.64	2.1E-01	J05082.1	NT	Vampire bat (D.rotundus) plasminogen activator mRNA, complete cds
5554	18144	30504	17.71	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
7202	19787	32608	1.21	2.1E-01	AJ223392.1	NT	Doko fragilis mitochondrial 16S rRNA gene, partial cds
7305	19717	32520	2.39	2.1E-01	U04842.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7888	20325	33190	0.7	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7886	20325	33191	0.7	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7899	20338		2.11	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
8250	20687	33557	1.73	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
8305	20720	33614	1.47	2.1E-01	AF088887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8305	20720	33615	1.47	2.1E-01	AF088887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8373	20787		0.56	2.1E-01	T87354.1	EST_HUMAN	y083001.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114783 5'
8667	21122		1.15	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1B), mRNA
9004	21437	34347	5.11	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
9212	21644	34552	0.95	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614 5'
9212	21644	34553	0.95	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614 5'
9367	21789	34707	0.92	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
9702	22125	35051	2.83	2.1E-01	X97378.1	NT	A.thaliana mRNA for AtRanBP1b protein

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9777	22180	35115	1.24	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10261	22682	35624	1.4	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10279	22680	35842	1.82	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
11241	23609		2.05	2.1E-01	A1141875.1	EST_HUMAN	(80 KD DIACYLGLYCEROL KINASE)
11315	23879		2.2	2.1E-01	11036847	NT	ga66f08.x1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691751 3'
11555	24446		1.37	2.1E-01	X57624.1	NT	Homo sapiens paracretic polypeptide 2 (PPY2), mRNA
12109	24254		1.65	2.1E-01	AF217490.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12345	24837		1.51	2.1E-01	L32588.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12547	24535	30838	1.7	2.1E-01	BE672330.1	EST_HUMAN	Human granulosa gene
206	12809	26227	2.13	2.0E-01	AB017437.1	NT	7a59e02.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3'
552	13124		2.54	2.0E-01	7705601	NT	Gallus gallus mRNA for avana, complete cds
719	13280	25702	1.17	2.0E-01	M77085.1	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
833	13390	25829	2.98	2.0E-01	AF027865.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype V-Ha2
1038	13586	26026	0.91	2.0E-01	D90905.1	NT	Mus musculus Major Histocompatibility Locus class II region
1152	13695	26135	3.41	2.0E-01	AL163213.2	NT	Synectocystis sp. POC8803 complete genome, 7127_781449-920916
1287	13822	26274	1.32	2.0E-01	AJ132695.5	NT	Homo sapiens chromosome 21 segment HS21C013
1340	13876	26329	1.42	2.0E-01	AW384937.1	EST_HUMAN	Homo sapiens rac1 gene
1515	14047	26512	2.31	2.0E-01	4503408	NT	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1576	14106	26569	2.31	2.0E-01	AB007974.1	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1579	14110	26575	1.08	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1715	14243		1.32	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1748	14275		2.67	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 87 of 150 of the complete genome
2243	14752		1.62	2.0E-01	XB2877.1	NT	H. sapiens Nat-D-glucose cotransport regulator gene
3463	16007	28428	0.81	2.0E-01	P46607	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3557	16099		0.83	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCL CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3703	16244	26849	1	2.0E-01	P34641	SWISSPROT	MER21 repetitive element ;
4238	16763	29147	1.04	2.0E-01	AF143738.1	NT	GED-11 PROTEIN
4802	17118		8.61	2.0E-01	BE826165.1	EST_HUMAN	Passer montanus recombination activating protein 1 (RAG-1) gene, partial cds
5147	17651	30017	7.62	2.0E-01	8922080	NT	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5194	18007	28428	0.72	2.0E-01	P46607	SWISSPROT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5248	17749	30118	1.17	2.0E-01	Y19216.1	NT	Homo sapiens putative pshHbD pseudogene for hair keratin, exons 1 to 9
5288	17787		5.18	2.0E-01	AF078448.1	NT	Dicystostellum discoidaleum cytochrome c oxidase assembly protein (coxA) gene, complete cds
6369	17867	30227	3.78	2.0E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
5702	18286	30711	2.48	2.0E-01	X56600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
6017	18391	31277	2.6	2.0E-01	11432540	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6127	18396	31393	0.83	2.0E-01	X91856.1	NT	Fructose DNA encoding for valyl-tRNA synthetase
6368	18924	31659	6.47	2.0E-01	U16300.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6488	18043		0.84	2.0E-01	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
6610	19160	31910	0.57	2.0E-01	P02487	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6769	19311	32077	3.4	2.0E-01	XG1033.1	NT	M. auratus mu class glutathione transferase gene
6880	18420	32185	4.71	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141098-001-g08 CT0247 Homo sapiens cDNA
7752	20198	33058	1.45	2.0E-01	AF260371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (Pfkc) gene, exons 3 through 7
7930	20367	33232	0.79	2.0E-01	P64422	SWISSPROT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8335	20750	33847	0.73	2.0E-01	V00726.1	NT	Mouse germ line gene coding for beta-globin (Y2)
8598	21033		5.49	2.0E-01	AF028028.1	NT	Andes virus strain Q123133 glycoprotein G1 and G2 precursor, gene, partial cds
8778	21212	34115	3.25	2.0E-01	X91151.1	NT	M. musculus scp2 gene exon 14
8884	22007	34835	0.94	2.0E-01	U82511.1	NT	Dicystostellum discoidaleum random slug cDNA19 protein (rsc19) mRNA, partial cds
9812	22027	34955	0.85	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9736	22063		5.89	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
9964	22368		2.1	2.0E-01	AF146892.1	NT	Homo sapiens filarin 2 (FLN2) mRNA, complete cds
10068	22469	35426	2.14	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10068	22469	35427	2.14	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10307	22707	35872	0.91	2.0E-01	X97121.1	NT	R. norvegicus mRNA for NTR2 receptor
12087	24238		1.24	2.0E-01	AF206637.2	NT	Plimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12308	24749		1.43	2.0E-01	AF302773.1	NT	Homo sapiens rhinein-Lm isoform (rhinein) mRNA, complete cds
12320	24885	30797	1.39	2.0E-01	AW975297.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12663	24454	30869	3.8	2.0E-01	AJ023592.1	EST_HUMAN	ov80e10.s1 Soares, testis NHT Homo sapiens cDNA clone IMAGE:1843610 3'
12387	24429		8.44	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
12542	24531	30862	1.44	2.0E-01	11528495	NT	Mus musculus fructosamine 3 kinase (Fn3k), mRNA
114	12726		8.89	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arlnt1), mRNA
366	12658	26373	6.47	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
675	13240	25694	1.67	1.9E-01	U32581.2	NT	Homo sapiens lambda101a protein kinase C-interacting protein mRNA, complete cds
675	13240	25655	1.67	1.9E-01	U32581.2	NT	Homo sapiens lambda101a protein kinase C-interacting protein mRNA, complete cds
682	13247	25662	6.39	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0602-261199-011-001 BT0502 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
683	13247	25662	8.68	1.9E-01	BE070801.1	EST_HUMAN	RC3-B10502-251199-011-d01 BT0502 Homo sapiens cDNA
1012	13583		1.39	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (IL2rg), mRNA
1131	13675	28115	7.88	1.9E-01	AA358813.1	EST_HUMAN	EST6784 Fetal lung II Homo sapiens cDNA 5' end
1403	13937	26393	4.48	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1484	13997		5.41	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rpb-2) gene, complete cds
2187	14698		8.41	1.9E-01	AF163822.1	NT	Arabidopsis thaliana endoxylglucan transferase (EXGT-AA) gene, complete cds
2278	14786	27308	2.24	1.9E-01	B922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2877	15432	27860	3.82	1.9E-01	U66066.1	NT	Sigmoidon hispidus p53 gene, partial cds
2892	15448		7.53	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3373	15920	28338	4.19	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3455	15999	28418	5.94	1.9E-01	R18487.1	EST_HUMAN	y42f10.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:129547 5'
3911	16348	28749	0.75	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4008	16540	28938	5.73	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4089	16630	29019	1.97	1.9E-01	AW754108.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4248	16773	29158	1.08	1.9E-01	BE634943.1	EST_HUMAN	MR1-FN0010-290700-007-404 FN0010 Homo sapiens cDNA
4503	17021	29403	0.87	1.9E-01	AL161483.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
4824	17336	29716	0.84	1.9E-01	Z63780.1	NT	Fugu rubripes genes encoding carbamoyl phosphate synthetase III, myosin light chain, MAP2
4894	17504	29880	7.09	1.9E-01	P25082	SWISSPROT	CELL SURFACE GLYCOPROTEIN PRECURSOR (S-LAYER PROTEIN)
5083	17593	29890	3.41	1.9E-01	AW848203.1	EST_HUMAN	IL3-CT0215-180200-087-D02 CT0215 Homo sapiens cDNA
5113	17621		0.94	1.9E-01	Q95239	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
6139	17643	30006	0.94	1.9E-01	O95239	SWISSPROT	KINESIN-LIKE PROTEIN KIF4
5238	17740	30110	5.84	1.9E-01	AJ251178.1	NT	Phoca vitulina partial ear2B gene for alpha adrenergic receptor 2B
5354	17853	30210	0.86	1.9E-01	7705331	NT	Homo sapiens cytokine receptor-like molecule 9 (CREME9), mRNA
5379	17898		2.19	1.9E-01	AE004894.1	NT	Pseudomonas aeruginosa PA01, section 155 of 520 of the complete genome
5399	17898	30253	2.97	1.9E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMAGA) mRNA
5871	18450		4.97	1.9E-01	AW130149.1	EST_HUMAN	x229a07.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb.M73779 RETINOIC
5913	18491	31174	8.26	1.9E-01	AF127837.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN)
6128	18695	31392	0.83	1.9E-01	AF091216.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
6175	18743		3	1.9E-01	AU133118.1	EST_HUMAN	Mus musculus Wrm protein (Wrm) gene, complete cds
6260	18824		0.52	1.9E-01	AE001299.1	NT	AU133118 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6657	19205	31955	0.89	1.9E-01	AI162391.1	EST_HUMAN	Chlamydia trachomatis section 26 of 87 of the complete genome
							wis4h02.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2394099 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6724	19270	32029	0.79	1.8E-01	AW148452.1	EST_HUMAN	x11408.x1 NCL_CGAP_Kid0 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7398	18057	30397	1.66	1.8E-01	R43212.1	EST_HUMAN	yg09a12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31883 3' similar to contains MER13 repetitive element;
7392	18061	30402	0.46	1.9E-01	X88276.1	NT	P. sativum PS-JAA4/S gene
7418	19923	32753	0.93	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7418	19923	32764	0.93	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7712	20157	33018	0.65	1.9E-01	U73846.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7988	20404	33274	0.6	1.8E-01	U93698.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsl), enterotoxin (ent), and integrase (int) genes, complete cds
7985	20429	33298	1.3	1.8E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
8049	20481	33355	3.19	1.8E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
8485	20897		0.47	1.9E-01	AF165980.1	NT	Mus musculus recombination breakpoint containing region
8623	21068	33968	1.65	1.8E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
9126	21558	34464	15.05	1.8E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
9305	21737	34844	1.77	1.9E-01	M14598.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9305	21737	34845	1.77	1.9E-01	M14598.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
10535	22982	35982	2.52	1.8E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11258	23824	36672	2	1.8E-01	M22253.1	NT	Rattus norvegicus sodium channel I mRNA, complete cds
11446	23806	36865	3.3	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12136	24269		1.65	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
12519	24739		1.9	1.9E-01	AF001188.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
33	12653	25043	2.78	1.8E-01	U73200.1	NT	Mus musculus p110Rip mRNA, complete cds
273	15280	25287	1.46	1.8E-01	AB022090.1	NT	Mus musculus Ctg gene for chaparrin containing TOP-1 gamma subunit, partial cds
385	12972	25394	1.55	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
767	13327	25758	0.74	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OGC1, complete cds
1007	13558	26000	0.97	1.8E-01	AB12212.1	EST_HUMAN	wd7102.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1118	13861	26101	1.28	1.8E-01	AF000590.1	NT	Dictyostellium discoideum plasmid Ddp5, complete genome
1321	13856	26308	8.2	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1531	14093	26523	1.77	1.8E-01	6763947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1531	14093	26524	1.77	1.8E-01	6763947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA

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1838	14358		1.05	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE:
1870	14392	28884	1.05	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2640	15135		3.08	1.8E-01	AW635728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA
2851	18407		1.64	1.8E-01	AF184589.1	NT	Jonopsidium oculale LEAFY protein (LEAFY2) gene, partial cds
2856	15411	27832	0.85	1.8E-01	AW182300.1	EST_HUMAN	X41403.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3085	15630	28048	1.05	1.8E-01	AW095178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3344	15690	28312	1.02	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3618	16158	28567	1.04	1.8E-01	H03369.1	EST_HUMAN	Y45601.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:161704 3' similar to contains Alu repetitive element;
3618	16158	28568	1.04	1.8E-01	H03369.1	EST_HUMAN	Y45601.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:161704 3' similar to contains Alu repetitive element;
4356	16878		1.09	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4592	17108	29497	6.07	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4825	17337	29717	2.49	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4937	17448	29823	8.08	1.8E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
5119	17628	29987	0.59	1.8E-01	X79794.1	NT	N.tabacum mRNA pNLA-35
5163	17657	30019	2.08	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151289-112-g06 ST0203 Homo sapiens cDNA
5232	17734	30103	2.49	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5266	17767	30136	1.04	1.8E-01	AI439881.1	EST_HUMAN	tt57e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5550	18140	30499	0.87	1.8E-01	BE082628.1	EST_HUMAN	RC6-BT0641-500300-011-H03 BT0641 Homo sapiens cDNA
6092	18691	31355	1.06	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6222	18788	31495	0.95	1.8E-01	N28626.1	EST_HUMAN	Y438108.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264063 5'
6441	18997	31728	1.31	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6441	18997	31729	1.31	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6882	19402	32178	1.53	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6911	19450		2.48	1.8E-01	N04853.1	EST_HUMAN	Y92902.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278163 5'
7204	19769		0.57	1.8E-01	11430157	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
7427	19932	32784	1.25	1.8E-01	AB018561.1	NT	Citrus latifolia mRNA for wsvs, complete cds
7427	19932	32765	1.25	1.8E-01	AB018561.1	NT	Citrus latifolia mRNA for wsvs, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7488	19892	32488	0.76	1.8E-01	BE981353.1	EST_HUMAN	601648361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
7931	20368	33233	0.82	1.8E-01	AP001511.1	NT	Bacillus halodurans genome DNA, section 5/14
9579	22002	34929	1.62	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9802	22082	35009	1.61	1.8E-01	9626232	NT	Bacteriophage Ika, complete genome
9749	22152	35082	1.13	1.8E-01	P16272	SWISSPROT	AMP NUCLEOSIDASE
9749	22152	35083	1.13	1.8E-01	P16272	SWISSPROT	AMP NUCLEOSIDASE
9775	22178	35111	0.9	1.8E-01	M26019.1	NT	S. commune oridine-5'-phosphate decarboxylase (URA1) gene, complete cds
9775	22178	35112	0.9	1.8E-01	M26019.1	NT	S. commune oridine-5'-phosphate decarboxylase (URA1) gene, complete cds
9884	22287	35228	0.93	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9888	22289	35230	0.87	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 80 of 150 of the complete genome
10139	22540		0.86	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10283	22684	35646	1.45	1.8E-01	X63440.1	NT	M. musculus mRNA for P19-protein tyrosine phosphatase
10434	22888	35863	3.24	1.8E-01	X77336.1	NT	A. thaliana mRNA for ribonucleotide reductase R2
10469	22919	35897	5.95	1.8E-01	U36906.1	NT	Bacteriophage r11 integrase, repressor protein (rrp), dUTPase, holin and lysin genes, complete cds
10520	19832	32764	2.19	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wus, complete cds
10520	19932	32765	2.19	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wus, complete cds
10521	22968	35948	4.88	1.8E-01	AF019107.1	NT	Dicystostellum discoidium unknown (DG1041) gene, complete cds
11214	22868	35841	3.31	1.8E-01	X57033.1	NT	B. taurus mRNA for potassium channel
11471	23829	36897	2.94	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
11661	23977		1.57	1.8E-01	10986561	NT	Bovine ephraim fever virus, complete genome
11727	24019	31011	1.52	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NC1 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12221	24333		2.63	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12553	24413		13.68	1.8E-01	R24494.1	EST_HUMAN	yH48H10.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:133027 5'
12397	24435		1.73	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hdx1)
594	13164	25567	1.37	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
828	13385	25825	2.74	1.7E-01	X53330.1	NT	P. aumerill histone gene cluster for core histones H2A, H2B, H3 and H4
985	13538		1.77	1.7E-01	P35516	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1084	13630	26069	1.03	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolyhedrovirus, complete genome
1084	13630	26070	1.03	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolyhedrovirus, complete genome
1926	14445		1.99	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2814	15371	27788	1.72	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2814	15371	27787	1.72	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2881	15438	27855	1.78	1.7E-01	AA398909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2951	15508	27928	1.28	1.7E-01	AJ238736.1	NT	Naja naja atra cbx-1 gene, exons 1-3
2951	15508	27927	1.28	1.7E-01	AJ238736.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3088	15820	28027	2.81	1.7E-01	AF081614.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3343	15889	28311	0.9	1.7E-01	N85763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3424	15968	28381	1.51	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3951	18488	28895	5.56	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4480	15371	27786	1.78	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
4480	15371	27787	1.78	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
4596	17112		1.88	1.7E-01	X62936.1	NT	Schistosoma gregaria alpha repetitive DNA
4897	17408	29780	1.34	1.7E-01	AI247635.1	EST_HUMAN	qh57e09.x1 Soares_fetal_liver_spleen_1NFUS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element;
5170	17874		6.18	1.7E-01	U28376.1	NT	Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds
5213	17716	30081	0.98	1.7E-01	BF688719.1	EST_HUMAN	602186630F1 NIH_MGC 49 Homo sapiens cDNA clone IMAGE:4298848 5'
5333	17832	30180	0.84	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3827197 5'
5384	17882	30220	242.34	1.7E-01	BE398671.1	EST_HUMAN	601309660F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3631167 5'
5394	17882	30221	242.34	1.7E-01	BE398671.1	EST_HUMAN	601309660F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3631167 5'
5486	17981	30309	1.61	1.7E-01	D45354.1	NT	Arabidopsis thaliana AME2 mRNA for protein kinase, complete cds
5684	18249	30649	1.99	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI CGAP_Cc3 Homo sapiens cDNA clone IMAGE:881068 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5684	18249	30650	1.99	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI CGAP_Cc3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5860	18439	31114	0.8	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6659	19207	31958	12.08	1.7E-01	HT2118.1	EST_HUMAN	ys02g06.s1 Soares fetal liver spleen 1N1FS Homo sapiens cDNA clone IMAGE:213858 3'
6688	19236		0.51	1.7E-01	AJ238270.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4
6723	19269	32027	0.57	1.7E-01	AJ370978.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6723	19269	32028	0.57	1.7E-01	AJ370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
7251	18025	30408	0.73	1.7E-01	BE300286.1	EST_HUMAN	600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
7284	18789		1.93	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7421	18926		0.77	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7668	20114	32987	0.88	1.7E-01	AF000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7766	20200	33062	10.65	1.7E-01	BE734178.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5'
7980	20419	33284	1.26	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLFO PROTEIN)
8001	24641	33300	0.93	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
8426	20842	33741	0.45	1.7E-01	BF328982.1	EST_HUMAN	QV3-BN0047-020800-284-d08 BN0047 Homo sapiens cDNA
8428	20842	33742	0.45	1.7E-01	BF328982.1	EST_HUMAN	QV3-BN0047-020800-284-d08 BN0047 Homo sapiens cDNA
8460	20873	33774	0.46	1.7E-01	AL114656.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8534	20969	33670	1.34	1.7E-01	AF000573.1	NT	Homo sapiens homotensinase 1,2-dioxygenase gene, complete cds
8834	21268	34174	6.68	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8834	21268	34175	6.68	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
9156	21598	34496	2.34	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
9248	21650	34589	1.04	1.7E-01	AF217413.1	NT	Homo sapiens neuridin 3 isoform gene, complete cds, alternatively spliced
9248	21650	34590	1.04	1.7E-01	AF217413.1	NT	Homo sapiens neuridin 3 isoform gene, complete cds, alternatively spliced
9758	22181	35094	10.02	1.7E-01	AF001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9845	22248	35183	2.25	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9898	22300	35242	0.92	1.7E-01	AJ261748.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10200	22601		2.77	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10299	22699	35664	1.38	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
10300	22700	35665	1.51	1.7E-01	AA827972.1	EST_HUMAN	nc80s07.s1 NCI_CGAP_Cc9 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:125081
10471	22921	35900	8.94	1.7E-01	BE390835.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
10586	23032		1.65	1.7E-01	U37768.1	NT	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
10589	23034	36017	3.82	1.7E-01	AA814617.1	EST_HUMAN	Hantaan virus S segment nucleocapsid protein mRNA, complete cds
10894	23326	36327	15.92	1.7E-01	7106300	NT	643a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1428924 3'
10894	23326	36328	15.92	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Ebt1 (Ebt1), mRNA
10894	23326	36328	15.92	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Ebt1 (Ebt1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11434	23785		2.02	1.7E-01	P16272	SWISSPROT	AMP NUCLEOSIDASE
11557	24448		1.2	1.7E-01	AJ272884.1	NT	Blobellia aurantiaca mitochondrial partial COII gene for cytochrome c oxidase subunit II
11561	23911	37001	5.33	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
11696	24872		1.36	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11992	24703		1.34	1.7E-01	AI824404.1	EST_HUMAN	tx69g05.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC
12315	24391		10.33	1.7E-01	U01317.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
130	12738	30885	2.14	1.7E-01	AF217832.1	NT	Human beta globin region on chromosome 11
699	15258	25678	1.43	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate Kinase gene, exon 6 and 7
1548	14077	26538	3.48	1.6E-01	AF298117.1	NT	yt75f12.f1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135699 5'
1877	14399	26893	1.27	1.6E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
1928	14447		1.89	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2282	15333	27310	2.15	1.6E-01	X94232.1	NT	Crossotrea gigas RNA polymerase II largest subunit mRNA, partial cds
2396	14900	27419	2.19	1.6E-01	AB037729.1	NT	H. sapiens mRNA for novel T-cell activation protein
2845	15401	27818	14.02	1.6E-01	AF185589.1	NT	Homo sapiens mRNA for KIAA1303 protein, partial cds
2845	15401	27819	14.02	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3631	16171	28580	1.11	1.6E-01	AJ003165.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3631	16171	28581	1.11	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3773	16311	28712	0.75	1.6E-01	AE000962.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
4014	16847		2.83	1.6E-01	AE004413.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4351	16873	29257	10.86	1.6E-01	AF178680.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete genome
4488	17005		3.37	1.6E-01	AW686601.1	EST_HUMAN	Homo sapiens apelin gene, complete cds
4498	17014		4.78	1.6E-01	0753319	NT	EST380677 IMAGE resequences, MAGJ Homo sapiens cDNA
4941	17452	29828	1.87	1.6E-01	Z28330.1	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4941	17452	29829	1.97	1.6E-01	Z28330.1	NT	S. cerevisiae chromosome XI reading frame ORF YKR105c
						NT	S. cerevisiae chromosome XI reading frame ORF YKR105c
5003	17513	29887	0.97	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE
							PROTEINS ALPHA, BETA, DELTA AND GAMMA]
5027	17537	29908	1.32	1.6E-01	AA088343.1	EST_HUMAN	z184h09.s1 Stragelene colon (#837204) Homo sapiens cDNA clone IMAGE:611361 3' similar to TR:E221955
5061	17571	29939	1.03	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
5081	17571	29940	1.03	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5284	17785	30150	2.43	1.6E-01	AL353984.1	EST_HUMAN	Lycopodium obscurum RsaI fragment 2, satellite region
5284	17785	30151	2.43	1.6E-01	AL353984.1	EST_HUMAN	DKFZp434O1729_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O1729 5'
5348	17847	30204	1.73	1.6E-01	AI874074.1	EST_HUMAN	DKFZp434O1729_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O1729 5'
							wm48c08.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2439182 3'

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5397	17894	30261	0.89	1.6E-01	P98158	SWISSPROT	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN) (GLYCOPROTEIN 330)
5843	18230	30631	0.88	1.6E-01	L40608.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5784	18365	30828	3.05	1.6E-01	AW197496.1	EST_HUMAN	HYPOHETICAL 127.6 KD PROTEIN ; xm4301.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2886969 3' similar to TR:O75984 O75984
5784	18365	30827	3.05	1.6E-01	AW197496.1	EST_HUMAN	xm4301.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2886969 3' similar to TR:O75984 O75984
5786	18377	31036	2.81	1.6E-01	AF034716.1	NT	HYPOHETICAL 127.6 KD PROTEIN ; Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6332	18890	31622	1.03	1.6E-01	BE925803.1	EST_HUMAN	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6578	19129	31874	0.63	1.6E-01	BF183584.1	EST_HUMAN	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6578	19129	31876	0.83	1.6E-01	BF183584.1	EST_HUMAN	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6767	19310	32075	2.03	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6767	19310	32076	2.03	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7167	19880	32704	0.97	1.6E-01	AA308047.1	EST_HUMAN	z88904.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:729611 5'
7167	19898	32725	0.72	1.6E-01	AA308047.1	EST_HUMAN	Homo sapiens mRNA for KIAA1566 protein, partial cds
7241	19852		0.65	1.6E-01	BF693630.1	EST_HUMAN	602139855F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301004 5'
7379	18049	30387	6.28	1.6E-01	AW291215.1	EST_HUMAN	UI-H-B12-egl-b-08-0-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7760	20204	33068	0.69	1.6E-01	Z49832.1	NT	S.cerevisiae chromosome X reading frame ORF YJR132w
7998	20432		0.53	1.6E-01	BE925803.1	EST_HUMAN	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
8337	20752	33648	1.49	1.6E-01	AW246359.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8382	20796	33694	0.57	1.6E-01	6763237	NT	Mus musculus Cxcr2-dependent activator protein for secretion (Cadps), mRNA
8397	20811		1.11	1.6E-01	AU136525.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone IMAGE:1004466 5'
8539	20974	33875	1.64	1.6E-01	L49349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
9234	21666	34576	1.08	1.6E-01	R13873.1	EST_HUMAN	y60h08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
9321	21753	34681	2.06	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9417	21849		0.83	1.6E-01	AF111167.2	NT	Homo sapiens lun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9800	22203		1.82	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA
9801	22204	36141	2.18	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9827	22290		1.28	1.6E-01	BE156694.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA
10450	22801	35879	2.91	1.6E-01	AW950853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
10781	23219	36201	1.98	1.6E-01	BE259849.1	EST_HUMAN	601145783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
10868	23328		3.35	1.6E-01	AF106094.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11166	23546	36586	4.61	1.6E-01	6871552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Aptb1), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11574	24886		1.81	1.6E-01	6879466	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
11699	24002	36562	2.89	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLOEMF07 5'
12019	24196	30950	1.41	1.6E-01	L14933.1	NT	Rat convertase PC5 mRNA, 5' end
12052	24218		1.37	1.6E-01	AW639711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12157	24680		12.88	1.6E-01	AB045310.1	NT	Gucumis sativus KS mRNA for ent-kaurene synthase, complete cds
12340	24405		2.83	1.6E-01	AK024466.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12433	24467		2.85	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qlu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12461	24481	30878	1.91	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
12593	24570		1.3	1.6E-01	BF672698.1	EST_HUMAN	602162004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283145 5'
261	12859	25276	1.47	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
261	12859	25277	1.47	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
604	15257		1.92	1.5E-01	AV711696.1	EST_HUMAN	AV711698 DCA Homo sapiens cDNA clone DCAADH08 5'
805	13364	25789	1.28	1.5E-01	AL183284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1119	13663	26103	0.85	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1124	13668	26107	3.08	1.5E-01	AJ261885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1140	13684		1.45	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1247	13785	26231	1.69	1.5E-01	AW195516.1	EST_HUMAN	zn39411.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2686085 3'
1308	13843	26292	4.36	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1308	13843	26293	4.36	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1510	14042	26509	1.57	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
2663	15158	27668	2.95	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247637 5'
2668	15423		1.02	1.5E-01	AW572516.1	EST_HUMAN	xw56a02.x2 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_ma1
2984	15549	27861	0.6	1.5E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3013	15568	27980	0.66	1.5E-01	O76887	SWISSPROT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3325	15872	28294	4.88	1.5E-01	AA935049.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3345	15891	28313	0.71	1.5E-01	Z23104.1	NT	cc68a05.s1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3345	15891	28314	0.71	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
						NT	L. stagnalis mRNA for G protein-coupled receptor
						NT	L. stagnalis mRNA for G protein-coupled receptor
3757	16298	28697	1.99	1.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3769	16307	28708	0.98	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3783	16320	28719	0.8	1.5E-01	M97882.1	NT	XYNA; Thermomonas bacterium; xyna; 4182 base-pairs
3873	16409	28813	2.35	1.5E-01	AW665983.1	EST_HUMAN	h11006.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
3890	16425	28830	0.88	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3890	16425	28831	0.88	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
4002	16593	28885	1.06	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-191089-012-c09 HT0149 Homo sapiens cDNA
4199	16724	29112	10.61	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4522	17040	29419	0.6	1.5E-01	BE791263.1	EST_HUMAN	601583988F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838345 5'
4522	17040	29419	0.6	1.5E-01	BE791263.1	EST_HUMAN	601583988F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838345 5'
4604	17120		4.26	1.5E-01	AF030694.2	NT	Plasmodium falciparum strain Dd2 heat shock protein 88 (HSP88), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (qrt), CG9 (cg9), CG1 (cg1), CG8 (cg8), CG2 (cg2), and CG7 (cg7) genes, complete cds
4777	17291	29676	1.19	1.5E-01	BF687685.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4805	17168	27668	2.48	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
5098	17609	29870	1.95	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5235	17737	30108	1.02	1.5E-01	5579481	NT	Homo sapiens calbindin 1, (28kD) (CALB1), mRNA
5508	18097	30340	2.32	1.5E-01	P07998	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5536	18129	30481	1.07	1.5E-01	AF236852.1	NT	Caiman crocodilus MHC class II beta chain (hcIIbeta) gene, complete cds
5581	18169		5.93	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5800	18381	31040	5.12	1.5E-01	AW650754.1	EST_HUMAN	(SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5844	18424	31093	8.43	1.5E-01	U65016.1	NT	IL3-CT0219-160200-084-F10 CT0219 Homo sapiens cDNA
5844	18424	31094	8.43	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6200	18766	31469	0.78	1.5E-01	4508810	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6308	18869	31595	1.85	1.5E-01	6753659	NT	Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA
6308	18869	31596	1.85	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6349	18907	31640	2.41	1.5E-01	AJ276505.1	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6509	19063	31804	3.11	1.5E-01	BE727658.1	EST_HUMAN	Mus musculus genomic fragment, 279 Kb, chromosome 7
6568	19119		2.37	1.5E-01	4508398	NT	601584322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:38383981 5'
							Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6874	19222	31970	1.8	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6852	24616	32168	1.81	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6882	19422	32196	5.43	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C8ORF3), mRNA
6893	19433	32209	1.67	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6941	19479	32258	2.71	1.5E-01	Q28482	SWISSPROT	AMELOGENIN
7054	19588	32382	0.96	1.5E-01	AA714760.1	EST_HUMAN	hw30d10.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
7085	19619	32414	1.9	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7396	18065	30405	5.81	1.5E-01	AW970295.1	EST_HUMAN	EST382378 MAGC resequences, MAGK Homo sapiens cDNA
7441	24631		0.76	1.5E-01	AA811645.1	EST_HUMAN	ob73f02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element:
7662	20108		2.36	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7824	20266	33126	0.54	1.5E-01	AJ223986.1	NT	Leucophaea mederae mRNA for lipocalin, Lma-P22
7869	20308	33174	1.78	1.5E-01	AJ973157.1	EST_HUMAN	wr62c08.xt NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
8112	20538	33416	1.2	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
8112	20538	33417	1.2	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
8124	20548	33424	1.6	1.5E-01	AW600611.1	EST_HUMAN	UI-HF-BND-ekb-4-05-O-UJ.r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3077409 5'
8124	20548	33425	1.6	1.5E-01	AW600611.1	EST_HUMAN	UI-HF-BND-ekb-4-05-O-UJ.r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3077409 5'
8292	20708	33601	0.88	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds
8976	21111	34013	1.16	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8784	21228	34135	0.99	1.5E-01	AA970317.1	EST_HUMAN	0085g12.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8859	21293		1.15	1.5E-01	BE894799.1	EST_HUMAN	601610523F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912004 5'
8932	21366		11.57	1.5E-01	C16900.1	EST_HUMAN	C16900 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-528H09 5'
8956	21388	34300	2.01	1.5E-01	L27835.1	NT	Pangaslanodon gigas growth hormone (GH) mRNA, complete cds
9064	21496	34405	2.11	1.5E-01	D84476.1	NT	Homo sapiens mRNA for ASK1, complete cds
9242	21674	34584	2.03	1.5E-01	4501972	NT	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9413	21845	34769	3	1.5E-01	N74226.1	EST_HUMAN	za59e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:266866 3' similar to
9470	21901	34824	1.24	1.5E-01	BF685465.1	EST_HUMAN	PIR:S44443 S44443 RAD23 protein homolog2 - human;
9476	21906		2.51	1.5E-01	AV754819.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9557	20948	33847	6.93	1.5E-01	U00455.1	NT	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9884	22386	35336	8.93	1.5E-01	AF007570.1	NT	Acipenser transmontanus vitellogenin mRNA, partial cds
9884	22386	35337	8.93	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10179	22580	35547	2.52	1.5E-01	X98852.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10245	22846	35611	2.35	1.5E-01	AJ814046.1	EST_HUMAN	P. leniusculus mRNA for integrin beta subunit
10245	22846	35612	2.35	1.5E-01	AJ814046.1	EST_HUMAN	wk53h12.xt NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:2419173 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10245	22846	35612	2.35	1.5E-01	AJ814046.1	EST_HUMAN	wk53h12.xt NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);

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Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10285	22696	35682	1.27	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax6b (Pax6) mRNA, complete cds
10399	22798	39774	1.44	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10399	22799	35775	1.44	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10483	22833	35910	1.63	1.5E-01	BE088482.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
10483	22833	35911	1.63	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
10606	23050	36034	4.24	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10606	23050	36035	4.24	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10857	23280	36283	2.33	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
10895	23327	36329	2.33	1.5E-01	AA425488.1	EST_HUMAN	zw48d02.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:773091 5' similar to contains element MER22 repetitive element;
10943	20308	33174	1.86	1.5E-01	AI973157.1	EST_HUMAN	wf52c08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2481310 3'
11487	23845		1.86	1.5E-01	AI984404.1	EST_HUMAN	wm32a05.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437616 3' similar to TR:Q135539 Q13539 MARINER TRANSPOSASE; contains Alu repetitive element
11652	24740		36.22	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286549 6'
12051	24217		1.71	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12097	24246		1.19	1.5E-01	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12118	24760		6.73	1.5E-01	R83077.1	EST_HUMAN	vp87e04.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194430 5'
12216	24786		2.25	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA04 5'
12339	24894	30774	6.42	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 116
12590	24559	30846	3.52	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
313	12808		1.69	1.4E-01	AF008663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S8P to TCRBV21S2A2 region
933	13487		3.29	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1292	13827		2.61	1.4E-01	T91964.1	EST_HUMAN	yf54c01.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112032 3'
1740	14267		0.89	1.4E-01	6678980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1742	14269	26754	1.23	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1928	14448		13.45	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2371	14876	27395	1.32	1.4E-01	P30708	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2806	15101	27618	2.31	1.4E-01	BE439741.1	EST_HUMAN	HTM1-598F HTM1 Homo sapiens cDNA
2751	15241	27755	7.79	1.4E-01	AI933496.1	EST_HUMAN	wm74d01.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3525	16088		0.98	1.4E-01	BF341524.1	EST_HUMAN	602013527F1 NCI CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4149126 5'
4190	16717	29105	9.94	1.4E-01	AI989094.1	EST_HUMAN	b56c02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4190	16717	29106	9.94	1.4E-01	AI989094.1	EST_HUMAN	b56c02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4254	16779	29183	4.34	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4437	18957		0.65	1.4E-01	AA76287.1	EST_HUMAN	z50b01.s1 Soares_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:U01057_mai INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4832	17443	28820	1.11	1.4E-01	AV689659.1	EST_HUMAN	AV689659 GKCC Homo sapiens cDNA clone GKCDUG09 5'
5202	17708	30069	0.89	1.4E-01	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5239	17741		5.7	1.4E-01	AW866022.1	EST_HUMAN	QV3-SN0022-100500-188-h09 SN0022 Homo sapiens cDNA
5370	17868	30228	1.65	1.4E-01	BE969740.1	EST_HUMAN	601670690F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949799 5'
5589	18148	30510	6.12	1.4E-01	T80877.1	EST_HUMAN	yef16t11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5582	18170	30533	6.06	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5582	18170	30534	6.06	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6625	19174	31928	3.39	1.4E-01	BE328891.1	EST_HUMAN	tr07c02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
6830	19371	32148	3.99	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6830	19371	32149	3.99	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6924	19463	32241	4.2	1.4E-01	AW082798.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6938	19477		1.57	1.4E-01	BE268536.1	EST_HUMAN	601183523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537681 5'
6961	19498	32277	2.63	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-409 UM0036 Homo sapiens cDNA
7586	20016		0.82	1.4E-01	AL118568.1	EST_HUMAN	DKFZb761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZb761A0910 5'
7863	20302		1.9	1.4E-01	AW015373.1	EST_HUMAN	U1-H-BID-eat-c-09-0-UJ.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7891	20330	33196	0.84	1.4E-01	F08746.1	EST_HUMAN	HSC1D8011 normalized Infant brain cDNA Homo sapiens cDNA clone c-1db01
7847	20384		0.62	1.4E-01	A1762827.1	EST_HUMAN	w04f12.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389285 3' similar to SW:ICE4_HUMAN P49662 CASPASE-4 PRECURSOR;
8152	20575	33450	0.7	1.4E-01	U85846.1	NT	Oryctolagus cuniculus fructose 1,6, biphosphate aldolase (AldB) gene, complete cds
8307	20722	33616	0.69	1.4E-01	A1305192.1	EST_HUMAN	q180b12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878683 3'
8982	21415		1.28	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH08 3'
9288	21721	34631	5.23	1.4E-01	A3307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9424	21856	34772	1.25	1.4E-01	R92746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:138873 5'
9424	21856	34773	1.25	1.4E-01	R92746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:138873 5'
9465	21896	34818	10.2	1.4E-01	BF310958.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9532	21947	34870	1.43	1.4E-01	W93411.1	EST_HUMAN	zdb4a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element;
9589	22012	34941	1.13	1.4E-01	Y10198.1	NT	Homo sapiens PHEX gene
9589	22012	34942	1.13	1.4E-01	Y10198.1	NT	Homo sapiens PHEX gene
9654	20945	33845	1.83	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase lai (JAL), and zinc finger protein (DNZ1) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10024	22426	35374	1.02	1.4E-01	AF023813.1	NT	Macromitrium levatum small ribosomal protein 4 (rps4) g'ina, chloroplast gene encoding chloroplast protein, partial cds
10620	23063	36049	3.53	1.4E-01	R53400.1	EST_HUMAN	y70c05.r1 Soares breast 2NBHb1st Homo sapiens cDNA clone IMAGE:154088 5'
10879	23312	36310	2.3	1.4E-01	P08948	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11175	23655		1.89	1.4E-01	AL161496.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8
11220	22872	35947	2.66	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK),
11282	23647		2.25	1.4E-01	X52102.1	NT	triosephosphate isomerase (TPI) genes, complete cds
11634	24708	30782	1.22	1.4E-01	AB000890.1	NT	M.musculus p16K gene for 16 kDa protein
11965	24178	30945	3.82	1.4E-01	X74773.1	NT	Ephydaria fluviatilis mRNA for aldolase, partial cds
11999	24186		2.42	1.4E-01	11968117	NT	P.salina plastid gene secY
12027	24169		1.49	1.4E-01	BE984835.2	EST_HUMAN	Rattus norvegicus desmin (Des), mRNA
12049	24951		2.11	1.4E-01	BE513802.1	EST_HUMAN	601659490R1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3885674 3'
12162	24292		3.4	1.4E-01	AF083221.1	NT	60131569F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3634329 5'
12163	24289		2.44	1.4E-01	D04004.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transformylase (GART) genes, complete cds
12248	24971		4.26	1.4E-01	P10447	SWISSPROT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868787-3002865
12272	24366		1.33	1.4E-01	AA452305.1	EST_HUMAN	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12495	24495		1.36	1.4E-01	11425031	NT	z330e12.r1 Soares total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:788014 5' similar to contains
12498	24761		4.38	1.4E-01	D82983.1	NT	Alu repetitive element
12572	24554		2.3	1.4E-01	AW377998.1	EST_HUMAN	Homo sapiens ephrins-B3 (EFNB3), mRNA
336	12929	25345	2.87	1.3E-01	4759467	NT	Mus musculus mRNA for prolidase, complete cds
338	12929	25346	2.87	1.3E-01	4759467	NT	MR0-HT0208-221289-204-c08 HT0208 Homo sapiens cDNA
647	13119	25628	2.88	1.3E-01	AB013139.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
655	13220	25631	0.71	1.3E-01	AJ277606.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
655	13220	25632	0.71	1.3E-01	AJ277606.1	NT	Homo sapiens gene for NBS1, complete cds
867	13422	25870	0.87	1.3E-01	X53330.1	NT	Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
917	13471	25919	1.58	1.3E-01	AF139518.1	NT	Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
1052	13598	26037	1.59	1.3E-01	AL117078.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
1154	13697		2.35	1.3E-01	AL115265.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
							Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
							Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptar
1246	13784	26230	1.74	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1473	14005		1.16	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1829	14351	26950	2.86	1.3E-01	6880657	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
1908	14427	26924	1.5	1.3E-01	AL117078.1	NT	Bordetis chereia strain T4 cDNA library under conditions of nitrogen deprivation
2077	14591		1.36	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidophila pucB5, pucA5, pucB6, pucA7, pucB7, pucA8, pucB8, pucA8 and pucC genes and ORF151
2185	14696		1.03	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2277	14785		3.47	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2507	15008	27519	1.69	1.3E-01	M89918.1	NT	Cerassius auratus keratin type I mRNA, complete cds
3332	15879	28300	0.85	1.3E-01	AF198779.1	NT	Homo sapiens transcription factor GCHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel a2
3720	16260	28664	0.75	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3720	16260	28665	0.75	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3727	16267	28671	0.63	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrolid dehydrogenase 4 [AKR 1C4], exon 2
3782	16260	28664	0.63	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3782	16260	28665	0.63	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3809	16346	28747	0.63	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4002	16536		1.5	1.3E-01	AL161691.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4156	16683		1.06	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4175	16702		4.13	1.3E-01	AW394341.1	EST_HUMAN	QV3-DT0018-081289-036-a03 DT0018 Homo sapiens cDNA
4182	16709	28099	2.04	1.3E-01	AF028806.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4202	16727	28115	21.98	1.3E-01	AW273741.1	EST_HUMAN	xv23f10.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4337	16859		1.26	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4515	17033	29411	0.62	1.3E-01	M21572.1	NT	Homo sapiens chromosome 21 segment HS21C080
4570	17087	29474	2.62	1.3E-01	BE272339.1	EST_HUMAN	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4659	17185	29563	1.18	1.3E-01	BF679864.1	EST_HUMAN	601120096F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2890063 5'
5019	17529		0.99	1.3E-01	Y12594.1	NT	602164306F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4296544 5'
5130	17635		0.67	1.3E-01	BF091980.1	EST_HUMAN	H.sapiens gene encoding translin, exon 3
5294	17784	30160	2.58	1.3E-01	AL163284.2	NT	RC4-TN0077-180900-012-c05 TN0077 Homo sapiens cDNA
5294	17794	30161	2.58	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5578	18166	30531	0.85	1.3E-01	AW466988.1	EST_HUMAN	ha07b06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5618	18205	30602	2.07	1.3E-01	AW804417.1	EST_HUMAN	L1 repetitive element
							QV0-UM0093-100400-186-a08 UM0093 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5763	18344		0.84	1.3E-01	AF107783.1	NT	Emicollia nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5851	18430		0.72	1.3E-01	AF058880.1	NT	Hepatitis C virus 68_Q1.10 genome polyprotein gene, partial cds
5899	18573	31259	0.77	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4101119 5'
6287	18849	31569	0.59	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6287	18849	31570	0.59	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6831	19372	32150	0.78	1.3E-01	AB031328.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6921	19460	32238	1.79	1.3E-01	X88891.1	NT	Cjacchus intron 4 of visual pigment gene (red allele)
7157	19870	32693	0.45	1.3E-01	H73425.1	EST_HUMAN	y02d01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232609 5'
7173	19886		0.71	1.3E-01	W26387.1	EST_HUMAN	2673 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7436	19940		0.77	1.3E-01	BF529560.1	EST_HUMAN	602044345F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181866 5'
7715	20160		1.7	1.3E-01	H48694.1	EST_HUMAN	y33d02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
8349	20764		0.5	1.3E-01	BF681515.1	EST_HUMAN	602158643F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4297354 5'
8612	21047	33952	1.45	1.3E-01	11423284	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
8637	21072	33980	1.33	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC 49 Homo sapiens cDNA clone IMAGE:4298074 3'
8831	21265	34171	0.83	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8866	21320		4.57	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV, reading frame ORF YDL054c
8921	21355		4.5	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
9018	21451	34362	1.19	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC 49 Homo sapiens cDNA clone IMAGE:4298074 3'
9672	22019	34950	4.29	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K+-ATPase alpha 2a subunit mRNA, complete cds
10077	22478		1.2	1.3E-01	8363940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA
10137	22538	35506	0.93	1.3E-01	AW851599.1	EST_HUMAN	MR2-CT0222-201099-001-e01 CT0222 Homo sapiens cDNA
10298	24655	35663	1.29	1.3E-01	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
10431	22863		1.97	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA
11016	23443		2.52	1.3E-01	6871745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11343	23707	36762	3.4	1.3E-01	BE27949.1	EST_HUMAN	601158052F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3504804 5'
11825	24078	30988	1.73	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3868003 5'
11999	24165		3.19	1.3E-01	AJ242790.1	NT	Gallus gallus sox1 gene for lympholactin, exons 1-3
12373	24420		1.55	1.3E-01	AB026828.1	NT	Ephydrata fluviatilis mRNA for eALK-6, complete cds
12403	24438		1.77	1.3E-01	AW001114.1	EST_HUMAN	wu24d09.x1 Soares Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:060287 O60287 KIAA0539 PROTEIN.;
398	13014	26437	12.26	1.2E-01	AI421744.1	EST_HUMAN	tf39b02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2086339 3' similar to gb:U05760_rna1
441	12619		1.2	1.2E-01	U86912.1	NT	ANNEXIN V (HUMAN);
564	13135		3.63	1.2E-01	AF039442.1	NT	Dictyostelium discoideum ORF DG1016 gene, partial cds
							Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1409	13943	26399	3.93	1.2E-01	AU149148.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1409	13943	26400	3.93	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1415	13949		1.43	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cdA Homo sapiens cDNA clone cdAAJB11 5'
1534	14060		1.59	1.2E-01	AA897474.1	EST_HUMAN	aa897474.1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460564 3' similar to TR:Q16671 Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR.
1639	14170	26640	0.95	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1655	14180	26658	2.37	1.2E-01	A1285402.1	EST_HUMAN	q16909.x1 NCI CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
1756	14283		10.87	1.2E-01	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2511	15012	27523	0.89	1.2E-01	AW986568.1	EST_HUMAN	QV3-BN0046-220300-123-f10 BN0046 Homo sapiens cDNA
2682	15174	27685	2.84	1.2E-01	A1623388.1	EST_HUMAN	ts18g07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] contains element PTR5 repetitive element.
2798	15355	27775	1.49	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2855	15410	27831	1.76	1.2E-01	A1720470.1	EST_HUMAN	es80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:U05095
2898	15443	27866	3.38	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
2961	15519	27937	0.89	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3189	15742	28164	2.28	1.2E-01	AW370688.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3218	15770		0.81	1.2E-01	U87600.1	NT	QV1-BT0259-281089-021-d05 BT0259 Homo sapiens cDNA
3328	15875	28298	2.33	1.2E-01	AW503374.1	EST_HUMAN	Methanococcus jannaschii section 142 of 150 of the complete genome
3454	15908		0.78	1.2E-01	Z99118.1	NT	U1-HF-BNO-akw-a-10-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078427 5'
3502	16045	28466	0.85	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3502	16045	28467	0.85	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3600	15908		0.89	1.2E-01	Z99118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
4198	16723	29110	2.16	1.2E-01	Z64255.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
4198	16723	29111	2.16	1.2E-01	Z94255.1	NT	P.claridii mRNA; repeat region (ID 2MRT7)
4333	16855	29240	0.64	1.2E-01	M15861.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4772	17286	29871	0.98	1.2E-01	Z48183.1	NT	P.claridii mRNA; repeat region (ID 2MRT7)
5209	17712		1.01	1.2E-01	P16466	SWISSPROT	HEMOLYSIN PRECURSOR
5288	17788	30163	1.59	1.2E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
5434	17929	30282	1.02	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
5434	17929	30283	1.02	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
5483	17978	30322	0.88	1.2E-01	AW892592.1	EST_HUMAN	CN3-NN0004-100300-111-d08 NN0004 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5500	18091	30332	0.7	1.2E-01	AA744369.1	EST_HUMAN	ny63e04.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5553	18143	30503	0.76	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5563	18152	30513	2.63	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares_parenchymal_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5624	18211	30612	1.31	1.2E-01	Z89286.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5767	18348	30805	1.03	1.2E-01	Z48234.1	NT	M.domesica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6514	19067	31810	2.1	1.2E-01	BE620946.1	EST_HUMAN	601493618F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6569	19120	31863	0.8	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6626	19175	31929	2.39	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6698	19243	31994	1.57	1.2E-01	M26926.1	NT	Mouse galactosyltransferase mRNA, complete cds
6770	19313	32080	0.58	1.2E-01	AA747635.1	EST_HUMAN	mx85c01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'
7011	19547	32333	1.45	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158386 5'
7184	19898	32723	0.49	1.2E-01	AF285739.1	NT	JC Virus agnoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7435	19939	32773	0.42	1.2E-01	H47799.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193769 5'
7435	19939	32774	0.42	1.2E-01	H47799.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193769 5'
8121	20545	33422	0.74	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp78, drbp78 gamma, drbp78 alpha and ILF3)
8391	20805	33703	0.68	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8391	20805	33704	0.68	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8459	20872	33772	0.42	1.2E-01	BE728489.1	EST_HUMAN	601561036F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831585 5'
8459	20872	33773	0.42	1.2E-01	BE728489.1	EST_HUMAN	601561036F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831585 5'
8555	20990		1.45	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-280300-002-f09 BN0137 Homo sapiens cDNA
8604	21039	33944	3.19	1.2E-01	A1913753.1	EST_HUMAN	wc89g03.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II:
8930	21364		11.32	1.2E-01	AW083652.1	EST_HUMAN	xc49d07.x1 NCL_CGAP_E502 Homo sapiens cDNA clone IMAGE:2687697 3' similar to gb:M13462 LAMIN A (HUMAN);
8943	21378		4.5	1.2E-01	AF063772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8968	21401	34313	0.98	1.2E-01	J03936.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8968	21401	34314	0.98	1.2E-01	J03936.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
9071	21603		1.08	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
9128	21560		1.65	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
9747	22115	35043	1.87	1.2E-01	X77891.1	NT	S.cerevisiae HXT5 gene

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10037	22439	35386	1.6	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
10497	22947	35927	2.27	1.2E-01	BF314481.1	EST_HUMAN	601800763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
10689	23109		2.06	1.2E-01	D28184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
10846	23279		2.47	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
10927	23369		2.15	1.2E-01	BF314481.1	EST_HUMAN	601800763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11019	23446	38465	3.72	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17
11164	23544	38583	1.64	1.2E-01	9894174	NT	Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4 (B4GALT4), mRNA
11580	23921		2.08	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFB12 3'
11950	24163		2.86	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12034	24909	30453	3.38	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12156	24284		1.9	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntactin gene, partial cds
12158	13135		9.8	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12278	24371		2.29	1.2E-01	X53981.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
12354	24922	30480	2.04	1.2E-01	BE081418.1	EST_HUMAN	QV4-BT0234-11189-031-g10 BT0234 Homo sapiens cDNA
12377	24422	30897	7.72	1.2E-01	AI299903.1	EST_HUMAN	gn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12401	24436		3.12	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12405	24839		8.89	1.2E-01	O66433	SWISSPROT	CYCLIN T
12435	24468	30872	1.72	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 83 of the complete chromosome
581	13162	25558	1.07	1.1E-01	AI561003.1	EST_HUMAN	tn18d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3'
634	13198	25605	1.32	1.1E-01	AA569006.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_ma1 HEME OXYGENASE 1 (HUMAN);
1080	13626	26068	1.92	1.1E-01	BF697308.1	EST_HUMAN	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4288771 5'
1112	13659		1.81	1.1E-01	AL181580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1189	15303	26173	4.88	1.1E-01	AW972158.1	EST_HUMAN	EST394142 MAGE resequences, MAGL Homo sapiens cDNA
1282	13818	26271	1.9	1.1E-01	D64004.1	NT	Synchocystis sp. PCC6803 complete genome, 23/27, 2868767-3002956
1545	14076	26637	2.32	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2208	14718		1.71	1.1E-01	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
2445	15270		3.86	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2481	14892		0.9	1.1E-01	AW821909.1	EST_HUMAN	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2992	15547	27959	0.83	1.1E-01	F03295.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3314	15892		1.71	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3399	19546	28357	2.7	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627068 5'
3429	19973	28386	1.38	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3487	16011	28433	0.7	1.1E-01	R96946.1	EST_HUMAN	y62g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains Alu repetitive element;
3574	16116	28531	0.98	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
3698	16238		0.67	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3706	16247	28651	1.29	1.1E-01	X62708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4127	16656	29039	1.21	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4127	16656	29040	1.21	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4269	16784		10.12	1.1E-01	AF167063.1	NT	Drosophila melanogaster Klaricht protein (klar) mRNA, complete cds
4303	16828	29217	0.72	1.1E-01	AW802058.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4889	17400	29771	1.88	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
5125	16662		0.69	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex
5203	17706		1.18	1.1E-01	AF002726.1	NT	Trigona neophraga cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5839	18517		1.4	1.1E-01	AA747216.1	EST_HUMAN	nx76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
6015	18589	31275	1.53	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
6054	18626	31317	0.97	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6090	18659	31352	0.79	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186818 5'
6090	18659	31353	0.79	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186818 5'
6122	18691	31388	1.9	1.1E-01	X88851.1	NT	S.pombe ste8 gene encoding protein kinase
6159	18727	31430	4.77	1.1E-01	M88533.1	NT	Providencia rettgeri penicillin G amidase gene
6330	18886	31619	1.49	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6362	18910	31643	1.52	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
6372	18930	31666	8.4	1.1E-01	AW853598.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
6763	19306	32071	0.63	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6771	19314	32081	1.38	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6818	19359	32136	0.82	1.1E-01	AL216307.1	EST_HUMAN	q076d06.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6955	19502	32280	3.57	1.1E-01	O96935	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME)
7076	19610		2.82	1.1E-01	AF032922.1	NT	Homo sapiens syntroph 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
7180	19893	32718	2.53	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7478	19682	32478	0.64	1.1E-01	AE002166.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7478	19682	32479	0.64	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7631	24989		0.71	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050653 5'
7765	24636	33072	1.05	1.1E-01	AP000008.1	NT	Pyrococcus horikoshii OT3 genome DNA, 1166001-1485000 nt. position (6/7)
8046	20478	33351	9.11	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
8046	20478	33352	9.11	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
8105	20631	33408	0.6	1.1E-01	AA959508.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
8185	20608	33498	2.33	1.1E-01	P41087	SWISSPROT	TRAB PROTEIN
8195	20617		0.44	1.1E-01	AB015294.1	NT	Schizosaccharomyces pombe gene for Alp13, complete cds
8234	20653		0.71	1.1E-01	Z14098.1	NT	B. subtilis gene encoding hypothetical polyketide synthase
8235	20654	33545	2.84	1.1E-01	AA788784.1	EST_HUMAN	ah31b06.s1 Soares parathyroid tumor NIH-PA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
8414	20828	33728	0.58	1.1E-01	BE782290.1	EST_HUMAN	CHROMOGRANIN A PRECURSOR (HUMAN);
8608	21043	33948	1.01	1.1E-01	U67482.1	NT	601470055F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873229 5'
8783	21217	34121	1.76	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8783	21217	34122	1.78	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8817	21251	34157	1.15	1.1E-01	X91233.1	NT	nh04g10.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8847	21281		0.93	1.1E-01	AW817918.1	EST_HUMAN	H. sapiens IL15 gene
8891	21325	34237	1.81	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-409 ST0270 Homo sapiens cDNA
9228	21660	34569	1.72	1.1E-01	U02482.1	NT	DKFZp547P194_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547P194 5'
9288	21720	34630	0.94	1.1E-01	AI807474.1	EST_HUMAN	Pedococcus acidifaciens H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
9372	21804	34713	2.7	1.1E-01	AA192153.1	EST_HUMAN	wf48c01.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;
9372	21804	34714	2.7	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9450	21881	34800	2.65	1.1E-01	TT2875.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9635	22050		1.1	1.1E-01	BE142305.1	EST_HUMAN	yd19h03.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9690	22102		2.69	1.1E-01	BF085149.1	EST_HUMAN	CM3-HT0142-271089-028-g11 HT0142 Homo sapiens cDNA
10181	22582		2.11	1.1E-01	R80590.1	EST_HUMAN	MR2-GN0027-040800-005-a08 GN0027 Homo sapiens cDNA
10286	22687	35630	1.38	1.1E-01	U60529.1	NT	y96a09.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:147084 3'
10588	15547	27959	1.89	1.1E-01	F03265.1	EST_HUMAN	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10700	23139		3.31	1.1E-01	AF169032.1	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
							Cerassius auratus activin beta A precursor, mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10745	23183		1.97	1.1E-01	Q28279	SWISSPROT	CGMP-GATED CATION CHANNEL PROTEIN (CYCLIC NUCLEOTIDE GATED CHANNEL, PHOTORECEPTOR) (CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 1) (CNG CHANNEL 1) (CNG-1) (CNG1)
10825	23281	36246	3.31	1.1E-01	R23708.1	EST_HUMAN	yf35f12.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element:
10883	23412	36424	2.79	1.1E-01	Z11910.1	NT	Z.mobilis tgf and lig genes encoding tRNA guanine transglycosylase and DNA ligase
10983	23412	36425	2.79	1.1E-01	Z11910.1	NT	Z.mobilis tgf and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11075	23500	36528	4.61	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11516	23874	36954	1.78	1.1E-01	AF207568.1	NT	Brassica napus 4-coumarate:CoA ligase (4CL-C) gene, partial cds
11686	23992		1.25	1.1E-01	AA192163.1	EST_HUMAN	zp83b12.r1 Stralagene muscle 837209 Homo sapiens cDNA clone IMAGE:627743 5'
11805	24067		3.25	1.1E-01	BE787023.1	EST_HUMAN	RG2-NT0112-120600-014-103 NT0112 Homo sapiens cDNA
12097	24698		2.18	1.1E-01	BE974558.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
12288	24375		1.28	1.1E-01	BE969888.2	EST_HUMAN	601660908R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915744 3'
12537	24528	30861	5.51	1.1E-01	BF239753.1	EST_HUMAN	601806350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1232	13771		1.21	1.0E-01	O82855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1305	13840	28289	2.45	1.0E-01	A1985499.1	EST_HUMAN	ws08d01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13 MER7 repetitive element:
1424	13957	28413	2.59	1.0E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2392	14898	27414	3.9	1.0E-01	AW461365.1	EST_HUMAN	UIH-B13-alc-d-07-0-ULe1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3493	16036	28457	1.14	1.0E-01	BF033891.1	EST_HUMAN	601456301F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3859849 5'
3717	16257	28661	0.81	1.0E-01	BF239818.1	EST_HUMAN	601806489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3987	16502	28910	3.03	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4432	16952	29340	1.3	1.0E-01	AE002265.2	NT	Chlamydomonas reinhardtii AR39, section 91 of 94 of the complete genome
4591	17107		0.88	1.0E-01	A1792349.1	EST_HUMAN	en32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4783	17277	29660	1.32	1.0E-01	U60450.1	NT	Drosophila melanogaster tyrosine Kinase p45 isoform (fer) mRNA, complete cds
4998	17508	29882	2.31	1.0E-01	AW952344.1	EST_HUMAN	EST364414 IMAGE resequences, MAGB Homo sapiens cDNA
5295	17795	30182	5.98	1.0E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
5329	17828	30187	0.82	1.0E-01	BE389100.1	EST_HUMAN	601286669F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613562 5'
5426	17921		5.14	1.0E-01	AV763960.1	EST_HUMAN	AV763960 MDS Homo sapiens cDNA clone MDSBQB11 5'
5574	18102		10.06	1.0E-01	W89490.1	EST_HUMAN	Zh62h04.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5874	18259		0.57	1.0E-01	X54015.1	NT	X.campestis genes for sensor and regulator protein
5757	18338		0.44	1.0E-01	Q36860	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
6168	18736		1.22	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6328	18887	31618	14.41	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6685	19213	31861	1.05	1.0E-01	AA481879.1	EST_HUMAN	z441910.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756258 3' similar to contains L1.13 L1 repetitive element;
6679	19227	31976	0.6	1.0E-01	AA406039.1	EST_HUMAN	z467c12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'
7447	19950		1.69	1.0E-01	R23821.1	EST_HUMAN	yf34h06.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
8287	20703		2.59	1.0E-01	Y12488.1	NT	M.musculus whn gene
8411	20825	33722	0.63	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8411	20825	33723	0.63	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8997	21430		1.08	1.0E-01	AW189797.1	EST_HUMAN	x09b01.x1 NCI CGAP U4 Homo sapiens cDNA clone IMAGE:2875689 3' similar to gb:U17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.13 TAR1 repetitive element;
9484	21895	34817	1.11	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synapton mRNA, complete cds
9696	22108		2.2	1.0E-01	M76729.1	NT	Human pro-alpha-1(V) collagen mRNA, complete cds
9730	22057		3.16	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9808	22310	35254	1.89	1.0E-01	BF240154.1	EST_HUMAN	60180558F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
9992	22394	35345	9.84	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1578 protein, partial cds
9992	22394	35346	9.84	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1578 protein, partial cds
10146	22547		0.9	1.0E-01	AW957425.1	EST_HUMAN	EST369615 IMAGE resequences, IMAGE Homo sapiens cDNA
10262	22663	35625	1.14	1.0E-01	BE792750.1	EST_HUMAN	60158460F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3639098 5'
10808	23244	36227	2.77	1.0E-01	BF242846.1	EST_HUMAN	601877703F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4105089 5'
10808	23244	36228	2.77	1.0E-01	BF242846.1	EST_HUMAN	601877703F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4105089 5'
11154	23535	36573	5.76	1.0E-01	BE790543.1	EST_HUMAN	601582559F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3636734 5'
11276	23843		2.42	1.0E-01	AF000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Salmonella) Inserted region, substrain:RIMD 0609952
11518	23876	36957	3.03	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLC8PG01 3'
11618	23876	36958	3.03	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLC8PG01 3'
11791	24426		3.86	1.0E-01	BE537719.1	EST_HUMAN	60106554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12048	24216		1.84	1.0E-01	X00954.1	NT	Drosophila melanogaster ftz gene
12350	24900		2.85	1.0E-01	U52691.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PTT) mRNA, complete cds
12393	24426		3.48	1.0E-01	BE537719.1	EST_HUMAN	60106554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12431	24495		1.54	1.0E-01	BE159905.1	EST_HUMAN	QV4-HT0401-211289-064-g03 HT0401 Homo sapiens cDNA
12448	24870		18.35	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12514	24516		8.09	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2738	15228	27740	3.62	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2746	15235	27748	1.45	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2745	15235	27749	1.45	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3228	15780	28197	1.11	9.9E-02	AF098810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
3985	16500	28908	0.66	9.9E-02	A821637.1	EST_HUMAN	zu45c03.x5 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740932 3'
4727	17243	28025	0.91	9.9E-02	BE674249.1	EST_HUMAN	7d77c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'
7263	18768	32576	0.82	9.9E-02	BE613498.1	EST_HUMAN	601504252F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906084 5'
7386	18055	30394	7.8	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
9518	21981	34907	1.61	9.9E-02	6765111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
580	13151		1.61	9.9E-02	X56338.1	NT	O. sativa RAmY3C gene for alpha-amylase
3105	15858	28069	3.98	9.9E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4241	16768	29151	12.98	9.9E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
4241	16768	29152	12.98	9.9E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
7982	20417		1.02	9.9E-02	X54133.1	NT	Human HP1TP delta mRNA for protein tyrosine phosphatase delta
9516	21978		1.14	9.9E-02	M61943.1	NT	Human laminin B1 chain gene, exon 26
11211	22863	35637	1.76	9.9E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3864287 5'
11755	24036		1.63	9.9E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mept), mRNA
1803	14134		0.99	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2164	14876	27201	1.81	9.7E-02	BE168560.1	EST_HUMAN	QV1-HT0518-070300-095-a04 HT0518 Homo sapiens cDNA
3997	16531		3.99	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5599	18187	30551	0.7	9.7E-02	AF098189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5599	18187	30552	0.7	9.7E-02	AF098189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6318	18878	31605	1.91	9.7E-02	AW954473.1	EST_HUMAN	EST368548 MAGC resequences, MAGC Homo sapiens cDNA
7759	20203	33085	4.78	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2997771 to 3213410
8620	21055	33982	1.33	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8620	21055	33963	1.33	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9263	21685	34596	1.25	9.7E-02	A1853984.1	EST_HUMAN	wx78b06.x1 NCI_CGAP_OV48 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:U62851_ma1
10989	23398		1.85	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
4397	16889	29270	6.95	9.6E-02	Z32886.2	NT	Mus musculus ligandin (Lgln) mRNA, partial cds
5103	17612	28674	1.2	9.6E-02	AW966230.1	EST_HUMAN	Protein mirabilis fibrillar operon, strain HI4320
5441	17836		5.6	9.6E-02	A1708160.1	EST_HUMAN	EST378303 MAGC resequences, MAGI Homo sapiens cDNA
							es38d02.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318459 3'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9414	19971		3.18	9.6E-02	BE910039.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8500	20912		0.53	9.0E-02	8678753	NT	Mus musculus lymphocyte antigen 78 (L78), mRNA
9726	22148	35079	0.86	9.6E-02	AV887898.1	EST_HUMAN	AV887898 GKC Homo sapiens cDNA clone GKCAAH02 5'
9947	22349		0.86	9.6E-02	BE94895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10066	22467	35424	1.25	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10066	22467	35425	1.25	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10149	22550	35516	1.69	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10149	22550	35517	1.69	9.6E-02	AB013986.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10216	22618	35584	3.49	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
10526	22973	35953	7.85	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
11441	23801	36859	1.89	9.6E-02	AA925755.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
12421	24459		1.85	9.6E-02	H14599.1	EST_HUMAN	zu91g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
4118	16648	29034	1.72	9.6E-02	AW992395.1	EST_HUMAN	ym18h03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
5272	17773	30140	10.23	9.6E-02	U63374.1	NT	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5934	18512	31188	0.83	9.6E-02	P51854	SWISSPROT	Lycopodium obscurum polygalacturonase isoenzyme 1 beta subunit gene, complete cds
7526	19976	32811	0.48	9.6E-02	AA780728.1	EST_HUMAN	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7764	20208	33071	5.3	9.6E-02	AB003473.1	NT	ac88a06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:367736 3'
8084	20512	33392	8.48	9.6E-02	AL161538.2	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
8237	18512	31198	0.74	9.6E-02	P51854	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
8547	20982	33860	2.34	9.6E-02	BF035861.1	EST_HUMAN	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8547	20982	33861	2.34	9.6E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10470	22920	35898	3.39	9.6E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10470	22920	35899	3.39	9.6E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1808	14331	26824	2.72	9.4E-02	BF071063.1	EST_HUMAN	602160882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281917 5'
3888	16423	28828	5.87	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
6845	19193	31945	0.78	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8118	20543	33420	0.61	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and p35 genes, partial cds
9070	21502		2.68	9.4E-02	Z46863.1	NT	Acinetobacter sp. oysD, cobQ, cobM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
10710	20543	33420	2.47	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and p35 genes, partial cds
11633	24769		3.38	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
12592	24568	30850	1.41	9.4E-02	U27699.1	NT	Human pepHBT-1 betaine-GABA transporter mRNA, complete cds
2944	15499		1.83	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
2988	15543		6.84	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3217	15769	28190	1.88	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4169	16698	29084	4.2	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4169	16698	29085	4.2	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4487	17015		2.27	9.3E-02	U88092.1	NT	Ehrlichia sensu lato operon: GroES (ESGroES) and GroEL (ESGroEL) genes, complete cds
4786	17300		1.98	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HITFAUA06 5'
5174	17678	30039	0.95	9.3E-02	U38804.1	NT	Porphyria purpurea chloroplast, complete genome
5831	18509		0.69	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8465	20878	33777	0.47	9.3E-02	M75994.1	NT	Human hepatocyte growth factor gene exon 18, 3' and
8483	20898	33791	0.62	9.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9843	22246	35182	2.67	9.3E-02	BE982631.2	EST_HUMAN	601655989R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3655981 3'
10171	22572	35538	3.25	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10171	22572	35539	3.25	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10266	22666		3.96	9.3E-02	AW206117.1	EST_HUMAN	U1-H-B11-efx-h-05-0-J1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
11912	24718		1.75	9.3E-02	AJ249850.1	NT	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit
12314	24748		17.31	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
12540	24798						Mus musculus major histocompatibility locus class II region; Fas-binding protein Daax (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr-
240	12841	26252	1.95	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
240	12841	25253	6.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
240	12841	25254	6.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2133	14646		1.31	9.2E-02	R54166.1	EST_HUMAN	y88107.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5'
3136	16689	28108	4.45	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3269	16820	28236	0.72	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.s1 NCL_CGAP_Oc3 Homo sapiens cDNA clone IMAGE:826138 3'
3578	16120		1.27	9.2E-02	6756215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4255	16780		1.19	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region
4327	16849		1.41	9.2E-02	BE299722.1	EST_HUMAN	600944385F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860176 5'
4684	17200	26578	1.3	9.2E-02	X96402.1	NT	G.gallus M1a-CK gene
8841	21076	33984	2.07	9.2E-02	T49920.1	EST_HUMAN	ya89c09.r1 Stragene placenta (#837225) Homo sapiens cDNA clone IMAGE:89808 5' similar to similar to gb-X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8780	21194	34096	2.2	9.2E-02	X95258.1	NT	H.vulgaris xylose isomerase gene
11422	23793	36844	1.78	9.2E-02	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
12517	24976		2.4	9.2E-02	11466872	NT	Podospira anserina mitochondrion, complete genome
440	12618	25008	3.42	9.1E-02	X77665.1	NT	O. cuniculus k12 keratin gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3669	16209		0.99	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA
4520	17038	29418	1.77	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
6005	18679	31268	1.26	9.1E-02	AF129766.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7770	24990		0.55	9.1E-02	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7894	20303	33168	13.59	9.1E-02	AW180658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
8212	20632	33521	1.15	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 417
8264	20671	33561	0.83	9.1E-02	U36073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
9285	21727	34835	1.18	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10323	22723		2.54	9.1E-02	T02894.1	EST_HUMAN	FB18F10 Fetal brain, Strategene Homo sapiens cDNA clone FB18F10 3'end
10346	22748	35713	1.04	9.1E-02	S74059.1	NT	Tg618=Cy1 actin [Tripneustes gratilis=sea urchins, embryos, Genomic, 5275 nt]
11570	23915		2.09	9.1E-02	9633494	NT	Bacteriophage Mu, complete genome
11821	24908		1.89	9.1E-02	AA179801.1	EST_HUMAN	zp38h12.s1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:811783 3' similar to
11901	24126		1.59	9.1E-02	AF052895.1	NT	SW:TRT3_HUMAN P46378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12404	24742		7.91	9.1E-02	AJ291390.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
						NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
							FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
765	13325	25755	4.51	9.0E-02	P15328	SWISSPROT	h39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
1842	14173	26842	6.78	9.0E-02	BE220482.1	EST_HUMAN	IL5-UM0067-240300-050-h06 UM0067 Homo sapiens cDNA
2275	14783	27305	2.8	9.0E-02	AW801364.1	EST_HUMAN	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
2761	15251	27768	2.84	9.0E-02	AF138522.1	NT	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
2761	15251	27767	2.94	9.0E-02	AF138522.1	NT	Dictyostellium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
3309	15857	28277	1.03	9.0E-02	AF279135.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4318	18841	28232	0.61	9.0E-02	S88757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4318	18841	28233	0.61	9.0E-02	S88757.1	NT	Plasmidium falciparum P-type ATPase 3 gene
4711	17227	28611	1.92	9.0E-02	X65740.2	NT	za68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to
6298	18860	31562	11.35	9.0E-02	W58037.1	EST_HUMAN	PIR:S62171 S52171 small G protein - human ;
7094	19627		1.08	9.0E-02	BF062651.1	EST_HUMAN	7h63d03.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element;

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7148	19861	32679	0.83	9.0E-02	R02805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
12231	24339		1.48	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CasD (casD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1466	13999	28463	1.24	8.9E-02	BF701593.1	EST_HUMAN	602128030F2 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4285951 5'
1468	13999	28484	1.24	8.9E-02	BF701593.1	EST_HUMAN	602128030F2 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4285951 5'
2285	14792	27312	7.53	8.9E-02	BE153572.1	EST_HUMAN	PMO-HT0339-251189-003-d01 HT0339 Homo sapiens cDNA
4215	16740		1.92	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFib2 protein (AtranFib2) gene, partial cds
4680	17188	29572	4.15	8.9E-02	AA424887.1	EST_HUMAN	2w03d04.s1 Soares_NHMP_u_S1 Homo sapiens cDNA clone IMAGE:768199 3'
6137	18706	31403	2.44	8.9E-02	AW452122.1	EST_HUMAN	U1-H-B13-elo-f-08-Q-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:3068294 3'
6137	18706	31404	2.44	8.9E-02	AW452122.1	EST_HUMAN	U1-H-B13-elo-f-08-Q-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:3068294 3'
6154	18722	31426	3.41	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
7637	20084	32838	1.77	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]
8073	20502		2.18	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6PA20F8
8668	21103	34006	0.93	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
9068	21500	34409	4.35	8.9E-02	AA308319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
11632	24746		1.52	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
11763	24060		4.35	8.9E-02	BF686918.1	EST_HUMAN	602128082F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4286180 5'
11863	24163		1.35	8.9E-02	6680220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hlat1), mRNA
1408	13940	26396	1.43	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3913	16448	28555	0.84	8.8E-02	AA289128.1	EST_HUMAN	EST11695 Uterus Homo sapiens cDNA 5' end
4047	16579		5.19	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII-130) (TAFII30)
4256	16781		1.35	8.8E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4321	16844		0.91	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
5394	17891		1.69	8.8E-02	P14548	SWISSPROT	CYTCHROME C OXIDASE POLYPEPTIDE III
6476	17971	30316	5.87	8.8E-02	7019568	NT	Homo sapiens vacuolar sorting protein 4 (VPS4), mRNA
8057	20488		0.76	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
9332	21784	34670	2.07	8.8E-02	AA151872.1	EST_HUMAN	zr09a05.s1 Stratiagene cdon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
10898	23330	36331	4.28	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3535648 5'
10898	23330	36332	4.28	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3535648 5'
11032	23459	36479	4.86	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3691	16231	28640	3.95	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3691	16231	28641	3.95	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4756	17270	28653	1.4	8.7E-02	AF178638.1	NT	Mus musculus JNK Interacting protein-3a (Jip3) mRNA, complete cds
5243	17744		1.15	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5567	18155	30517	6.73	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5567	18155	30518	5.73	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
7240	19851	32671	0.8	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7240	19851	32672	0.8	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7472	19678	32472	0.67	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
10496	22846		3.45	8.7E-02	L04758.1	NT	Cyclolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11859	24108		2.68	8.7E-02	X17116.1	NT	Homo DNA for Immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12066	24224		1.75	8.7E-02	6879057	NT	Mus musculus ridogen 2 (Nid2), mRNA
1285	13820	28272	7.28	8.6E-02	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2162	14685	27188	3.2	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3145	16688	28116	2.75	8.6E-02	L05488.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3644	16184		4.11	8.6E-02	AF153362.1	NT	Dicystostellium discoideum adenylyl cyclase (acrA) gene, complete cds
3781	16319		0.82	8.6E-02	U29187.1	NT	Mus musculus long incubation prion protein (Prnpb) and prion-like protein (Prnd) genes, complete cds
5297	17797		3.82	8.6E-02	L13419.1	NT	Chromatium vinosum tetraheme cytochrome c gene, 3' end, bacterial ankryrin homologue, flavocytochrome o
5476	17970	30315	1.51	8.6E-02	BF358207.1	EST_HUMAN	heme subunit fccA (complete cds), and flavin subunit, fccB (3' end)
6402	18959	31084	4.75	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6707	19254	32007	1.7	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6707	19254	32008	1.7	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
8059	20525	33405	1.08	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8584	21019	33918	1.2	8.6E-02	5730068	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8584	21019	33919	1.2	8.6E-02	5730068	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8723	21158		0.9	8.6E-02	U00168.1	NT	Dicystostellium discoideum proteasome subunit C2 homolog PTC (ptc) gene, complete cds
8857	22260	35188	1.09	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9880	22283		1.02	8.6E-02	AW682153.1	EST_HUMAN	h220c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872846 3'
10151	22552	35619	0.89	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
11015	23442	36460	3.52	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11015	23442	36461	3.52	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11188	22840	35812	27.94	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11324	23688	36739	2.82	8.6E-02	AF283660.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2280	14803	27321	2.37	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5938	18516	31201	0.69	8.5E-02	AA985491.1	EST_HUMAN	oq83b07.s1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1592917 3' similar to gb:K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5979	18555		2.4	8.5E-02	P08089	SWISSPROT	MPTROTEIN, SEROTYPE 0 PRECURSOR
6315	18876	31601	7.27	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
9074	21606	34415	2.14	8.5E-02	6764779	NT	Mus musculus myosin XV (Myo15), mRNA
9820	22322	35269	3.77	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
9920	22322	35270	3.77	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10365	22785	35733	0.84	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
10834	23368		0.75	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
10946	23377	36386	5.86	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12290	24674		1.98	8.5E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
12478	24493		2.53	8.5E-02	AA362834.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2605	18343	27617	3.79	8.4E-02	W69330.1	EST_HUMAN	zd44e11.t1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5155	17659		2.63	8.4E-02	X01472.1	NT	Drosophila melanogaster cople-like element 17.6
5259	17760	30128	1.12	8.4E-02	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
5259	17760	30129	1.12	8.4E-02	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
5565	18153	30515	11.11	8.4E-02	BE287153.1	EST_HUMAN	601180436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
7059	19593	32387	1.63	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8682	21087	33995	7.15	8.4E-02	BE095074.1	EST_HUMAN	CN3-BT0780-260400-162-d08 BT0780 Homo sapiens cDNA
9246	21678	34587	0.84	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
10281	22682	35644	1.78	8.4E-02	A735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:088312
11776	24051	31023	1.39	8.4E-02	R79408.1	EST_HUMAN	Y83H12.t1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:145895 5'
3595	19127	28540	7.64	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3615	19155	28563	2.3	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3615	19155	28564	2.3	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4320	16843		0.62	8.3E-02	M54984.1	NT	C.hummi A2b region open reading frame, complete cds
5415	17911	30262	1.72	8.3E-02	BE546188.1	EST_HUMAN	601071212F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3457202 5'
6582	19133	31879	0.84	8.3E-02	A1942338.1	EST_HUMAN	w078f11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
6899	19246	31697	3.16	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
8818	21053	33959	3.51	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dnp2) mRNA, complete cds
8642	21077		1.57	8.3E-02	AA865285.1	EST_HUMAN	cg88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.L1 L1 L1
8850	21284		1.59	8.3E-02	AA987873.1	EST_HUMAN	repetitive element ;
9722	22145	35072	1.4	8.3E-02	AW583603.1	EST_HUMAN	cc81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
9731	22058		2.09	8.3E-02	AL161895.2	NT	la06h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
11876	24911		1.96	8.3E-02	BE98458.1	EST_HUMAN	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE ;
1411	13945		12.99	8.2E-02	Y08170.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
1524	14056	26519	2.98	8.2E-02	AF167077.2	NT	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929893 5'
3035	15590		2.13	8.2E-02	AL163206.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
3808	16345		1.53	8.2E-02	AL161498.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
4021	16554	28951	1.08	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4301	16826	29212	7.55	8.2E-02	P48960	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4301	16826	29214	7.55	8.2E-02	P48960	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
5211	17714	30079	3.64	8.2E-02	U76009.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5588	18176	30541	1.66	8.2E-02	BE97030.1	EST_HUMAN	LEUCOCYTE ANTIGEN CD97 PRECURSOR
7448	18951	32786	3.17	8.2E-02	AF309555.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
8282	20699		0.56	8.2E-02	AV743341.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
9193	21625	34635	3.04	8.2E-02	AW875126.1	EST_HUMAN	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
9764	22167	35100	6.27	8.2E-02	X04197.1	NT	AV743341 CB Homo sapiens cDNA clone GBLANF07 5'
9875	22278	35218	2.07	8.2E-02	BE254318.1	EST_HUMAN	RC2-PT0004-031289-011-d05 PT0004 Homo sapiens cDNA
11882	24118	31003	6.33	8.2E-02	AE002246.2	NT	Beet necrotic yellow vein virus RNA-2
12317	24664		3.58	8.2E-02	AF275360.1	NT	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355598 5'
1523	14055	26518	1.04	8.1E-02	AB017138.1	NT	Chlamydia pneumoniae AR39, section 73 of 84 of the complete genome
5039	17549	28919	0.92	8.1E-02	BF343921.1	EST_HUMAN	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5039	17949	28920	0.92	8.1E-02	BF343921.1	EST_HUMAN	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
							602015608F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151640 5'
							602015608F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151640 5'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptar
6033	18607	31295	1.09	8.1E-02	AE004008.1	NT	Xylella fastidiosa, section 162 of 228 of the complete genome
6713	19259	32015	0.96	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7641	20088		0.83	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
8100	20528		1.13	8.1E-02	AI682681.1	EST_HUMAN	wd8608.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
9978	22380		1.77	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
11255	23621	36669	3.13	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5	15274	25014	6	8.0E-02	AW954653.1	EST_HUMAN	EST366723 MAGE resequences, MAGC Homo sapiens cDNA
960	13512	25954	0.75	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1695	15318	26704	11.91	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1695	15318	26705	11.91	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1804	14386	26877	2.68	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2268	14776	27297	7.07	8.0E-02	D90915.1	NT	Synechocystis sp. PCC8803 complete genome, 1727, 2137268-2267259
2268	14776	27288	7.07	8.0E-02	D90915.1	NT	Synechocystis sp. PCC8803 complete genome, 1727, 2137268-2267259
2365	14870		5.48	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2779	13662	26102	0.89	8.0E-02	M23449.1	NT	Dictyoselium discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2853	16408	27828	0.73	8.0E-02	AL445087.1	NT	Thermoplasma acidophilum complete genome, segment 6/5
3824	16361	28761	0.89	8.0E-02	AW966118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
4086	16617		0.61	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4871	17383		7.19	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
4895	17505	29881	0.62	8.0E-02	M28074.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene.s
5369	17857	30216	2.73	8.0E-02	S78215.1	NT	complete cds, and small nuclear RNAs (uRNAs)
5365	17863	30222	0.77	8.0E-02	AW207037.1	EST_HUMAN	protein phosphatase 1 alpha [rats, striatum, mRNA, 1404 nt]
6018	18592	31278	0.45	8.0E-02	AW851139.1	EST_HUMAN	UH-HB1-aid-4-10-0-UI.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721547 3'
6181	18748	31448	4.08	8.0E-02	AF275948.1	NT	EST363209 MAGE resequences, MAGA Homo sapiens cDNA
7624	18748	31448	1.72	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8722	21157	34084	3.52	8.0E-02	AL114983.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
11913	24136	30870	4.24	8.0E-02	AJ005375.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
12535	16617		2.14	8.0E-02	4503034	NT	Drosophila arena hunchback region
2081	14595	27114	2.23	7.9E-02	BE250008.1	EST_HUMAN	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2834	15489	27910	12.46	7.9E-02	AI582029.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5'
							60S RIBOSOMAL PROTEIN L38 (HUMAN);

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3800	16337	28739	4.19	7.9E-02	AF030694.2	NT	Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), O38 (o38), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG9 (cg9), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds
3857	16393	28794	4.71	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3857	16393	28795	4.71	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4869	17381		1.31	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
4979	17490	29887	1.22	7.9E-02	L24757.1	NT	Human bone sialoprotein (BSP) gene, exons 2, 3 and 4
4988	17498		16.84	7.9E-02	AW081738.1	EST_HUMAN	xb70a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581626 3'
5605	18193		0.44	7.9E-02	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel α
7087	19601		1.28	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
8654	21089	33998	3.28	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds
10056	22457	35407	6.05	7.9E-02	A1081644.1	EST_HUMAN	cu63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
10056	22457	35408	6.05	7.9E-02	A1081644.1	EST_HUMAN	cu63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
1241	13779	26225	1.54	7.9E-02	A1783275.1	EST_HUMAN	cc59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element
1241	13779	26226	1.54	7.9E-02	A1783275.1	EST_HUMAN	cc59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element
2295	14802	27319	3.08	7.9E-02	AF221942.1	NT	Sus scrofa telomerase RNA pseudogene
2295	14802	27320	3.08	7.9E-02	AF221942.1	NT	Sus scrofa telomerase RNA pseudogene
3749	16288		4.86	7.9E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959893 5'
5219	16288		2.3	7.9E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959893 5'
7509	19712	32515	1.33	7.9E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7509	19712	32516	1.33	7.9E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
9380	21812	34725	0.9	7.9E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FVE-DSP1b mRNA, complete cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9380	21812	34728	0.9	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9592	22072	34997	1.19	7.8E-02	AA469354.1	EST_HUMAN	nc88b06.r1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:771731
10467	22908	36887	117.61	7.8E-02	U32323.1	NT	Human Interleukin-11 receptor alpha chain gene, complete cds
12318	24393	30888	1.29	7.8E-02	U72847.1	NT	Homo sapiens envoplakin (EVPL) gene, exons 16 through 18
1431	16310	26420	1.16	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3679	16121		2.3	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5090	17600	29885	1.02	7.7E-02	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
5293	17793	30159	6.53	7.7E-02	U39680.1	NT	Mycoplasma genitalium section 2 of 51 of the complete genome
5807	18387	31048	0.44	7.7E-02	AF062636.1	NT	Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
8512	20824	33820	0.48	7.7E-02	BE674473.1	EST_HUMAN	7e04f03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281501 3' similar to TR:085415 O85415 I3 PROTEIN. ;
8568	21003	33901	4.83	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEDOME ASSOCIATED PROTEIN. ;
9919	22321	35268	4.41	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10138	22639	35507	0.83	7.7E-02	AJ186682.1	EST_HUMAN	ta80b08.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26878 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10138	22639	35508	0.83	7.7E-02	AJ186682.1	EST_HUMAN	ta80b08.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26878 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10791	23229	36213	4.41	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
12122	24759		2.07	7.7E-02	11436859	NT	Homo sapiens Interferon regulatory factor 7 (IRF7), mRNA
2377	14882	27400	1.48	7.6E-02	AW178789.1	EST_HUMAN	PM3-HT0125-020688-001-B01 HT0125 Homo sapiens cDNA
3365	15911	28332	2.28	7.6E-02	BE614432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634803 5'
3385	15931	28345	1.13	7.6E-02	AA298447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3546	16088	28505	0.6	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6405	18962	31697	0.84	7.6E-02	AJ061276.1	EST_HUMAN	an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
6687	19235	31985	1.08	7.6E-02	BE379328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9599	22079	35008	1.22	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
9868	22370		1.59	7.6E-02	AL193076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 6/6
10423	22823	35783	0.87	7.6E-02	X92696.1	NT	L.esculentum mRNA for triose phosphate translocator
10423	22823	35794	0.87	7.6E-02	X92696.1	NT	L.esculentum mRNA for triose phosphate translocator
11411	23772	36831	2.17	7.6E-02	AW996845.1	EST_HUMAN	QV3-BN0046-150400-161-e04 BN0046 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
807	13368	25801	1.48	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
807	13368	25802	1.48	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4545	17082	29445	0.7	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for Interleukin-18, Intron 1 and exon 2
6139	18707	31406	1.15	7.5E-02	AB048714.1	EST_HUMAN	wq24h09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472267 3'
8881	21315	34228	1.64	7.5E-02	AB049387.1	EST_HUMAN	wf52b02.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
9007	21440	34350	1.22	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000284 5'
10424	22824	35795	0.91	7.5E-02	X79460.1	NT	C.fiml DSM 20113 16S rDNA
495	13068	25487	4.35	7.4E-02	AW838547.1	EST_HUMAN	RC5L T0054-260100-011-H09 LT0054 Homo sapiens cDNA
1489	14021		1.17	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2500	15001		1.49	7.4E-02	6755089	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3588	16130	28543	0.79	7.4E-02	AB078851.1	EST_HUMAN	wf43h01.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2368385 3'
4754	17268	29050	1.59	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4846	17358	29743	2.79	7.4E-02	6978442	NT	Rattus norvegicus Actin receptor like kinase 1 (Acvrl1), mRNA
6023	17533	29905	1.84	7.4E-02	6878492	NT	Mus musculus ubiquitin C-terminal hydrolase related polypeptide (Uchrlp), mRNA
6844	19386		1.82	7.4E-02	R17477.1	EST_HUMAN	y014g08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:32339 5'
7965	20401	33271	0.58	7.4E-02	AA05132.1	EST_HUMAN	no71d02.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
8563	20998	33895	1.25	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3896284 5'
9003	21436	34346	1.09	7.4E-02	U56089.1	NT	Human perlecan tyrosinase protein 2 (PW2) gene, exons 15 to 21, and complete cds
9451	21882	34801	1.19	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2987881 5' similar to SW:SCA2_HUMAN
9451	21882	34802	1.19	7.4E-02	AW629605.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.;
9903	22305	35248	0.94	7.4E-02	U62293.1	NT	hh67d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2987881 5' similar to SW:SCA2_HUMAN
11361	23724	36784	1.65	7.4E-02	AI25063.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.;
11835	24087		1.37	7.4E-02	11525893	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
12114	24883		3.57	7.4E-02	AW378431.1	EST_HUMAN	eo11d07.s1 Barstead aorta HPLRB3 Homo sapiens cDNA clone IMAGE:1726285 3' similar to gb:M86492
12220	24332		1.27	7.4E-02	AF180355.1	NT	GLIA MATURATION FACTOR BETA (HUMAN);
12287	24376	30907	1.31	7.4E-02	BF035089.1	EST_HUMAN	Human histone deacetylase 5 (NY-CQ-9), mRNA
486	13090	26477	1.65	7.3E-02	BE984981.2	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
							Brassica oleracea isolate B265 AB11 protein (ABI1) gene, partial cds; RPS2 protein (RPS2) and N-myristoyl transferase (N-MYR) genes, complete cds; and CK1a protein (CK1a) gene, partial cds
							601453813F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857738 5'
							601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
486	13060	25478	1.65	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
704	13266	25682	2.86	7.3E-02	AE001789.1	NT	Thermotoga maritima section 101 of 130 of the complete genome
1509	13312	28508	3.41	7.3E-02	AW900281.1	EST_HUMAN	CMD-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1817	15323		13.24	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3771	16309		0.63	7.3E-02	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TORBV27S1P, TORBV22S1A2N1T, TORBV9S1A1T, TORBV7S1A1N2T, TORBV5S1A1T, TORBV13S3, TORBV6S7P, TORBV7S3A2T, TORBV13S2A1T, TORBV8S2A2PT, TORBV7S2A1N4T, TORBV13S9/13S>
5097	17607		0.97	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6765	18338	32109	1.07	7.3E-02	AA779877.1	EST_HUMAN	424402.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to 9b:LO2426 26S PROTEASE SUBUNIT 4 (HUMAN);
7662	20398	33267	1.97	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7662	20398	33268	1.97	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8379	20793		0.42	7.3E-02	BF516087.1	EST_HUMAN	601866047F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125515 5'
8762	21186		1.37	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9483	21914		1.87	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
124	12734	25150	1.04	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
124	12734	25151	1.04	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1504	14036	28499	3.24	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1504	14036	28500	3.24	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2460	14962		2.14	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
3694	16429	28835	0.78	7.2E-02	AW298322.1	EST_HUMAN	U1-H-BW0-e-aj-e-05-Q-U1.s1 NCI CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2732049 3'
4369	16890	29271	3.88	7.2E-02	BF572307.1	EST_HUMAN	602077157F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
4743	17257	28637	0.76	7.2E-02	11466563	NT	Rhodomonas salina mitochondrion, complete genome
4927	17438	29813	1.49	7.2E-02	AW027569.1	EST_HUMAN	wv74g12.x1 Soares_thymus_NHFTn Homo sapiens cDNA clone IMAGE:2535334 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element;
4927	17438	29814	1.49	7.2E-02	AW027569.1	EST_HUMAN	wv74g12.x1 Soares_thymus_NHFTn Homo sapiens cDNA clone IMAGE:2535334 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element;
5188	17692	30053	0.65	7.2E-02	AB001662.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5539	18129	30486	2.96	7.2E-02	U07531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5540	18130	30487	8.69	7.2E-02	P11120	SWISSPROT	CALMODULIN

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6429	18985		0.65	7.2E-02	BF217598.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4098224 5'
7611	20060	32913	1.33	7.2E-02	BF216086.1	EST_HUMAN	801883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7629	20077	32930	0.63	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmps), and putative zinc metalloprotease (zmpB) genes, complete cds
7656	20101		1.61	7.2E-02	5834897	NT	Strongyloides purpuratus mitochondrion, complete genome
9774	22177	35110	2.28	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAAUG01 5'
9872	22276	35216	4.73	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9878	22381	35330	1.02	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028436 5'
10035	22437	35384	2.48	7.2E-02	AW873187.1	EST_HUMAN	h24f11.x1 NCL_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
10172	22573	35540	0.83	7.2E-02	AA768204.1	EST_HUMAN	ca62c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10273	22674	35637	2.27	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10359	22759	35726	5.39	7.2E-02	BE565003.1	EST_HUMAN	601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10373	22773		3.41	7.2E-02	BE59214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10692	23131	36112	4.92	7.2E-02	AF048874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11737	24026	31013	1.49	7.2E-02	AA773666.1	EST_HUMAN	af81a04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
11775	24050		3.28	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranck P) Homo sapiens cDNA clone PS13D5 3'
11837	24089		1.76	7.2E-02	AA594465.1	EST_HUMAN	nc05h08.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1098339 3'
11802	24127		2.17	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
11915	24722		7.1	7.2E-02	AW900862.1	EST_HUMAN	CM4-NN1009-200300-118-c11 NN1009 Homo sapiens cDNA
12453	24476		1.46	7.2E-02	AA401778.1	EST_HUMAN	zf57c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454 6'
1865	14387	26878	0.99	7.1E-02	L02280.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2188	14999	27218	4.82	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
8566	21001	33898	1.23	7.1E-02	A115284.1	EST_HUMAN	q92a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738922 3'
11613	23944		6	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3051234 5'
546	13118	25527	0.98	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1528	14060		1.9	7.0E-02	X96677.1	NT	Martellia Mitcut-1 gene
2989	16544	27857	1.73	7.0E-02	AW138162.1	EST_HUMAN	U1-H-B11-acy-o-07-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3907	16442	28848	0.87	7.0E-02	AA815438.1	EST_HUMAN	al65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4056	16588	28978	1.13	7.0E-02	BE070284.1	EST_HUMAN	QV4-BT0407-280100-030-e10 BT0407 Homo sapiens cDNA
4157	16684		1.22	7.0E-02	AW792982.1	EST_HUMAN	CMD-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4229	16754	29143	1.45	7.0E-02	AF077821.1	NT	Canis familiaris Inducible nitric oxide synthase mRNA, complete cds
5008	17518	29892	9.58	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4050071 5'
5633	18220		0.98	7.0E-02	Y08143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7880	20319	33184	0.69	7.0E-02	AV689285.1	EST_HUMAN	AV689285 GK Homo sapiens cDNA clone GKCCAE08 5'
8133	20558	33433	0.68	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for partial accorin, XL spliced variant (acc gene)
9407	21839	34763	1.32	7.0E-02	9828113	NT	African swine fever virus, complete genome
9782	22165	35099	1.32	7.0E-02	K02901.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
11129	23581	36822	2.52	7.0E-02	AA724295.1	EST_HUMAN	af98a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb.L14837
532	13104	25513	12.83	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN)
532	13104	25514	12.83	6.8E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1365	13899		1.54	6.9E-02	4507968	NT	Homo sapiens chromosome 21 segment HS21C010
3785	16332	28733	1.54	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3785	16332	28734	1.54	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
6214	18780		0.61	6.9E-02	AF161384.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
8145	20588		0.7	6.9E-02	AF164987.1	NT	Homo sapiens HSPC101 mRNA, partial cds
8870	21105		1.21	6.9E-02	U12022.1	NT	Canine distemper virus strain A7517, complete genome
9037	21469	34378	0.83	6.9E-02	BE567435.1	EST_HUMAN	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
9037	21469	34378	0.83	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
11769	24047		3.75	6.9E-02	X74315.1	NT	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
12188	24308		3.31	6.9E-02	AF195953.1	NT	Xlaevis XFD2 mRNA for fork head protein
1866	14388	28878	2.94	6.8E-02	AF156673.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4589	17105		0.72	6.8E-02	BE141076.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
6982	19519		0.6	6.8E-02	P20792	SWISSPROT	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
7307	19719		1.25	6.8E-02	BE061890.1	EST_HUMAN	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
7737	20181	33042	8.67	6.8E-02	AL163268.2	NT	RC1-BT0254-080300-017-009 BT0254 Homo sapiens cDNA
8222	20641	33631	0.74	6.8E-02	U16856.1	NT	Homo sapiens chromosome 21 segment HS21C068
8843	21277	34187	6.61	6.8E-02	AJ249287.1	NT	Dicystosium discoidium myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8843	21277	34188	6.61	6.8E-02	AJ249287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11525	23883	36968	6.04	6.8E-02	M38526.1	NT	Pyrococcus abyssi complete genome; segment 6/6
11560	24938		1.9	6.8E-02	T03214.1	EST_HUMAN	S. pombe retrotransposon Tf1-107
							FB4A8 Fetal brain, Stratiogene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11697	24001		2.4	6.8E-02	AA758014.1	EST_HUMAN	ah67f05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
12382	24425		2.56	6.8E-02	9910585	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1551	14083		2.02	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OmyTAP1) mRNA, OmyTAP1'01 allele, complete cds
1857	14379	26870	1.31	6.7E-02	AJ220285.1	EST_HUMAN	cg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841408 3'
3715	16255	28658	4.95	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD4 (HOXA)
3968	16503	28911	0.72	6.7E-02	U53783.1	NT	Cyprinus carpio Rep1b mRNA, complete cds
3968	16503	28912	0.72	6.7E-02	U53783.1	NT	Cyprinus carpio Rep1b mRNA, complete cds
4605	17121		3.32	6.7E-02	P07198	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (68 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1380	13915	26371	1.36	6.6E-02	AJ735509.1	EST_HUMAN	at12e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW/LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
1402	13938	26392	1.82	6.6E-02	AF245118.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2088	14602	27119	2.12	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3440	15984	28401	11.47	6.6E-02	R64306.1	EST_HUMAN	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138579 3'
3453	15987	28416	2.81	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3453	15987	28417	2.81	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4096	16627	28017	1.73	6.6E-02	AF260226.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5074	17584	28950	11.71	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5074	17584	28951	11.71	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5120	17627	29988	0.64	6.6E-02	AA393244.1	EST_HUMAN	z174e07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728062 5' similar to gb.L04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
5120	17627	29989	0.64	6.6E-02	AA393244.1	EST_HUMAN	z174e07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb.L04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
5430	17925	30278	2.55	6.6E-02	AF023424.1	NT	Hepatitis GB virus A complete genome
6937	19476	32256	3.04	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6972	19509	32289	0.52	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
6972	19509	32290	0.52	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
7185	19509	32289	0.78	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
7185	19509	32290	0.78	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
7514	19716	32519	0.69	6.6E-02	A1243328.1	EST_HUMAN	q141d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847233 3'
8482	20895		0.73	6.6E-02	D14567.1	NT	Pericentriolar urticaria mitochondrial rRNA (large rRNA) gene and its flanking region
8596	21031	33934	1.75	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
9283	21725	34632	1.06	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9293	21725	34633	1.06	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10105	22606	35470	1.55	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, mp22 and bam22 genes
10743	23181	36168	6.96	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-e12 SN0064 Homo sapiens cDNA
12182	24302		2.12	6.6E-02	9937997	NT	Mus musculus DIPB gene (Dipb), mRNA
12524	24521		1.4	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
599	13188	25572	2.12	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1013	13566	26010	1.98	6.5E-02	7708068	NT	Homo sapiens E2F-like protein (LOC61270), mRNA
1423	13956	28412	5.47	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1729	14266	28741	1.23	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 98 of 109 of the complete genome
5337	17838	30194	2.49	6.5E-02	D45899.1	NT	Caenorhabditis elegans DNA for ryanodine receptor, complete cds
5823	18403	31067	2.05	6.5E-02	AA443991.1	EST_HUMAN	z465h12.s1 Soares ovary tumor NIHOT Homo sapiens cDNA clone IMAGE:758743 3' similar to gb:M26038
6894	19434	32210	0.78	6.5E-02	BF668340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7389	18058	30398	0.88	6.5E-02	U22661.1	NT	60211887F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276028 5'
10436	22888	35864	4.42	6.5E-02	AA195648.1	EST_HUMAN	Azotobacter vinelandii ATCC 8046 negative regulator MucB (mucB) gene, partial cds
11539	23896	36978	2.95	6.5E-02	AW604112.1	EST_HUMAN	z32905.s1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
11592	23922		7.83	6.5E-02	M21496.1	NT	PM4-NN1043-310300-001-d01 NN1043 Homo sapiens cDNA
11959	24160		4.09	6.5E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
592	13182	25565	1.95	6.4E-02	X94549.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
2973	15528	27949	3.05	6.4E-02	6998923	NT	A. carterae precursor of peridinin-chlorophyll-protein (PCP) gene
5400	17897		5.26	6.4E-02	AA147572.1	EST_HUMAN	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5707	18291	30717	1.02	6.4E-02	AI191966.1	EST_HUMAN	z51e04.r1 Soares_pregnant_uterus_Nbi-FPU Homo sapiens cDNA clone IMAGE:505470 5' similar to contains Alu repetitive element
6170	18738	31439	0.67	6.4E-02	7305188	NT	q607b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element
6424	18980	31713	2.77	6.4E-02	AF052733.1	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6424	18980	31714	2.77	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6740	19286	32046	0.81	6.4E-02	AI672896.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
7208	19919	32748	4.46	6.4E-02	BE574449.1	EST_HUMAN	wa73g12.x1 Soares Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346780 3'
7946	20363	33250	0.49	6.4E-02	AL162757.2	NT	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3650503 3'
8879	21313		2.76	6.4E-02	6753323	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 817
9115	21547	34450	4.33	6.4E-02	AA093305.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
9427	21859	34778	0.84	6.4E-02	AF150195.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 6'
9847	22260	35185	2.16	6.4E-02	AB011126.1	NT	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
							Homo sapiens mRNA for KIAA0554 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11431	23782	36853	2.58	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11431	23782	36854	2.58	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11855	24838		3.62	6.4E-02	AF107890.1	NT	Homo sapiens much 5B (MUC5B) gene, partial cds
11806	24130	30965	2.06	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1745	14272	26757	1.21	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3588	16139		3.02	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
5485	17980		1.05	6.3E-02	AF182346.1	NT	Yushania exilis NADH dehydrogenase (ndhF) gene, partial cds; chloroplast gene for chloroplast product
6449	19005	31737	0.99	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7691	20136		1.02	6.3E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
9544	21959	34882	1	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Domina gene, exons 1-3
10043	22445	35393	3.81	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polypeptide (NS5A region), partial cds, strain: CMR-152
10225	22626		1.09	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GK Hom sapiens cDNA clone GKCAHE01 5'
10501	18005	31737	2.78	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
2378	14883	27401	7.78	6.2E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4267	16782	29175	4.78	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4360	16882		1.13	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4021	17137		20.89	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
4865	17476		0.84	6.2E-02	AV705701.1	EST_HUMAN	AV705701 ADB Homo sapiens cDNA clone ADBBAB03 5'
7181	19894	32719	0.7	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
8158	20581	33459	0.97	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8490	20902		0.63	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
9679	22091	35020	1.38	6.2E-02	6577898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdfir2), mRNA
11106	23559	36600	2.44	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chyl gene)
11684	24868		8.22	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12129	24264	30932	3.53	6.2E-02	BF112039.1	EST_HUMAN	7137108.X1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9Y456 Q9Y456 HYPOTHETICAL 30.3 KD PROTEIN. [1];

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
269	12887	25284	7.6	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
4005	16539		9.78	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
4689	17215	28585	1.05	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
4699	17215	29586	1.05	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
5382	17879		2.71	6.1E-02	A1220330.1	EST_HUMAN	gg90e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842470 3'
6231	18788	31504	0.51	6.1E-02	7662463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6231	18788	31905	0.51	6.1E-02	7662463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6425	18981		1.72	6.1E-02		NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
7590	20039	32887	0.54	6.1E-02	AJ001487.1	NT	Homo sapiens AFG3L1 gene, exon 2
8824	21258	34163	3.62	6.1E-02	X99288.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
10514	22963	36942	3.55	6.1E-02	BE179543.1	EST_HUMAN	IL3-H10818-110500-136-C06 HT0618 Homo sapiens cDNA
11638	24877		11.24	6.1E-02	X70899.1	NT	S. japonicum mRNA for serine-enzyme
12402	24437		4.95	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1295	13830	26279	1.41	6.0E-02	AE001777.1	NT	Thermoplasma maritima section 89 of 136 of the complete genome
2615	16110	27626	5.99	6.0E-02	AW968848.1	EST_HUMAN	EST1380924 IMAGE resequences, MAGJ Homo sapiens cDNA
2731	15221		1.82	6.0E-02	AB031289.1	NT	Mesocricetus auratus mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2890	12717	25130	1.08	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2890	12717	25131	1.08	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3188	15741	28162	1.83	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3188	15741	28163	1.83	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3634	16174		0.62	6.0E-02	BE664443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5065	17575	29944	1.1	6.0E-02	Z87739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5654	18240		0.67	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-073-B04 BT0253 Homo sapiens cDNA
6533	18085	31826	0.99	6.0E-02	AI807537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 L1 repetitive element
7405	18074	30367	2.86	6.0E-02		NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7405	18074	30368	2.86	6.0E-02	5174598	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7632	20079	32932	2.43	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
7748	20192	33053	0.44	6.0E-02	BF210488.1	EST_HUMAN	601874710F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101074 5'
8218	20638	33528	1.93	6.0E-02	A1204275.1	EST_HUMAN	qf58b08.x1 Soares_festis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
8947	21380		3.88	6.0E-02	11466495	NT	Recellomonas americana mitochondrion, complete genome
9529	21944	34866	0.94	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9529	21944	34867	0.94	6.0E-02	A123167.1	EST_HUMAN	ts78e09.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:237362 3'
9623	22038	34871	1.85	6.0E-02	A1245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9623	22038	34872	1.85	6.0E-02	A1245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
11905	24129	30864	1.23	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12328	24397		2.69	6.0E-02	A1809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:060288
241	12842	25255	4.84	5.9E-02	AW634719.1	EST_HUMAN	RC1-DT0001-290100-012-s10 DT0001 Homo sapiens cDNA
2938	16493	27915	2.95	5.9E-02	AF180288.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4931	17442	28819	1.84	5.9E-02	AF008304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
7288	24627	32814	0.61	5.9E-02	AF145880.1	NT	Drosophila melanogaster LD23107 sting (slng) mRNA, complete cds
9080	21612	34421	2.68	5.9E-02	9055249	NT	Mus musculus Iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
9655	20948		0.97	5.9E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'
10567	23014		2.05	5.8E-02	6679870	NT	Mus musculus follistatin-like (Fstl), mRNA
957	13509		5.45	5.8E-02	D80110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
3682	18202	28608	1.84	5.8E-02	AE001775.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
4376	18898	29280	4.47	5.8E-02	AW051927.1	EST_HUMAN	w24c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2644578 3'
4378	18898	29281	4.47	5.8E-02	AW051927.1	EST_HUMAN	w24c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2644578 3'
4583	17099	29488	5.09	5.8E-02	A1247505.1	EST_HUMAN	q156101.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4583	17099	29489	5.09	5.8E-02	A1247505.1	EST_HUMAN	q156101.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4812	17128		1.92	5.8E-02	AF096294.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6202	18768	31472	0.57	5.8E-02	AA190994.1	EST_HUMAN	zp88a11.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627088 3'
8216	20636	33525	2.77	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8216	20636	33526	2.77	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
11782	24059		2.18	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12104	24955		6.12	5.8E-02	AA604269.1	EST_HUMAN	no75e11.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:112684 3'
3018	15573	27984	1.32	5.7E-02	A1091844.1	EST_HUMAN	cu63b05.s1 NCL_CGAP_B12 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WIP:C37A2.2
3032	15587	27998	1.19	5.7E-02	AF119117.1	NT	CE09611;
3704	16245		0.64	5.7E-02	AF001292.1	NT	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
3808	16343	28744	2.67	5.7E-02	AW968791.1	EST_HUMAN	EST378865 MAGE resequences, MAGE Homo sapiens cDNA
4733	17248		0.95	5.7E-02	M95099.1	NT	Bos taurus lysoczyme gene (cow 3), complete cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6280	17781	30147	1.84	5.7E-02	AB017105.1	NT	Mus musculus gene for DNA helicase Q1, complete cds
6167	18735		0.86	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7959	20395	33202	0.59	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7959	20395	33263	0.59	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
8051	20483	33357	0.71	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8051	20483	33358	0.71	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8740	21174	34077	1.7	5.7E-02	AJ286080.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
10963	23392	36403	4.02	5.7E-02	AJ752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
10963	23392	36404	4.02	5.7E-02	AJ752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
12009	24762		8.05	5.7E-02	D50320.1	NT	Pig DNA for SPA-2, complete cds
12187	24307		1.27	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12286	24832		2.17	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12418	24944		6.38	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
12568	24550	30843	1.22	5.7E-02	R48513.1	EST_HUMAN	y64d10.s1 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:163523 3' similar to contains L1 repetitive element
4686	17202	28580	1.52	5.6E-02	AB013100.1	NT	Lycopersicon esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4746	17260	29840	1.33	5.6E-02	AA290899.1	EST_HUMAN	z645c01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700419 3'
4848	17360	29746	0.89	5.6E-02	AA873479.1	EST_HUMAN	ch77f12.s1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1473071 3' similar to contains element, MER19 repetitive element
7028	19562	32349	4.64	5.6E-02	AW172708.1	EST_HUMAN	x02c10.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2856050 3' similar to TR:084979 094979 KIAA0906 PROTEIN.
7296	19801	32812	1.35	5.6E-02	AA666182.1	EST_HUMAN	od47f12.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu . repetitive element; contains element L1 repetitive element
7592	20041	32860	3.81	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-280400-214-q07 BN0147 Homo sapiens cDNA
7605	20054	32906	0.53	5.6E-02	AI983738.1	EST_HUMAN	wz34f05.x1 NCL_CGAP_Bim53 Homo sapiens cDNA clone IMAGE:2859969 3' similar to gb:X08409 RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
8456	20889	33769	0.65	5.6E-02	AI183583.1	EST_HUMAN	qd84g11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9216	21648	34558	2.08	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453278 5'
9216	21648	34559	2.06	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453278 5'
9901	22303	35246	1.38	5.6E-02	AA482864.1	EST_HUMAN	nf49d07.s1 NCL_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C.

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11316	23680		2.11	5.0E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2691	16087	27601	4.13	5.5E-02	X97899.1	NT	H. sapiens gene encoding La autoantigen
3173	15728	28147	4.1	5.5E-02	6756501	NT	Mus musculus SH3 domain protein 1B (SH3d1B), mRNA
5928	18506	31190	3.15	5.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6329	18506	31190	4.24	5.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7851	20291	33154	1.94	5.5E-02	6756502	NT	Mus musculus tufelin 1 (Tuf1), mRNA
8717	21152	34057	0.85	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8717	21152	34058	0.85	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8864	22267	35206	1.38	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
10797	23234	38216	5.9	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
12594	24807	30452	1.25	5.5E-02	11421332	NT	Homo sapiens hypothetical protein SIPP-b2 (SIPP-b2), mRNA
2979	15534		0.97	5.4E-02	AJ277468.1	NT	Oryza sativa rbb3-1 gene for putative Bowman Birik trypsin inhibitor
3400	17963		10.5	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3923	16458	28966	0.76	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-28 homolog mRNA, complete cds
8720	21155		1.02	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2395281 to 2813730
10486	22938	35914	1.86	5.4E-02	U20790.1	NT	Neurospora crassa ublquihol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11892	24745		2.03	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1079	13625	26064	1.54	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1079	13625	26065	1.54	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1533	14085	26526	1.6	5.3E-02	T94759.1	EST_HUMAN	ye87112.1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:118951 5' similar to gb:K01508
2402	14908	27424	7.76	5.3E-02	AJ279408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2896	15451	27876	0.98	5.3E-02	M59417.1	NT	Pseudomonas putida tgs gene
2896	15451	27877	0.98	5.3E-02	M59417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3111	15684	28076	4.39	5.3E-02	AJ279408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
4849	17361	29746	1.22	5.3E-02	AL161535.2	NT	Pseudomonas putida tgs gene
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
5220	17722	30089	0.63	5.3E-02	AB051897.1	NT	Mus musculus Soya6, Soya6, Soya16-ps, Soya5 genes for small inducible cytokine A5 precursor, small inducible cytokine A9 precursor, Soya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5222	17724	30091	9.96	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5572	18160	30624	2.26	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5572	18180	30525	2.28	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6411	18968	31704	0.73	5.3E-02	MB5289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7289	18784	32603	3.71	5.3E-02	9895413	NT	Lymphocystis disease virus 1, complete genome
7531	19982	32816	1.14	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7833	20273		2.38	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
9426	21858	34776	1.7	5.3E-02	X03127.1	NT	Podospora anserina mitochondrial epsilon-sen DNA
11278	23644		9.75	5.3E-02	Z72955.1	NT	S.cerevisiae chromosome VII reading frame ORF YGR170W
12569	24551	30844	1.67	5.3E-02	AF278815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2181	14692		44.24	5.2E-02	5031808	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEPTA) mRNA
3075	15629	28036	2.62	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3075	15629	28036	2.62	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3952	16487	28898	0.8	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4294	16819	29202	3.98	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nrf-1 mRNA, complete cds
6213	18779	31484	0.57	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
8418	18975		0.94	5.2E-02	AB309095.1	EST_HUMAN	w80e04.x1 NCJ_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains MER15.b1 MER15 repetitive element;
7728	20172	33032	1.25	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8772	21206		3.19	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9854	22257	35194	1.91	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9854	22257	35185	1.91	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12153	24283		1.82	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
2257	14765		1.05	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_J1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D073 5'
7041	19576	32387	0.86	5.1E-02	AF280369.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds
7258	18032	30415	1.75	5.1E-02	BF378625.1	EST_HUMAN	QV0-JM0051-250800-350-b08 UM0061 Homo sapiens cDNA
8815	21249	34153	1.01	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8815	21249	34154	1.01	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8887	21321	34232	1.65	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydrocyclohexane 3beta-reductase
9899	22301	35243	7.92	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10164	22565	35631	2.04	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10610	23053	36038	2.79	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
10610	23053	36039	2.79	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12159	24285		2.24	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
500	13074	25490	2.52	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1235	13773	26220	2.82	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1934	14453	26955	3.51	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2777	13564	26009	1.37	5.0E-02	U72742.1	NT	Oryzias latipes cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3310	15858		1.49	5.0E-02	7305610	NT	Mus musculus Uno-51 like kinase 2 (C. elegans) (Ull2), mRNA
3589	16131		1	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3683	16223	28631	6.64	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
4678	17390		0.93	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
5062	17572	29941	1.78	5.0E-02	AF188530.1	NT	Homo sapiens ubiquitous tetrapeptide containing protein RoXaN mRNA, partial cds
6443	18999	31731	0.79	5.0E-02	AF068264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6636	19184		1.01	5.0E-02	AJ242025.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7406	18076	30369	0.62	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
8050	20482	33366	11.82	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
8268	20702		0.51	5.0E-02	AW062464.1	EST_HUMAN	MRQ-CT0064-100899-002-g10 CT0084 Homo sapiens cDNA
10176	22677	35545	1.3	5.0E-02	AF305238.1	NT	Mus musculus Fes-interacting serine/threonine kinase 3 (Fis3) mRNA, complete cds
11247	23613	36658	2.82	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
11649	24790		5.39	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
232	12833		35.01	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
384	12971	25392	3.81	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
384	12971	25393	3.81	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2827	15383	27795	0.77	4.9E-02	U32636.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3250	15801	28218	5.83	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3559	16101		0.84	4.9E-02	AA188940.1	EST_HUMAN	z48a12.s1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632928 3' similar to contains Alu repetitive element contains element MSR1 repetitive element ;
3584	16128	28538	1.01	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3584	16128	28538	1.01	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4308	16933		1.17	4.9E-02	M23929.1	NT	Drosophila melanogaster developmental protein (rough) gene, complete cds
4898	17409	29781	1.93	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4898	17409	29782	1.93	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
6438	17933		6.11	4.9E-02	AE001774.1	NT	Thermotoga maritima section 88 of 138 of the complete genome
5626	18213	30614	1.63	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5626	18213	30615	1.63	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7582	20031	32878	1.04	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9179	21911	34522	1.08	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
11156	23537	36575	3.96	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12072	24226		2.85	4.9E-02	8923980	NT	Homo sapiens CS box-containing WD protein (LOC55984), mRNA
12368	24417		3.72	4.9E-02	M18964.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
344	12935	25351	1.53	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
345	12935	25351	3.07	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
506	13080	25495	9.38	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2173	14884	27208	1.42	4.8E-02	W51983.1	EST_HUMAN	z049b02.s1 Soares, senescent, fibroblasts, NBHSF Homo sapiens cDNA clone IMAGE:325811 3' similar to
3167	15720	28142	2.5	4.8E-02	X17144.1	NT	gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
5301	17801	30167	0.71	4.8E-02	U91914.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
8128	21163	34068	1.38	4.8E-02	AW388497.1	EST_HUMAN	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
5287	17980		0.91	4.7E-02	AW98984.1	EST_HUMAN	MR2-ST0129-221099-012-b02 ST0129 Homo sapiens cDNA
7223	19835	32652	3.4	4.7E-02	W01153.1	EST_HUMAN	MRO-BN0070-180200-001-408 BN0070 Homo sapiens cDNA
7280	18785	32604	0.77	4.7E-02	BF686625.1	EST_HUMAN	yz87109.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element
7290	19795	32605	0.77	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7327	18739	32643	1.75	4.7E-02	M62752.1	NT	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
8268	20883		0.51	4.7E-02	11431898	NT	Rat statin-related protein (s1) gene, complete GDS
8813	21247	34151	9.73	4.7E-02	X15543.1	NT	Homo sapiens protein x 0001 (LOC51185), mRNA
8310	21742	34650	1.32	4.7E-02	X89211.1	NT	B.taurus mRNA for RF-38-DNA-binding protein
9325	21757		3.31	4.7E-02	AB026878.1	NT	H.sapiens DNA for endogenous retroviral like element
9497	21928	34852	7.87	4.7E-02	X15543.1	NT	Gallus gallus Wpckl-8 gene, complete cds
11873	24967		1.64	4.7E-02	AV848521.1	EST_HUMAN	B.taurus mRNA for RF-38-DNA-binding protein
12256	24959		2.1	4.7E-02	P62951	SWISSPROT	AV848521 GLC Homo sapiens cDNA clone GLCBK02 3'
12521	24519		1.64	4.7E-02	AJ277662.1	NT	HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)
284	12881	25299	0.6	4.6E-02	BE193583.1	EST_HUMAN	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
760	13320	25749	3.04	4.6E-02	AE000445.1	NT	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
1324	13859		1.09	4.6E-02	AI014255.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1391	13925	26383	3.42	4.6E-02	AV727059.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533
							P90533 LIMA; contains element LTR1 repetitive element;
							AV727059 HTC Homo sapiens cDNA clone HTCBWC01 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2391	14895	27413	2.69	4.8E-02	AW238023.1	EST_HUMAN	nm2af03.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2894653 3' similar to SW:GRF1_HUMAN Q12849 G-RICH SEQUENCE FACTOR-1;
2768	12881	25298	1.43	4.8E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251198-003-g05 HT0339 Homo sapiens cDNA
2866	15521	27942	0.63	4.8E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251198-003-g05 HT0339 Homo sapiens cDNA
3301	15521	27942	0.68	4.8E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251198-003-g05 HT0339 Homo sapiens cDNA
3472	15521	27942	0.71	4.8E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251198-003-g05 HT0339 Homo sapiens cDNA
4140	16668		1.31	4.8E-02	AF220365.1	NT	Mus musculus nucleolar RNA helicase II/Gu (dd21) gene, complete cds
6009	18583	31269	1.64	4.8E-02	AF076962.1	NT	Haplochromis burtoni gonadotrophin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
6549	19101	31843	3.18	4.8E-02	XG1624.1	NT	C.reinhardtii alp2 (atpB) mRNA
6549	19101	31844	3.18	4.8E-02	XG1624.1	NT	C.reinhardtii alp2 (atpB) mRNA
7186	19897	32724	1.83	4.8E-02	AI149574.1	EST_HUMAN	qc60b06.x1 Soares_placenta_8tccweeks_2NbtHP8tcc9W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1.13 L1 repetitive element;
8447	20861	33762	0.54	4.8E-02	6878720	NT	Rattus norvegicus Cathepsin H (Clsh), mRNA
9108	21540	34447	3.61	4.8E-02	BE154008.1	EST_HUMAN	PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11158	23638	36576	3.34	4.8E-02	AA913328.1	EST_HUMAN	ql27h09.e1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12230	24954		1.23	4.8E-02	L11692.1	NT	Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds
12485	24498		3.64	4.8E-02	X57808.1	NT	Human germ-line immunoglobulin lambda light chain gene
484	13038	25462	2.35	4.8E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1249	13787	26233	1.37	4.8E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1249	13787	26234	1.37	4.8E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1780	14305	26784	3.91	4.8E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2031	14547	27061	1.16	4.8E-02	AE003984.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3721	16261	28666	2.8	4.8E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6551	19103	31847	1.69	4.8E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6857	19397	32173	1.01	4.8E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7283	19788	32597	0.64	4.8E-02	L26487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdhIA) gene; carbon monoxide dehydrogenase small subunit (cdhIB) gene, complete cds
7283	19788	32598	0.64	4.8E-02	L26487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdhIA) gene; carbon monoxide dehydrogenase small subunit (cdhIB) gene, complete cds
8927	21361	34274	2.5	4.8E-02	AF036884.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
8988	22401	35351	4.32	4.8E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 6' end similar to neuro-D4 protein
10189	22580	35556	0.92	4.8E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11870	24113	30599	1.5	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RPPL3), mRNA
12299	24840	30596	4.55	4.5E-02	AA191097.1	EST_HUMAN	z44311.1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
227	12829		12.15	4.4E-02	BE927233.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2019	14535		5.57	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2393	14897	27415	2.94	4.4E-02	AW875473.1	EST_HUMAN	QV2-PT0012-D10300-070-g02 PT0012 Homo sapiens cDNA
3639	16179	28587	1.68	4.4E-02	AF159160.1	NT	Myxobolus xenithus serine/threonine kinase Ptk10 (pkr10) gene, complete cds
4671	17187	29584	1.04	4.4E-02	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
4671	17187	29565	1.04	4.4E-02	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
4794	17308		0.98	4.4E-02	AJ222889.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
5446	17941	30280	1.44	4.4E-02	AF081575.1	NT	Petunia x hybrida flavonoid 3',5'-hydroxylase (Hf1) gene, complete cds
7657	20007	32849	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7557	20007	32850	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8391	20776	33674	0.59	4.4E-02	11525968	NT	Homo sapiens hypothetical protein PRO2492 (PRO2492), mRNA
8391	20776	33675	0.59	4.4E-02	11525968	NT	Homo sapiens hypothetical protein PRO2492 (PRO2492), mRNA
8177	21609	34519	2.52	4.4E-02	AA736989.1	EST_HUMAN	hw13h03.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1239221 3'
10853	23286	36277	2.89	4.4E-02	AF060689.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
10974	23403	39413	6.25	4.4E-02	AA498739.1	EST_HUMAN	ac33f04.1 Geseler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
11578	23920		1.92	4.4E-02	AB040928.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
11771	24970		1.41	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4107418 5'
803	13362	25797	10.06	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2309	14816	27333	5.44	4.3E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2309	14816	27334	5.44	4.3E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3407	15952	28365	9.33	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3658	16198		1.19	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6845	19366	32160	6.35	4.3E-02	P30427	SWISSPROT	PLECTIN
6845	19366	32161	6.35	4.3E-02	P30427	SWISSPROT	PLECTIN
7111	19844	32440	0.73	4.3E-02	AA632268.1	EST_HUMAN	ns69c12.s1 NCI_CGAP_P2 Homo sapiens cDNA clone IMAGE:1188986
8461	20874		0.47	4.3E-02	L15299.1	NT	Yeast para-aminobenzoate synthase gene, complete cds
9215	21647	34556	1.27	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
9215	21647	34557	1.27	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
845	13402	28843	2.12	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM200020 5'

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
889	13444		2.37	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 6'
919	13473	25621	1.41	4.2E-02	AW003645.1	EST_HUMAN	wk34901.x1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 MRNA ; contains L1.13 L1 L1 repetitive element ;
1717	14245		1.02	4.2E-02	AL445088.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
3663	16203	28609	1.75	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
5885	18464	31140	0.83	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5885	18464	31141	0.83	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7400	18089	30360	8.97	4.2E-02	BE288285.1	EST_HUMAN	601124596F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2988319 5'
8033	20485	33339	3.95	4.2E-02	AF276762.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
8059	20490	33366	0.78	4.2E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5'
9221	21863	34564	4.42	4.2E-02	P06095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10158	22559	35527	1.35	4.2E-02	Q16950	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
10820	23266	36241	5.64	4.2E-02	AA976118.1	EST_HUMAN	an33b11.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65290
11078	23501	36529	3.54	4.2E-02	BE816822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11078	23501	36530	3.54	4.2E-02	BE816822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
12154	24890		4.25	4.2E-02	A1983494.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
528	13100	25512	0.72	4.1E-02	AF200628.1	NT	w49g10.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
4507	17025		9.94	4.1E-02	AF200628.1	NT	Homo sapiens HPS1 gene, Intron 5
5911	18489	31171	1.11	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-164-706 NN0012 Homo sapiens cDNA
5911	18489	31172	1.11	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343858 6'
7287	19782		0.98	4.1E-02	X75881.1	NT	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343858 6'
7538	19988	32825	1.1	4.1E-02	AE002132.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
8019	20451	33322	1.93	4.1E-02	7682347	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
						NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
8128	20551	33427	0.85	4.1E-02	L02110.1	NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
8321	20736	33630	3.28	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8441	21872	34780	1.04	4.1E-02	AA372998.1	EST_HUMAN	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12508	24881	30577	15.92	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3203	16766	28173	3.28	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3803	16340	28741	0.99	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5288	17789	30154	0.71	4.0E-02	AB042297.1	NT	Homo sapiens PTS gene for 8-pyruvoyltransferin synthase, complete cds
5635	18222	30622	8.01	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6531	19083	31824	1.06	4.0E-02	BF110434.1	EST_HUMAN	7n52h07 x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75298 O75296 R28124.1;
8228	20847	33539	6.17	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
8304	20719	33631	0.5	4.0E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
8322	20737	33631	0.94	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8322	20737	33632	0.94	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8376	20780	33689	0.46	4.0E-02	AF288153.1	NT	Homo sapiens erythrocyte tropomodulin (E-TMOD) gene, exon 7
9147	21679	34485	2.98	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9795	22198	35149	0.87	4.0E-02	BF079378.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284724 5'
9808	22212	35149	2.42	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
10022	22424		1.04	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11480	23838		1.68	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Ca++ ATPase
11756	24694	30778	10.94	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1147	13691	26132	3.56	3.9E-02	BF516149.1	EST_HUMAN	UI-H-BW1-anch-08-Q-U1.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084193 3'
1376	13911	26366	2.66	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1910	14428	26926	1.91	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2653	15146		6.28	3.9E-02	4506892	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 16kD (SDHC) mRNA
5160	17694	30025	1.19	3.9E-02	U61380.1	NT	Bacillus megaterium germination protein (gerAA, gerAC, gerAB) genes, complete cds
5160	17694	30026	1.19	3.9E-02	U61380.1	NT	Bacillus megaterium germination protein (gerAA, gerAC, gerAB) genes, complete cds
5316	17818	30179	0.66	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0258-171189-021-C08 ST0258 Homo sapiens cDNA
6334	17833	30181	0.97	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5334	17833	30192	0.97	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5470	17995		2.32	3.9E-02	Y15802.1	NT	Hordeum vulgare Ss2 gene
5756	18337	30782	0.92	3.9E-02	D50508.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5758	18337	30783	0.92	3.9E-02	D50808.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
6008	18680	31287	1.06	3.9E-02	BE968841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
6144	18712	31414	0.59	3.9E-02	BF675203.1	EST_HUMAN	602138192F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7489	18693	32489	1.01	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
8505	20917	33813	0.51	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
8523	20958	33860	1.31	3.9E-02	BF239613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
11804	24849		6.48	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12308	24386		1.38	3.9E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY3, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
12439	24763		8.05	3.9E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 6 gene, Zinc finger protein 275, Zinc finger protein 92, nmrxq28orf
5697	18282	30706	1.05	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
6395	18952	31687	1.13	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7782	20224	33084	1.49	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8116	20541		0.41	3.8E-02	AA382700.1	EST_HUMAN	EST95937 Testis I Homo sapiens cDNA 5' end
9114	21548		1.42	3.8E-02	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
10445	22898	35873	2.16	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1018	13569	28013	5.5	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1420	13953	28409	1.05	3.7E-02	L14581.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2144	14857	27181	3.67	3.7E-02	A1984806.1	EST_HUMAN	wf85c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2484502 3'
2498	14967	27511	1.87	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3010	15565	27978	1.31	3.7E-02	P78844	SWISSPROT	ECM-SODERMIN
3012	15567	27978	5.33	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
6945	19483	32282	0.42	3.7E-02	AJ132405.1	NT	Homo sapiens GDF-9B gene
7512	24988		0.98	3.7E-02	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 8/7
8231	20650	33542	0.68	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
10044	22446		1.01	3.7E-02	AA782516.1	EST_HUMAN	af55c08.s1 Soares parathyroid tumor NblHPA Homo sapiens cDNA clone 1360812 3'
11647	23969	37012	6.47	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12370	24731	30676	1.83	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3854	16194	28601	0.91	3.6E-02	X73221.1	NT	H. vulgare Sst1 gene for sucrose synthase

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3681	18201	28807	0.95	3.6E-02	AL068808.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5683	18268	30670	0.71	3.6E-02	X59403.1	NT	C-glutamylcysteine synthetase, phosphoglycerate kinase and triosephosphate isomerase
5683	18268	30688	0.71	3.6E-02	X59403.1	NT	C-glutamylcysteine synthetase, phosphoglycerate kinase and triosephosphate isomerase
5762	18343	30800	0.74	3.6E-02	AF181722.1	NT	Homo sapiens RUC2AS (RUC2) mRNA, complete cds
7078	19813	32406	4.82	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7078	19813	32407	4.82	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7373	18043	30427	0.59	3.6E-02	U67575.1	NT	Methanococcus jannaschii section 117 of 150 of the complete genome
7522	19873	32807	1.92	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cx2 precursor (egp2) gene, complete cds
7769	20212	33075	2.71	3.6E-02	AA714521.1	EST_HUMAN	mw20605.s1 NCL CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_ma2
8164	20586	33485	0.75	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN)
9813	22028	34956	2.18	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9813	22028	34957	2.18	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
918	13472	25920	1.14	3.6E-02	U09506.1	NT	Drosophila melanogaster liggrin mRNA, complete cds
1035	13584	26025	1.23	3.6E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1584	14116	26592	1.12	3.6E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1584	14116	26583	1.12	3.6E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4228	16763	29142	1.67	3.6E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4338	16860	29245	1.51	3.6E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6539	18091	31832	1.27	3.6E-02	J01238.1	NT	Maize actin 1 gene (MACT), complete cds
8618	21051		0.81	3.6E-02	H29951.1	EST_HUMAN	yp44a05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190266 5' similar to contains Alu repetitive element;
9085	21517	34427	2.84	3.6E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928737 3'
10047	22449	35397	1.32	3.6E-02	X76842.1	NT	L.lactis MG1363 gfpE and dnaK genes
11251	23617	36663	2.29	3.6E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
11251	23617	36664	2.29	3.6E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
12384	24777		3.96	3.6E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
595	13165	25568	1	3.6E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
595	13165	25569	1	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
598	13165	25568	2.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
599	13165	25569	2.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1077	13623	26082	2.56	3.4E-02	AW274020.1	EST_HUMAN	xi28407.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1237	13775		5.29	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2289	14796	27314	1.31	3.4E-02	T67160.1	EST_HUMAN	yc20e08.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER28 repetitive element
3408	15933	28366	1.34	3.4E-02	AL183208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3776	16314	28714	0.79	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
3933	16468	28877	3.83	3.4E-02	AW784952.1	EST_HUMAN	RC8-UJ0015-210200-021-A10 UM0015 Homo sapiens cDNA
4638	17154	29534	2.62	3.4E-02	X69789.1	NT	M.musculus S-antigen gene promoter region
5179	17693		2.56	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5207	17710	30074	1.76	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6520	18073		0.67	3.4E-02	BF131628.1	EST_HUMAN	601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5'
7292	18026	30409	5.13	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8822	21296		3.3	3.4E-02	AI869629.1	EST_HUMAN	w189d04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433031 3'
9173	21805	34515	1.21	3.4E-02	AA694886.1	EST_HUMAN	nu70108.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element, contains element MER25 MER25 repetitive element ;
							zq04f11.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
8291	21723		5.55	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRNFTEITAE.NLTKESVTADAGRVEITAANSSGTTKAFINIVLDRPG
387	12974		4.05	3.3E-02	AA398735.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGGQVNTYLLKRETSTAVWTEVSATVARTMKVMKL ... ;
1197	13738	28181	17.95	3.3E-02	AB035897.1	NT	z175e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1647	14178	26647	0.88	3.3E-02	AF110763.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1731	14268		0.91	3.3E-02	AE000700.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2009	14525		1.19	3.3E-02	R09112.1	EST_HUMAN	Aquifex aeolicus section 32 of 109 of the complete genome
3337	16894	28305	0.91	3.3E-02	H02389.1	EST_HUMAN	yf25c08.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:127888 5'
4194	14178	26647	3.66	3.3E-02	AF110763.1	NT	y35h02.r1 Soares placenta Nb2fP Homo sapiens cDNA clone IMAGE:150771 5'
4601	17019	29402	2.03	3.3E-02		NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
6769	18312	32078	19.22	3.3E-02	BF245995.1	EST_HUMAN	Mus musculus tumor rejection antigen gp96 (Trat), mRNA
6769	18312	32078	19.22	3.3E-02	BF245995.1	EST_HUMAN	601833910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6769	18312	32079	19.22	3.3E-02	BF245995.1	EST_HUMAN	601833910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6952	18499		0.42	3.3E-02	L31625.1	NT	Canis familiaris intercellular adhesion molecule-1 (ICAM-1) mRNA, complete cds

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8014	20446	33317	0.55	3.3E-02	AF124162.1	NT	Nicotiana plumbaginifolia methylglutathione synthase sulphurylase (cmt6) gene, partial cds
9567	21990	34917	0.91	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.xt NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3582423 3'
9567	21990	34918	0.91	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.xt NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3582423 3'
10801	23333	36336	3.65	3.3E-02	BF691107.1	EST_HUMAN	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
11856	24103		1.88	3.3E-02	T86545.1	EST_HUMAN	y648f11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
11982	24175		1.85	3.3E-02	AF289565.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
12013	24192		3.11	3.3E-02	M81890.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
136	12742	25182	1.61	3.2E-02	AJ002005.1	NT	Oryzobolus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1153	13688	28136	11.06	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1153	13688	28137	11.08	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
3095	16649	28080	13.9	3.2E-02	BE867353.1	EST_HUMAN	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3711	16251	28856	0.62	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3974	16509	28916	0.64	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
3974	16509	28916	0.64	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4233	16758		20.12	3.2E-02	X94768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4819	17331	28710	3.89	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5030	17540		4.37	3.2E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70L and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5797	18378	31036	2.61	3.2E-02	X68709.1	NT	S.griseocarneum whiG-Stv gene
5797	18378	31037	2.61	3.2E-02	X68709.1	NT	S.griseocarneum whiG-Stv gene
6874	19414	32189	1.63	3.2E-02	M32437.1	NT	Ratpolyomavirus left junction in cell line W98.14
6877	19417		36.16	3.2E-02	T89367.1	EST_HUMAN	y633h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
6966	19503	32281	4.08	3.2E-02	AF173845.1	NT	Alu repetitive element; contains LTR1 repetitive element;
8318	20733	33627	0.9	3.2E-02	11424049	NT	Segulus oedipus tissue kallikrein gene, complete cds
8499	20911	33807	0.58	3.2E-02	AA555015.1	EST_HUMAN	Homo sapiens cytochrome P450, subfamily 11B (phenobarbital-inducible) (CYP2B), mRNA
8851	21265	34196	4.12	3.2E-02	6880565	NT	nt07d11.s1 NCI_CGAP_Pt11 Homo sapiens cDNA clone IMAGE:1029621 similar to gb:X65923 UBIQUITIN-LIKE PROTEIN FUBI (HUMAN);
9495	21928	34849	1.1	3.2E-02	A1278871.1	EST_HUMAN	Mus musculus kinesin family member 3c (Kif3c), mRNA
9495	21928	34850	1.1	3.2E-02	A1278871.1	EST_HUMAN	qm17b04.xt NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10081	22482		4.86	3.2E-02	AA718795.1	EST_HUMAN	zg54b12.s1 Soares pineal gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to
10277	22678	35640	1.17	3.2E-02	U96762.1	NT	gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
							Macaca mulatta chemokine receptor CCR5 mRNA, complete cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11371	23733	36791	4.52	3.2E-02	AB10410.1	EST_HUMAN	q072002.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1914051 3' similar to SW:ILBP_HUMAN
1293	13828		1.98	3.1E-02	4503416	NT	P81161 GASTROTROPIN;
1337	13873	26323	1.96	3.1E-02	P18845	SWISSPROT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1856	14378	26869	1.02	3.1E-02	6871564	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1919	14438		1.06	3.1E-02	Z60087.1	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5162	17666		1.98	3.1E-02	BE091889.1	EST_HUMAN	Drosophila melanogaster mRNA for headcase protein
5514	18104	30348	1.47	3.1E-02	U78104.1	NT	IL2-BT0733-130400-067-A08 BT0733 Homo sapiens cDNA
5616	18203		2.56	3.1E-02	AA278478.1	EST_HUMAN	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5916	18494	31177	0.79	3.1E-02	BF687742.1	EST_HUMAN	z881a08.11 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5989	24597	31251	0.45	3.1E-02	AJ391284.1	NT	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
10059	22460	35412	3.04	3.1E-02	AF034779.1	NT	Nelisseria meningitidis DNA for region 2 (flaB- and flhA-homologs, unknown genes) and flanking genes, strain FAM18
1634	14166		1.77	3.0E-02	AF187125.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
2506	16007	27518	1.13	3.0E-02	AA402242.1	EST_HUMAN	Ptyokines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
3554	16096	28513	1.1	3.0E-02	M94178.1	NT	z665f03.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3653	16193	28600	3.06	3.0E-02	AF247844.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3744	16283		0.78	3.0E-02	AW820223.1	EST_HUMAN	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3960	16495		1.02	3.0E-02	AA364003.1	EST_HUMAN	QV2-ST0296-150200-040-e09 ST0296 Homo sapiens cDNA
5164	17668	30029	8.92	3.0E-02	AF281074.1	NT	EST74530 Pineal gland II Homo sapiens cDNA 5' end
5164	17668	30030	8.92	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5292	17792	30158	5.5	3.0E-02	BE889917.1	EST_HUMAN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5847	18234		3.7	3.0E-02	AB046793.1	NT	601649872R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933928 3'
6576	19127	31870	0.65	3.0E-02	N99816.1	EST_HUMAN	Homo sapiens mRNA for KIAA1573 protein, partial cds
6576	19127	31871	0.65	3.0E-02	N99815.1	EST_HUMAN	z399a10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284908 5' similar to contains element TAR1 repetitive element;
7176	19898	32711	3.07	3.0E-02	AJ242806.1	NT	z399a10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284908 5' similar to contains element TAR1 repetitive element;
7314	19726	32528	2.85	3.0E-02	BE889948.1	EST_HUMAN	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
7314	19726	32528	2.85	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7504	19708	32508	2.23	3.0E-02	AF213884.1	NT	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
							Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7604	19708	32509	2.23	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7680	20125	32978	1.2	3.0E-02	M86524.1	NT	Human dystrophin gene
8101	20527		0.59	3.0E-02	BF246361.1	EST_HUMAN	601854881F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
9209	21641		2.04	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10349	22749	35716	2.13	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
11000	23429	36447	1.73	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11420	23781	36841	5.3	3.0E-02	AA483216.1	EST_HUMAN	ne87f04.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
11982	24946	30466	2.73	3.0E-02	R32019.1	EST_HUMAN	YH63d04.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:134407 3'
12355	24414		7.21	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187405 NN0038 Homo sapiens cDNA
12398	24940		3.43	3.0E-02	AF048887.1	NT	Rattus norvegicus UDP-Gal:glucosylcaramide beta-1,4-galactosyltransferase mRNA, complete cds
2334	15334	27356	4.7	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3548	16060	28508	0.59	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
3941	18476	28886	0.83	2.9E-02	H72805.1	EST_HUMAN	y407e10.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:233130 5'
6389	18927	31692	1.41	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6617	19167	31920	7.16	2.9E-02	BF032233.1	EST_HUMAN	601452681F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855598 5'
7365	19822	32836	0.49	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flacC-homologs, unknown genes) and flanking genes, strain FAM18
7698	20143	33000	10.68	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7908	20347	33214	0.71	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
8508	20920	33816	0.48	2.9E-02	AE003932.1	NT	Xylella fastidiosa, section 78 of 228 of the complete genome
8633	21068	33977	0.84	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlectendalla chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
8633	21068	33978	0.84	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlectendalla chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9803	22206	35143	1.93	2.9E-02	AW876979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9803	22206	35144	1.93	2.9E-02	AW876979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10270	22871	35634	1.13	2.9E-02	AP000054.1	NT	Aeropyrum pernix genomic DNA, section 77
10830	16090	28508	1.84	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
11538	23895	36978	2.42	2.9E-02	R01455.1	EST_HUMAN	y675a03.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:123532 5'
11984	24947		1.38	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002982 5'
582	13163		0.7	2.9E-02	AW970163.1	EST_HUMAN	EST382234 IMAGE resequences, MAGK Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2374	14879		2.34	2.8E-02	AA782516.1	EST_HUMAN	ai55c08.s1 Soares parathyroid tumor_NHHPA Homo sapiens cDNA clone 1360912 3'
4332	18864		0.68	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5190	17694	30055	1.73	2.8E-02	8878677	NT	Mus musculus leptin (Lep), mRNA
5330	17829						Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
5748	18330	30784	5.11	2.8E-02	U52111.2	NT	
7189	18910	32739	13.48	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948087 5'
8873	21307	34219	1.1	2.8E-02	T78860.1	EST_HUMAN	Yd21b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5'
8873	21307	34219	2.23	2.8E-02	AJ005820.1	NT	Craterostigma plantaginum mRNA for homeodomain leucine zipper protein (hb-1)
9352	21784	34692	0.86	2.8E-02	AA280762.1	EST_HUMAN	zs98a08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711468 5'
9481	21912	34836	1.01	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
12281	24771		1.46	2.8E-02	R08866.1	EST_HUMAN	Yf12h02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126875 5'
12289	24378		1.18	2.8E-02	X06322.1	NT	Yeast CNA31C chromosome III RAHS DNA (right arm transcription hot-spot)
1517	14049	28513					Human geminine T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
3409	15954	28367	1.06	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4218	16743	29131	3.05	2.7E-02	AL161494.2	NT	Y86h12.r1 Soares multiple sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:280487 5'
4218	16743	29132	1.89	2.7E-02	N47258.1	EST_HUMAN	Y86h12.r1 Soares multiple sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:280487 5'
5497	18088	30330	0.63	2.7E-02	BF245872.1	EST_HUMAN	60188481F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5698	18283	30707					Y63d08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to
6183	18759	31482	1.24	2.7E-02	R12245.1	EST_HUMAN	SP-JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6856	19493		0.75	2.7E-02	X81670.1	NT	T.aestivum pTTH20 mRNA for wheat type V thionin
7489	19703	32502	1.11	2.7E-02	X97580.1	NT	A.bisporus pgkA gene
8455	20868		1.91	2.7E-02	AA993571.1	EST_HUMAN	at66h03.s1 Soares total_fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1624661 3'
8494	20906	33801	0.63	2.7E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00048 protein, partial cds
8893	21327		0.68	2.7E-02	9258542	NT	Mus musculus G21 protein (G21), mRNA
588	13158	25562	1.26	2.7E-02	AI377036.1	EST_HUMAN	lc28g08.x1 Soares total_fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element
1400	13934		1.36	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2261	14769	27288	19.4	2.6E-02	AW850515.1	EST_HUMAN	IL3-CT0219-280100-082-C09 CT0219 Homo sapiens cDNA
2263	14771	27290	1.62	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:839595 3'
			1.87	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA

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2263	14771	27291	1.87	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2869	16424		1.12	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNIP genes, complete cds; G7A gene, partial cds; and unknown genes
3978	16513		1.2	2.6E-02	AW161945.1	EST_HUMAN	x188f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2662409 3'
4691	17177		2.66	2.6E-02	BE989822.1	EST_HUMAN	601649877R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933786 3'
4973	17484	28861	4.16	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5189	17693	30054	1.35	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 161 of 229 of the complete chromosome 1
5227	17729	30097	1.91	2.6E-02	AW241154.1	EST_HUMAN	x52b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2670383 3' similar to SW:Y069_HUMAN
6131	18700		0.41	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6180	18747		0.65	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6637	19089		7.25	2.6E-02	AI206030.1	EST_HUMAN	q92711.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1702317 3'
6764	19307	32072	2	2.6E-02	BE621748.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
7220	19832	32648	0.95	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeih
7220	19832	32649	0.95	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeih
7318	19730	32534	6.03	2.6E-02	6981271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7768	20202	33064	0.72	2.6E-02	P21894	SWISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
9008	21439	34349	0.89	2.6E-02	AA860946.1	EST_HUMAN	ak22f04.s1 Soares_Ieslis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
9591	22071	34898	1.37	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
10306	22706	35671	5.81	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11140	23591		2.08	2.6E-02	AA276351.1	EST_HUMAN	z984c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704182 5'
11314	23678	36730	1.52	2.6E-02	AW600547.1	EST_HUMAN	U1-HF-BN0-ak-6-10-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
11899	24932	30463	1.44	2.6E-02	BF343827.1	EST_HUMAN	602016501F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4160944 5'
550	13122	25531	1.74	2.6E-02	AI783130.1	EST_HUMAN	on26f08.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
550	13122	25532	1.74	2.6E-02	AI783130.1	EST_HUMAN	on26f08.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
832	13389	28828	23.18	2.6E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
892	13447	28896	6.93	2.6E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
2722	16212		1.88	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2910	15465	27887	2.05	2.5E-02	X99897.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/b binding protein, Fcp1
2910	15465	27888	2.05	2.5E-02	X99897.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/b binding protein, Fcp1
4057	17895	28979	1.12	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4057	17895	28980	1.12	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4221	16748	29136	5.12	2.5E-02	AW592114.1	EST_HUMAN	h36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
6240	17899		0.94	2.5E-02	AI754201.1	EST_HUMAN	cr21f11.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr21f11 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5985	18561	31246	0.82	2.5E-02	A1732776.1	EST_HUMAN	z883c10.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810354 3'
6507	18061		5.27	2.5E-02	BE570128.1	EST_HUMAN	7e30e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.H1 L1
6526	18078		3.68	2.5E-02	BE748888.1	EST_HUMAN	repetitive element:
6686	19214	31862	0.93	2.5E-02	L29029.1	NT	601676393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928064 5'
8199	20620	33506	1.79	2.5E-02	BF526722.1	EST_HUMAN	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
8199	20620	33507	1.79	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCL CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213408 5'
8451	20865	33767	0.68	2.5E-02	AF129498.1	NT	602070562F1 NCL CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213408 5'
10592	23037	36020	1.76	2.5E-02	Q10335	SWISSPROT	Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene, complete cds
10592	23037	36021	1.76	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
10646	23086	36071	2.24	2.5E-02	AJ237936.1	NT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
							Bos taurus partial stat5B gene, exons 17-19
10694	23104		2.65	2.5E-02	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Aalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds;
11474	23832		2.72	2.5E-02	AB007546.1	NT	butyrophilin-like (NG9), butyrophilin-like
11527	23865		6.1	2.5E-02	U51002.1	NT	Homo sapiens gene for LECT2, complete cds
11845	24882		1.82	2.5E-02	11420078	NT	Mus musculus Dix-2 gene, complete cds
12040	24719		1.74	2.5E-02	11433220	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
12145	24276		1.59	2.5E-02	U60169.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12171	24293	30638	2.88	2.5E-02	BE973327.1	EST_HUMAN	Dichytellum discoideum putative protein kinase Mica (mka) gene, complete cds
178	12781	26197	0.88	2.4E-02	AI378582.1	EST_HUMAN	601662366R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
1615	14146	26618	1.54	2.4E-02	H65884.1	EST_HUMAN	601662366R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
1976	15326	27001	1.08	2.4E-02	P01901	SWISSPROT	601662366R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
1975	15326	27002	1.08	2.4E-02	P01901	SWISSPROT	601662366R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
4390	16912	29296	1.11	2.4E-02	J05110.1	NT	y7511.1 Soares fetal liver spleen 1N1S Homo sapiens cDNA clone IMAGE:211149 5'
4557	17074	29459	1	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4557	17074	29459	1	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6632	16084	31825	1.17	2.4E-02	W66680.1	EST_HUMAN	T.thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
6693	19240	31890	0.5	2.4E-02	M31650.1	NT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6693	19240	31891	0.5	2.4E-02	M31650.1	NT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
7699	20115	32668	1.09	2.4E-02	Z20573.1	EST_HUMAN	z63104.st Soares fetal liver spleen 1N1S_S1 Homo sapiens cDNA clone IMAGE:416761 3'
7699	20131	32985	1	2.4E-02	X12925.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7699	20131	32986	1	2.4E-02	X12925.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
8493	20906	33769	0.68	2.4E-02	P88092	SWISSPROT	HSAAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
							Rat gene for uncoupling protein (UCP)
							HEMOCYTIN PRECURSOR (HUMORAL LECTIN)

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8493	20905	33800	0.98	2.4E-02	P98092	SWISSPROT	HEMOCTIN PRECURSOR (HUMORAL LECTIN)
9020	21453	34363	5.77	2.4E-02	N69442.1	EST_HUMAN	z335g11.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:294596 3' similar to gb K02909 RATSR7K Rat (fRNA); contains A3R.b1 A3R repetitive element;
9346	21778	34685	1	2.4E-02	AA625680.1	EST_HUMAN	z381c08.s1 Soares testis NH-T Homo sapiens cDNA clone IMAGE:745354 3' similar to gb J04422 ISLET
9896	22298	35240	2.22	2.4E-02	AV692854.1	EST_HUMAN	AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR XTR repetitive element;
10019	22421	35371	3.3	2.4E-02	AA493894.1	EST_HUMAN	AV692854 GKC Homo sapiens cDNA clone GK05C03 5'
11323	23687	36737	2.21	2.4E-02	AF109905.1	NT	nm07b12.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element;
11323	23687	36738	2.21	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11630	23957		1.88	2.4E-02	9627909	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11789	24056	31025	3.72	2.4E-02	6753635	NT	Bacteriophage bil67, complete genome
11847	24096	30994	1.42	2.4E-02	BE928869.1	EST_HUMAN	Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA
11936	24148		1.51	2.4E-02	AF163864.1	NT	MRO-FT0175-310800-202-a06 FT0175 Homo sapiens cDNA
12089	24240		5.66	2.4E-02	AB008569.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
12119	24260		1.72	2.4E-02	N42980.1	EST_HUMAN	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12294	24687	30775	1.28	2.4E-02	AA178693.1	EST_HUMAN	yy08a08.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270610 5'
1842	14364		3.66	2.3E-02	W05340.1	EST_HUMAN	zp13h01.r1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
1852	14374		4.94	2.3E-02	U94165.1	NT	z384g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299294 5'
2248	14754	27274	1.93	2.3E-02	Z74293.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
3681	16221	28629	8.23	2.3E-02	Z20377.1	EST_HUMAN	S.cerevisiae chromosome IV reading frame ORF YDL245c
3712	16252		0.76	2.3E-02	L23429.1	NT	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
4168	16695	28082	0.82	2.3E-02	L24789.1	NT	Canis beta-galactoside-binding lectin (LGALS3) mRNA, 3'end
4198	16695	28083	0.82	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4448	16988	28355	1.03	2.3E-02	AW899107.1	EST_HUMAN	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4479	16989	28381	0.76	2.3E-02	BE935225.1	EST_HUMAN	CM4-NN0080-290-400-160-b04 NN0080 Homo sapiens cDNA
4478	16989	28382	0.76	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4480	17886	28383	0.98	2.3E-02	AW593693.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
							xs25608.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2770871 3'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar: (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4480	17986	29384	0.98	2.3E-02	AW563893.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2770871 3'
4813	17129	28514	0.99	2.3E-02	BE143150.1	EST_HUMAN	MRO-HT0169-151089-001-e03 HT0169 Homo sapiens cDNA
4834	17150	28530	2.29	2.3E-02	BF028487.1	EST_HUMAN	601872279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4834	17150	28531	2.29	2.3E-02	BF028487.1	EST_HUMAN	601872279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5122	17628		9.31	2.3E-02	7662173	NT	Homo sapiens KIAA0547 gene product (KIAA0547), mRNA
5631	18218	30619	3.97	2.3E-02	U86303.1	NT	Caulobacter crescentius topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcdB) homolog gene, partial cds
6556	19108	31862	0.63	2.3E-02	BF106484.1	EST_HUMAN	601822921R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3'
6979	19516	32298	4.44	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7397	18066	30356	0.72	2.3E-02	BE141476.1	EST_HUMAN	MRO-HT0080-011089-002-c09 HT0080 Homo sapiens cDNA
7948	20385	33251	0.5	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8646	20981	33879	3.35	2.3E-02	U63810.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8980	21413	34327	1.08	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8980	21413	34328	1.08	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
9430	21862	34778	0.92	2.3E-02	P41998	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
8937	22339	35288	0.6	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10058	22459	35410	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10058	22459	35411	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10565	23012	35989	2.63	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE)(1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
11791	24702		5.69	2.3E-02	BE276331.1	EST_HUMAN	601178995F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12209	24325	30918	1.32	2.3E-02	BF528482.1	EST_HUMAN	602043629F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181454 5'
12209	24325	30919	1.32	2.3E-02	BF528482.1	EST_HUMAN	602043629F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181454 5'
12326	24395	30887	2.02	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12365	24973		2.16	2.3E-02	U11077.1	NT	Dictyostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
12608	24806		1.71	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRILL1), mRNA
758	13318	25747	4.07	2.2E-02	AF018287.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1739	14266		1.44	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1953	14471	26976	1.07	2.2E-02	Z62001.1	NT	S.pneumoniae pcpA gene and open reading frames
2680	15346	27682	1.29	2.2E-02	AF109633.1	NT	Mus musculus ets variant protein ER81 gene, exons 1 through 4
3412	16957		2.05	2.2E-02	AA577785.1	EST_HUMAN	hm24e04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3646	16196		3.83	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3859	16395	28798	0.98	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-503 BT0340 Homo sapiens cDNA
3932	16487	28876	1.01	2.2E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
5445	17940	30289	11.2	2.2E-02	BF540825.1	EST_HUMAN	602067538F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066889 5'
7693	20141	32888	3.22	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND003 3'
8909	21343	34259	2.11	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8909	21343	34260	2.11	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9824	22227	35163	2.74	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9824	22227	35164	2.74	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10180	22681		1.33	2.2E-02	6878140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
10981	23410	36422	2.71	2.2E-02	BE797601.1	EST_HUMAN	601684309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938571 5'
11526	23884	36967	2.68	2.2E-02	11423632	NT	Homo sapiens transmembrane protein 1 (TMEM1), mRNA
12045	24214		3.06	2.2E-02	AA503553.1	EST_HUMAN	he47h07.a1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
436	13010		6.39	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
466	13040		10.04	2.1E-02	AF029726.1	NT	Dictyostellum discoideum histidine Kinase C (dhkc) mRNA, complete cds
1298	13831	26280	7.72	2.1E-02	U72073.1	NT	Bacillus subtilis cotLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1419	13952	28407	3.36	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1419	13952	28408	3.36	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
2774	13360	25795	3.86	2.1E-02	N29266.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:264541 5'
3575	16117	28532	1.12	2.1E-02	AA461271.1	EST_HUMAN	z63b09.r1 Soares_total_tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786121 5'
4148	16678	29054	0.81	2.1E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
4329	18851	29237	0.72	2.1E-02	BF343855.1	EST_HUMAN	602015306F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4151161 5'
4475	16995	29377	1.77	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
4760	17274	29658	5.69	2.1E-02	Y08501.1	NT	A. thaliana mitochondrial genome, part A
4780	17294	29678	0.82	2.1E-02	AA665737.1	EST_HUMAN	ag55g12.a1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4878	17388	29760	0.63	2.1E-02	AI823432.1	EST_HUMAN	wf54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5908	18486	31168	0.72	2.1E-02	AW378528.1	EST_HUMAN	GM4-HT0244-111198-040-105 HT0244 Homo sapiens cDNA
7498	19702	32501	0.66	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120800-329-at12 GN0058 Homo sapiens cDNA
9012	21445	34367	0.87	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9784	22187	35123	2.52	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9784	22187	35124	2.52	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10021	22423	35373	1.38	2.1E-02	L29324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
11253	23619	36668	1.72	2.1E-02	6754265	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp68a), mRNA
11472	23830	36898	1.86	2.1E-02	AW844320.1	EST_HUMAN	RC4-NCN050-130200-012-h04_1 CN0050 Homo sapiens cDNA
12024	18008		8.15	2.1E-02	Y19213.1	NT	Homo sapiens putative psinHbA pseudogene for hair keratin, exons 2 to 7
12065	24639	30779	1.18	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12495	24502	30853	4.85	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
18	12638	25025	1.22	2.0E-02	BF002932.1	EST_HUMAN	7951c08.x1 NC1_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
19	12839	25028	10.27	2.0E-02	AW895535.1	EST_HUMAN	MER1 repetitive element;
272	12870	25286	3.51	2.0E-02	6753635	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
309	12904	25324	2.8	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
821	13379	25816	2.24	2.0E-02	6753635	NT	aa15b10.r1 Soares_NhHMPu_ST1 Homo sapiens cDNA clone IMAGE:813307 5'
1114	13658	26099	1.59	2.0E-02	AL096805.1	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1230	13769	26216	1.2	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens
1230	13769	26217	1.2	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1843	14385	26858	1.46	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1843	14385	26859	1.46	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2757	15247		1.56	2.0E-02	AL161632.2	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
3041	12638	25025	2.08	2.0E-02	BF002932.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3104	15657		1.34	2.0E-02	7305474	NT	7951c08.x1 NC1_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
3188	15739		1.72	2.0E-02	AF095588.1	NT	MER1 repetitive element;
4020	16553	28950	1.56	2.0E-02	M18095.1	NT	Mus musculus senna domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B
5250	17751	30119	10.86	2.0E-02	AF189388.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
5268	17769		0.64	2.0E-02	AF127199.1	EST_HUMAN	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5310	17810	30175	0.64	2.0E-02	AA456538.1	EST_HUMAN	Allozymes capsularis catalase isozyme A (CATA) mRNA, complete cds
5903	18481	31163	0.56	2.0E-02	U34778.1	NT	q183e03.x1 NC1_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1866076 3'
6188	18754	31456	0.98	2.0E-02	L35321.2	NT	aa15b10.r1 Soares_NhHMPu_ST1 Homo sapiens cDNA clone IMAGE:813307 5'
8055	20498	33374	0.86	2.0E-02	AP000004.1	NT	Caenorhabditis elegans sma-2 mRNA, complete cds
8065	20498	33375	0.86	2.0E-02	AP000004.1	NT	Dicystostellum discoidaleum class VII unconventional myosin (myo) gene, complete cds
						NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
						NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9950	22362		2.17	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10280	22681	35643	1.82	2.0E-02	AI640342.1	EST_HUMAN	wat7602.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
10439	22891	35867	3.2	2.0E-02	Z73966.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 93/182
11568	17810	30176	1.66	2.0E-02	AA456538.1	EST_HUMAN	aat5b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:313307 5'
12082	15247		1.95	2.0E-02	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
12576	24727		1.5	2.0E-02	BE786595.1	EST_HUMAN	601478816F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881477 5'
12583	24561		3.77	2.0E-02	T80037.1	EST_HUMAN	y04c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24675 5'
713	13274	25694	2.4	1.9E-02	AA572784.1	EST_HUMAN	nf10a07.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914186 similar to contains L1.t1 L1 repetitive element;
1871	14489	26997	2.11	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1971	14489	26998	2.11	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2414	14918	27435	1.96	1.9E-02	AL161650.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2858	15413	27833	10.15	1.9E-02	AA713856.1	EST_HUMAN	rw04f05.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2906	15461	27885	1.8	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3220	15772		0.71	1.9E-02	AB033811.1	NT	Utrichus talpoides mitochondrial gene for cytochrome b, complete cds
3605	16145		1.5	1.9E-02	N52250.1	EST_HUMAN	yz28b02.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:284331 3'
3700	16240		7.99	1.9E-02	BE738038.1	EST_HUMAN	601572882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
4059	16590	28982	1.46	1.9E-02	AF141940.1	NT	Mycoplasma litans Vha1 precursor (vha1) and Vha2 precursor (vha2) genes, partial cds
4209	16734	28124	1.83	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4209	16734	28125	1.83	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4577	17093	29481	2.77	1.9E-02	AA52989.1	EST_HUMAN	h4ed04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144561 3' similar to contains Alu repetitive element
4788	17302		3.39	1.9E-02	AF178754.3	NT	Homo sapiens lithium-sensitive myo-inositol monophosphatase A1 (IMPA1) gene, promoter region and partial cds
5114	14918	27435	2.25	1.9E-02	AL161650.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5263	17764	30133	2.78	1.9E-02	AW500705.1	EST_HUMAN	UHFF-BND-akm-e-08-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077487 5'
5599	18157	30521	0.98	1.9E-02	AF037382.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5727	18309	30740	1.62	1.9E-02	L47872.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
6071	18643		0.72	1.9E-02	AB019507.1	NT	Drosophila kanakel gene for glycerol-3-phosphate dehydrogenase, complete cds
7529	19980		0.52	1.9E-02	AF101236.1	NT	Naja sputatrix neutral phospholipase A2 (NPLA2) gene, complete cds
7540	19990	32827	1.3	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7540	19990	32828	1.3	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
9051	21483		1.14	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 3/7
9572	21995	34925	1.1	1.9E-02	BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125482 5'

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10072	22473	35430	1.4	1.8E-02	BF695932.1	EST_HUMAN	601852385F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076253 5'
11789	24707	30781	2.88	1.9E-02	AF101095.1	NT	Hirudo medicinalis intermediate filament gillrin mRNA, complete cds
360	12850	25384	1.91	1.8E-02	AW771104.1	EST_HUMAN	hm52c06.x1 NCL_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
705	13287	25683	0.58	1.8E-02	BF308122.1	EST_HUMAN	MER29 repetitive element
1180	13731	26174	1.53	1.8E-02	X17684.1	NT	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138883 5'
2820	15115	27629	5.81	1.8E-02	AE004544.1	NT	H.francisci mRNA for myelin basic protein (MBP)
3189	15722		0.53	1.8E-02	AI805829.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3896	16431	28837	1.09	1.8E-02	AW879122.1	EST_HUMAN	tes2a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3888	16431	28838	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4102	16633		1.13	1.8E-02	AA861446.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4459	16978	28385	1.74	1.8E-02	AW936363.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
5042	17582	29923	1.07	1.8E-02	CG0810	SWISSPROT	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
5453	17948	30289	0.8	1.8E-02	AA649300.1	EST_HUMAN	HYPOTHETICAL PROTEIN DJ846024.2
6721	19287	32024	0.53	1.8E-02	AE002518.1	NT	ns31g09.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1185280 3'
6721	19287	32025	0.53	1.8E-02	AE002518.1	NT	Neisseria meningitidis serogroup B strain MC58 section 160 of 206 of the complete genome
7200	19911	32740	4.66	1.8E-02	P14310	SWISSPROT	Neisseria meningitidis serogroup B strain MC58 section 160 of 206 of the complete genome
7953	20380	33287	0.59	1.8E-02	BF125690.1	EST_HUMAN	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5REGION
7981	20390	33257	0.59	1.8E-02	BF125690.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
							601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
9793	22198		2.08	1.8E-02	AA897543.1	EST_HUMAN	q182p09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb.L11672 ZINC
10085	22486	35443	1.78	1.8E-02	BE778274.1	EST_HUMAN	FINGER PROTEIN 91 (HUMAN);
10195	22590	35562	1.59	1.8E-02	X98933.1	NT	6017463545F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3866963 5'
11186	22838	35809	2.11	1.8E-02	AB002337.2	NT	L.slagnalis mRNA for myomodulin neuropeptide precursor
11186	22838	35810	2.11	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11359	23722	36782	3.64	1.8E-02	AF000008.1	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11375	23737	36785	2.05	1.8E-02	U82749.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (8/7)
							Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
12498	24682		1.24	1.8E-02	AF202180.1	NT	Plasmodium falciparum erythrocyte membrane-associated giant protein antigen 332 (Ag332) gene, partial cds
12560	24683		1.4	1.8E-02	AF047476.1	NT	Drosophila melanogaster projectin (projectin) gene, partial cds
929	13483	25929	1.28	1.7E-02	BE394869.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632180 5'
1769	14295	28780	1.42	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L.1.t1 L1 repetitive element

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1769	14295	28781	1.42	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains
1841	14363		1.87	1.7E-02	AL163204.2	NT	L1.11 L1 repetitive element;
2033	14549		8.99	1.7E-02	AB004816.1	NT	Homo sapiens chromosome 21 segment HS21C004
2577	15073		1.4	1.7E-02	7657495	NT	Oryctolagus cuniculus mRNA for mitoguanin28, complete cds
2952	16507	27928	0.84	1.7E-02	AI147615.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3492	16035		5.05	1.7E-02	AW827368.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3622	16162		0.82	1.7E-02	P04929	SWISSPROT	hm45a04.x1 NCL_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains
3815	16352	28750	0.8	1.7E-02	Q82503	SWISSPROT	MER18.b1 MER19 repetitive element;
3815	16352	28751	0.8	1.7E-02	Q82503	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4185	16712		1.15	1.7E-02	AA689818.1	EST_HUMAN	SEC14-LIKE PROTEIN
4216	16741		1.73	1.7E-02	R02506.1	EST_HUMAN	act19f04.s1 Stratiotes ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu
4484	17003	29389	1.19	1.7E-02	AI305278.1	EST_HUMAN	repetitive element; contains element MER24 repetitive element;
4564	17081	29467	1.34	1.7E-02	AW573183.1	EST_HUMAN	ys65f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124847 5'
4610	17126	29511	1.3	1.7E-02	AB003688.1	NT	qm08g07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X62359 ZINC
4610	17126	29512	1.3	1.7E-02	AB003688.1	NT	FINGER PROTEIN 30 (HUMAN);
4765	17279	29682	1.98	1.7E-02	V00641.1	NT	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains
4847	17359	29744	1.39	1.7E-02	P16170	SWISSPROT	L1.11 L1 repetitive element;
4870	17382		6.77	1.7E-02	AI015078.1	EST_HUMAN	Homo sapiens p27Kip1 gene for cyclin-dependent kinase inhibitor, 5'-flanking region and partial cds
5479	17974		19.51	1.7E-02	AJ006945.1	NT	Homo sapiens p27Kip1 gene for cyclin-dependent kinase inhibitor, 5'-flanking region and partial cds
6438	18994	31725	1.84	1.7E-02	AI769247.1	EST_HUMAN	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
6819	19360		0.46	1.7E-02	Z38383.1	NT	NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS:
6932	19471	32248	1.31	1.7E-02	AI038280.1	EST_HUMAN	N-CAM 140]
7481	19685	32482	1.54	1.7E-02	AF190930.1	NT	ov51a02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
7849	20095	32947	1.84	1.7E-02	8400716	NT	Homo sapiens KVLQT1 gene
7829	20270	33131	0.91	1.7E-02	L07899.1	NT	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to
							contains Alu repetitive element;
							T.niveum (ATCC34921) simA gene for cyclosporine synthetase
							ov51a03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
							Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
							Homo sapiens nebulin (NEB), mRNA
							Human apolipoprotein (a) gene, exon 1

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7829	20270	33132	0.91	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
8294	20710		1.72	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
9645	20936	33833	1.02	1.7E-02	U21854.1	NT	<i>Caenorhabditis elegans</i> cCAF1 protein gene, complete cds
9833	22236	35172	1.5	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434l0314_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434l0314.5
12400	24892	30578	3.14	1.7E-02	AW903482.1	EST_HUMAN	CM4-NN1030-040400-130-06 NN1030 Homo sapiens cDNA
528	13101		2.29	1.6E-02	AL021929.1	NT	<i>Mycobacterium tuberculosis</i> H37Rv complete genome, segment 13/162
1658	14189	26661	1.2	1.6E-02	Y18899.1	NT	<i>Treponema mallophilum</i> flaB2, flaB3 and fliD genes for flagellin subunit proteins and CAP protein homologue
2260	14788		2.7	1.6E-02	4507102	NT	Homo sapiens small nuclear RNA activating complex, polypeptide 2, 45kD (SNAPC2) mRNA
2479	14980	27494	1.34	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ11 gene
2579	15076	27593	4.43	1.6E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCJ CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910887
2642	15137		0.9	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
2978	16531	27950	0.78	1.6E-02	AF112282.1	NT	<i>Leishmania</i> sp. isolate lBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3507	16050	28471	5.77	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-180200-063-C07 CT0219 Homo sapiens cDNA
3854	16390	28780	1.04	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4192	16719		1.7	1.6E-02	AF110520.1	NT	<i>Mus musculus</i> major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
5298	17788		0.77	1.6E-02	N80155.1	EST_HUMAN	z695e07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:287444 3'
5351	17850	30207	0.91	1.6E-02	AL048802.1	NT	Novel human gene mapping to chromosome 13
5503	18094	30337	0.78	1.6E-02	AI281365.1	EST_HUMAN	qu42b09.x1 NCJ CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1967417 3'
5691	18470	31150	1.27	1.6E-02	6971716	NT	<i>Mus musculus</i> CD5 antigen (Cd5), mRNA
7008	19542	32328	2.16	1.6E-02	AB015281.1	NT	<i>Candida albicans</i> CaGCR3 gene, complete cds
7341	19753	32557	1.09	1.6E-02	AB027571.1	NT	<i>Saccharomyces cerevisiae</i> CAD2 gene for cadmium resistance protein, complete cds
7341	19753	32558	1.09	1.6E-02	AB027571.1	NT	<i>Saccharomyces cerevisiae</i> CAD2 gene for cadmium resistance protein, complete cds
8255	20672	33562	1.02	1.6E-02	AL161508.2	NT	<i>Arabidopsis thaliana</i> DNA chromosome 4, contig fragment No. 20
8762	21186		2.83	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
10087	22468		2.68	1.6E-02	AF079764.1	NT	<i>Drosophila melanogaster</i> enhancer of polycomb (E(Pc)) mRNA, complete cds
10315	22715	35681	1.49	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCJ CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN. (1);
10315	22715	35682	1.49	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCJ CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN. (1);
10680	24657	36110	2.03	1.6E-02	Z94628.1	NT	<i>G.gallus</i> microsatellite DNA (LEI0260 (=T16IIIET1))

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10887	23416	36430	2.43	1.6E-02	AL161608.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
10887	23416	36431	2.43	1.6E-02	AL161608.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11284	23630	36679	4.49	1.6E-02	AI373558.1	EST_HUMAN	qz86a10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
11772	18006	30328	1.58	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
11772	18006	30329	1.58	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12167	24291		1.54	1.6E-02	X82751.1	NT	R.norvegicus gene for choline acetyltransferase, exon 1 (non coding)
772	13332		70.31	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2055	14570	27084	2.38	1.5E-02	N39521.1	EST_HUMAN	W27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
2082	14589	27115	2.01	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3723	16263	28668	0.94	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
4160	16687	28073	0.91	1.5E-02	AA160987.1	EST_HUMAN	zq40g10.r1 Strategene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632226 5'
6619	19169	31922	1.35	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7783	20225		1.56	1.5E-02	11467282	NT	Cyanophora paradoxa cyanella, complete genome
7881	20320	33185	1.59	1.5E-02	11418773	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8403	20817	33715	0.8	1.5E-02	AE004347.1	NT	Vibrio cholerae chromosome II, section 4 of 93 of the complete chromosome
8544	20979	33878	1.64	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8548	20983	33882	4.21	1.5E-02	11417739	NT	Homo sapiens vally-IFNA synthetase 2 (VARS2), mRNA
8237	21089	34579	1.24	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4154504 5'
9746	22114	35042	1.58	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9800	22302	35244	0.97	1.5E-02	R32867.1	EST_HUMAN	Yn54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
9800	22302	35245	0.97	1.5E-02	R32867.1	EST_HUMAN	Yn54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10944	23375	36385	2.89	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12001	24763		1.71	1.5E-02	AW760834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
434	13008		1.85	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 68 of 94 of the complete genome
1146	13689	28129	4.42	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1289	13824		1.13	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1330	13866		3.5	1.4E-02	U67778.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
2517	15017	27531	10.35	1.4E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
3171	15724	28144	1.64	1.4E-02	AF160969.2	NT	Bifidobacterium longum Nav/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (eglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyIR) gene, partial cds
3376	15923	28340	0.85	1.4E-02	AW074212.1	EST_HUMAN	X509409.x1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2576793 3'
3480	16004	28423	6.39	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3460	16004	28424	6.39	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3500	16043	28464	0.6	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3656	16196	28603	8.28	1.4E-02	6869918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4525	17043	28423	9.9	1.4E-02	AW982688.1	EST_HUMAN	EST374761 IMAGE reserences, MAGG Homo sapiens cDNA
4525	17043	28424	9.9	1.4E-02	AW982688.1	EST_HUMAN	EST374761 IMAGE reserences, MAGG Homo sapiens cDNA
4935	17446	28821	6.98	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4935	17446	28822	6.98	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4988	17506		1.01	1.4E-02	BF329848.1	EST_HUMAN	RC5-BN0283-120800-033-E02 BN0283 Homo sapiens cDNA
5218	17721	30088	1.84	1.4E-02	D10014.1	NT	Homo sapiens CYP2E1 gene for cytochrome P4501E1, promoter region and partial cds
5229	17731	30100	0.65	1.4E-02	AW948453.1	EST_HUMAN	CMO-FN0041-120500-370-h09 FN0041 Homo sapiens cDNA
6074	24982		0.71	1.4E-02	X91338.1	NT	H.sapiens LaSS-B pseudogene 3
6754	19297	32062	4.91	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
6754	19297	32063	4.91	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
8729	21164		1.45	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
9276	21708	34618	0.83	1.4E-02	M81702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds
9442	21873	34791	1.47	1.4E-02	AJ27285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9820	22035	34966	2.42	1.4E-02	BE544581.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10408	22808		0.93	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11679	23988	36556	5.72	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12124	24262		2.19	1.4E-02	Z23080.1	NT	C.aetobutylicum dnaE and sigA genes for primase and major vegetative sigma factor
12388	24418		2.22	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1835	14357		0.9	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3826335 5'
1805	14424	26921	1.33	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3172	15725	28145	2.12	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3172	15725	28146	2.12	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3983	16518		1.59	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5495	18096	30380	1.36	1.3E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28arf
5495	18096	30381	1.36	1.3E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28arf
6478	19033	31771	1.04	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6512	18066	31808	0.8	1.3E-02	M62862.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7377	18047	30383	1.61	1.3E-02	AL161648.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
7377	18047	30384	1.61	1.3E-02	AL161648.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
8084	20521	33401	5.02	1.3E-02	A031593.1	EST_HUMAN	ow08g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
8517	20928	33825	0.51	1.3E-02	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8989	21422	34334	1.6	1.3E-02	AF156901.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10182	22683	35548	1.89	1.3E-02	M63707.1	NT	Mouse kidney endrogen-regulated protein (KAP) gene, complete cds
10231	22632	35596	1.03	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10773	23211	36183	4.28	1.3E-02	AW268563.1	EST_HUMAN	x34403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10773	23211	36194	4.28	1.3E-02	AW268563.1	EST_HUMAN	x34403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11685	24921		1.88	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
12063	24910		1.7	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2590451 to 2812870
12176	24288		2.16	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
12374	24073		10.5	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
12598	24960	30488	1.56	1.3E-02	AF009179.1	NT	Oryza sativa replication protein A1 (Os-RPA1) mRNA, complete cds
220	12822		0.68	1.2E-02	X87344.1	NT	H.sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
369	12858	25375	4.04	1.2E-02	AA059299.1	EST_HUMAN	z165g01.r1 Soares_reliha N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element
470	13044	25485	2.12	1.2E-02	F38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3 REGION
759	13319	25748	7.25	1.2E-02	A183522.1	EST_HUMAN	q468e12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.11 L1 repetitive element
2085	14599	27117	1.13	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2403	14907	27425	4.78	1.2E-02	BE538310.1	EST_HUMAN	601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2403	14907	27426	4.78	1.2E-02	BE538310.1	EST_HUMAN	601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2571	14848	27366	1.99	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659492 3'
3083	15817		7.19	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3249	15800	28217	2.25	1.2E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
3252	15803	28220	0.68	1.2E-02	A1668694.1	EST_HUMAN	zb66e07.x5 Soares_fetal_Jung_NbHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element
4778	17290	29675	4.02	1.2E-02	A1887378.1	EST_HUMAN	wm39f04.x1 NCJ_CGAP_U14 Homo sapiens cDNA clone IMAGE:2438335 3'
4942	17453	29830	2.84	1.2E-02	6754367	NT	Mus musculus Interferon regulatory factor 5 (IRF5), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4989	17499	29874	2.35	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5149	17663		1.33	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiq1 mRNA, partial cds
5215	17718	30084	1.66	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5955	18531		0.52	1.2E-02	AA759018.1	EST_HUMAN	si28f10.s1 Soares testis NIH HT Homo sapiens cDNA clone 1344235 3'
6031	18605	31292	2.17	1.2E-02	D78598.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6428	18984	31717	0.69	1.2E-02	AF049555.1	NT	Homo sapiens wbscr1 (WBSOR1) and wbscr5 (WBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7428	19833	32768	5.74	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7750	20184	33056	1.15	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7776	20218	33080	7.33	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
8071	20500	33379	0.67	1.2E-02	BF216650.1	EST_HUMAN	801882949f1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066253 5'
8632	21067	33976	2.16	1.2E-02	Q11205	SWISSPROT	CMF-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
8769	21203	34105	1.36	1.2E-02	AF183812.1	NT	Homo sapiens fringe protein mRNA, partial cds
8789	21203	34108	1.36	1.2E-02	AF183812.1	NT	Homo sapiens fringe protein mRNA, partial cds
9270	21702		0.97	1.2E-02	T76987.1	EST_HUMAN	y072a08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'
9790	22183	35130	2.68	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9812	22215	35151	1.36	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
11736	24025	31012	1.4	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU) (HPER)
12384	24427		5.09	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujlwara) Homo sapiens cDNA clone GEN-557G08 5'
12614	24584		1.24	1.2E-02	X95450.1	NT	Endogenous sheep retrovirus LTR, locus 6
1302	13837	26288	1.22	1.1E-02	AA070364.1	EST_HUMAN	zn69e1.1.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530824 3'
1704	14232	26716	1.6	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
1704	14232	26717	1.6	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
1970	14488	26996	3.17	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4163808 5'
2832	15388		3.63	1.1E-02	N98523.1	EST_HUMAN	z840e05.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5'
3504	16047	28489	2.98	1.1E-02	AI653508.1	EST_HUMAN	tq65b10.x1 NCI CGAP_OV23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW.XPF_HUMAN
4033	16568		3	1.1E-02	BE144637.1	EST_HUMAN	PM3-HT0175-300899-001-108 HT0175 Homo sapiens cDNA
4123	16652		0.9	1.1E-02	AW813786.1	EST_HUMAN	RC3-ST0197-120203-015-g11 S10197 Homo sapiens cDNA
4886	17398	28759	1.53	1.1E-02	AL046383.2	EST_HUMAN	DKFZp586E0924_g1 686 (synonym: huter1) Homo sapiens cDNA clone DKFZp586E0924

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5163	17667	30028	1.05	1.1E-02	AW975815.1	EST_HUMAN	EST387824 IMAGE resequences, MAGN Homo sapiens cDNA
5450	17945	30286	1.31	1.1E-02	AW197270.1	EST_HUMAN	nm41d05.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2886761 3' similar to contains OFR.b1 OFR repetitive element:
6482	19018	31752	0.95	1.1E-02	U69480.1	NT	Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynaB), YnaC (ynaC), YnaD (ynaD), YnaE (ynaE), YnaF (ynaF), YnaG (ynaG), YnaH (ynaH), YnaI (ynaI), YnaJ (ynaJ), xylan beta-1,4-xylanase
8122	20548	33423	1.77	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-107 HT0256 Homo sapiens cDNA
8404	20818	33716	0.65	1.1E-02	9831204	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
9279	21711	34622	8.16	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
8989	22391	35342	2.16	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stralagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10111	22512	35477	2.4	1.1E-02	AA314665.1	EST_HUMAN	EST186404 Cdon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10761	23188	36186	2.83	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
11477	23835	36903	1.68	1.1E-02	M80478.1	NT	Human platelet glycoprotein IX precursor (gPIX) gene, complete cds
11615	23946		2.71	1.1E-02	AA698239.1	EST_HUMAN	ab77111.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains Alu repetitive element:
12449	16852		1.45	1.1E-02	AW813786.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
6	12828	25015	9.5	1.0E-02	AW846120.1	EST_HUMAN	MR3-GT0176-111098-003-e10 GT0176 Homo sapiens cDNA
1547	14079	26540	1	1.0E-02	AW368128.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3052	15808	28016	3.27	1.0E-02	BE835556.1	EST_HUMAN	RC0-FN0025-250500-021-402 FN0025 Homo sapiens cDNA
3224	15776	28194	1.26	1.0E-02	BE868989.1	EST_HUMAN	601649867R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3833689 3'
3488	16031		0.72	1.0E-02	AW845621.1	EST_HUMAN	MRO-CT0060-081098-003-h10 CT0060 Homo sapiens cDNA
3889	16424	28829	0.94	1.0E-02	AI065088.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
3905	16440	28846	0.67	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HSZ1C102
4829	17341	28723	5.44	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4902	17413	28785	4.66	1.0E-02	R66567.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:199633 5'
5101	17610	29971	1.11	1.0E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5672	18297	30657	0.74	1.0E-02	H52881.1	EST_HUMAN	yq36h11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235841 5'
6025	18599	31288	0.7	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6427	18993	31716	1.27	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (SY2) gene, complete cds
6495	19049	31788	3.04	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6495	19049	31789	3.04	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
7143	19856	32676	0.88	1.0E-02	Z29842.1	NT	Zmays U3snRNA pseudogene
9614	22029	34958	2.44	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9814	22029	34959	2.44	1.0E-02	BF036331.1	EST_HUMAN	601459370F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177 5'
11125	23577	36619	3.43	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
11699	24980		1.89	1.0E-02	Q62203	SWISSPROT	SPUCEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
11762	24726	30874	3.46	1.0E-02	AW939521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
11781	24788		6.07	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12360	24850		3.86	1.0E-02	XG2654.1	NT	H. sapiens gene for Me497/CD63 antigen
12600	24574	30835	1.2	1.0E-02	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
816	13470	25918	2.26	9.0E-03	AJ766128.1	EST_HUMAN	wh4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1297	13832		1.89	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element
2263	14800	27318	3.26	9.0E-03	AL161559.2	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873348 5'
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2568	15066	27681	1.89	9.0E-03	AJ243727.1	NT	Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2568	15066	27582	1.89	9.0E-03	AJ243727.1	NT	Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2859	15414	27834	0.73	9.0E-03	AJ251744.1	EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
2859	15414	27835	0.73	9.0E-03	AJ251744.1	EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3688	16208	28613	1.05	9.0E-03	J05184.1	NT	S. acidoalcalarius thermophilus gene, complete cds
5065	17595	29962	1	9.0E-03	BE047849.1	EST_HUMAN	tz44e10.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291468 5'
5385	17882		0.81	9.0E-03	AV747729.1	EST_HUMAN	AV747729 NPCO Homo sapiens cDNA clone NPCBSF05 5'
6094	18663		1.21	9.0E-03	AJ809792.1	EST_HUMAN	wt77f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
6991	19528		4.71	9.0E-03	BE745998.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834732 5'
7952	20389	33256	0.77	9.0E-03	AJ242219.1	EST_HUMAN	qh87c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7971	20407	33277	0.81	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
8945	20980		0.85	9.0E-03	ALD39991.1	EST_HUMAN	DKFZp434L0412.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0412 5'
9940	22342	35291	1.64	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10767	23206		1.98	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
11920	24981		1.58	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0462 Homo sapiens cDNA
12160	24975		21.09	9.0E-03	BE348385.1	EST_HUMAN	hwt7f09.x1 NCI_CGAP_Lu24.Homo sapiens cDNA clone IMAGE:3183161 3'
12262	24353	30824	1.33	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
12482	24495		10.73	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0462 Homo sapiens cDNA
							zh30e03.s1 Soares_pneal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains
519	13092		2.43	8.0E-03	AA723007.1	EST_HUMAN	Alu repetitive element
1015	13587	26011	17.98	8.0E-03	AF106866.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2087	14582	27100	1.18	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2482	14984	27473		8.0E-03	P10266	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
3334	15881	28302	1.2	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3675	16215	28821	1.44	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3875	16215	28822	1.44	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4273	16788	29181	1.35	8.0E-03	BE840049.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4405	16927	29316	6.24	8.0E-03	BF363327.1	EST_HUMAN	CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
4768	17282	29688	0.77	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
4768	17282	29687	0.77	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5785	18368	30828	3.05	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fae-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Secm21 gene, partial>
6513	24610	31809	1.4	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
7130	19883	32458	6.46	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
7328	19740		1.2	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7653	20099	32851	1.43	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
8055	20487		1.91	8.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
9286	21718	34627	4.1	8.0E-03	AW80892.1	EST_HUMAN	MR1-ST0111-111189-011-h06 ST0111 Homo sapiens cDNA
9898	22400		6.6	8.0E-03	BE088509.1	EST_HUMAN	QV1-BT0877-040400-131-g03 BT0877 Homo sapiens cDNA
10549	22998	35979	5.7	8.0E-03	BE788441.1	EST_HUMAN	601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
10766	23204		2.46	8.0E-03	Z49852.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
11085	23510	36543	2.94	8.0E-03	BF363327.1	EST_HUMAN	CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
11437	23787	36858	6.85	8.0E-03	AF04589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
11825	23953		1.74	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
11874	23985		3.31	8.0E-03	AB038181.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
714	13275	25095	15.28	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
714	13275	25096	15.28	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1001	13552	25998	3.54	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1143	13687	26127	4.32	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF-10 5'
1396	13930		1.16	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCTYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HNF-2)
1427	13960	28418	3.39	7.0E-03	AA668298.1	EST_HUMAN	ab78609.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1530	14082	28522	2.95	7.0E-03	AW303599.1	EST_HUMAN	x121b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2162	15330	27189	1.19	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2663	15082		2.31	7.0E-03	AW772132.1	EST_HUMAN	hm67h07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032989 3' similar to contains Alu repetitive element
3545	16087	28504	0.69	7.0E-03	A1150273.1	EST_HUMAN	qf34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1761955 3'
3767	16306	28707	0.7	7.0E-03	AW444463.1	EST_HUMAN	UHH-B13-alk-o-10-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
3820	16357	28757	1.01	7.0E-03	AF196344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4361	16883		0.81	7.0E-03	U60088.1	NT	Dichytalium discoidium multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds
4571	17088		1.05	7.0E-03	AW117711.1	EST_HUMAN	ACIDIC 82 KDA PROTEIN ;
4639	17155		1.01	7.0E-03	AW630888.1	EST_HUMAN	hm89a05.y1 NCL_CGAP_GJ1 Homo sapiens cDNA clone IMAGE:2669938 5'
5087	17697		1.84	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6104	18873		0.8	7.0E-03	H71106.1	EST_HUMAN	yr82g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to
6423	24608		3.97	7.0E-03	AW861059.1	EST_HUMAN	gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
6842	19180	31941	1.58	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0288-050400-018-c08 CT0288 Homo sapiens cDNA
6888	19428	32202	2.88	7.0E-03	AA327129.1	EST_HUMAN	z333f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'
6918	19457	32235	0.96	7.0E-03	BE857385.1	EST_HUMAN	EST30674 Colon 1 Homo sapiens cDNA 5' end
7516	19763	32570	1.68	7.0E-03	BE928133.1	EST_HUMAN	7g34b10.x1 NCL_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
8028	20458	33332	4.17	7.0E-03	Z35838.1	NT	Q13387 HYPOTHETICAL PROTEIN 384D8_2. contains TAR1.12 TAR1 repetitive element ;
8028	20458	33333	4.17	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
8712	21147	34050	2.67	7.0E-03	BE176687.1	EST_HUMAN	S.cerevisiae chromosome II reading frame ORF YBL077w
9849	22522	35187	2.88	7.0E-03	P48982	SWISSPROT	S.cerevisiae chromosome II reading frame ORF YBL077w
9849	22522	35188	2.88	7.0E-03	P48982	SWISSPROT	RCB-HT0692-160300-011-D02 HT0592 Homo sapiens cDNA
10243	22844		1.19	7.0E-03	AV687378.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10366	22766		1.01	7.0E-03	AI799734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10608	23052	36037	2.4	7.0E-03	AB008852.1	NT	AV687378 GKC Homo sapiens cDNA clone GKCAC07 5'
10683	23123	36102	4.85	7.0E-03	AJ004802.1	NT	wc37e09.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:2320840 3'
10683	23123	36103	4.85	7.0E-03	AJ004802.1	NT	Bos taurus mRNA for NDP52, complete cds
12202	24987		1.59	7.0E-03	H94065.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
							ww15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12208	24324		1.88	7.0E-03	BE263253.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
12318	24392		1.56	7.0E-03	Y17485.1	NT	Homo sapiens LSFR2 gene, penultimate exon
12469	24963		1.65	7.0E-03	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
1273	13810	26260	10.91	6.0E-03	AW511148.1	EST_HUMAN	hcd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN O75489 ORPHAN NUCLEAR RECEPTOR PXR;
1273	13810	26261	10.91	6.0E-03	AW511148.1	EST_HUMAN	hcd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN O75489 ORPHAN NUCLEAR RECEPTOR PXR;
2730	15220	27734	3.93	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2844	16400	27816	3.08	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
2844	16400	27817	3.08	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3205	15757		2.14	6.0E-03	H76690.1	EST_HUMAN	y77h04.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:211351 5'
3288	15819		0.74	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3360	15906	28327	1.15	6.0E-03	U80880.1	NT	Fugu rubripes zinc finger protein, Isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3360	15906	28328	1.15	6.0E-03	U80880.1	NT	Fugu rubripes zinc finger protein, Isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3331	16074		1.49	6.0E-03	W37985.1	EST_HUMAN	zz13a11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3659	16199	28605	3.04	6.0E-03	BF510986.1	EST_HUMAN	UI-H-B14-epm-c-08-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3778	16316	28716	1.15	6.0E-03	6764028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3935	16470	28860	0.79	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240989-021-b10 CT0204 Homo sapiens cDNA
3970	16506		1.6	6.0E-03	BE250108.1	EST_HUMAN	600942904FT NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2858513 5'
4348	16870		4.03	6.0E-03	N58948.1	EST_HUMAN	yyd2h10.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:278179 3'
4385	16907		1.63	6.0E-03	A1016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4745	17259	29639	8	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5277	17778		1.02	6.0E-03	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
5363	17861	30219	0.71	6.0E-03	AA889972.1	EST_HUMAN	ajp5p09.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404256 3'
5403	17899	30254	0.89	6.0E-03	P38650	SWISSPROT	DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C)
5442	17937		1.31	6.0E-03	BE047451.1	EST_HUMAN	hq75h07.x1 NCI_CGAP_Ov41 Homo sapiens cDNA clone IMAGE:3125245 3' similar to TR:O70395 O70395
6466	24609	31755	0.88	6.0E-03	9827621	NT	MYOSIN XV, contains Alu repetitive element; contains element TAR1 repetitive element;
7207	19918	32747	0.89	6.0E-03	O14994	SWISSPROT	Varola virus, complete genome
7254	18028	30411	0.81	6.0E-03	BE253748.1	EST_HUMAN	SYNAPSIN III
7699	20144	33001	0.45	6.0E-03	AA289442.1	EST_HUMAN	601112333F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
							EST11849 Uterus tumor 1 Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7699	20144	33002	0.45	6.0E-03	AA289442.1	EST_HUMAN	EST11949 Uterus tumor 1 Homo sapiens cDNA 5' and
8177	20599	33485	0.76	6.0E-03	AF128394.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-18 and complete cds
8394	20808	33707	0.68	6.0E-03	P17684	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
8450	20864	33766	0.64	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55 ow13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element;
8531	20969	33868	5.04	6.0E-03	AI033980.1	EST_HUMAN	RCO-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8613	21048	33953	2.91	6.0E-03	AW799337.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
8664	21098		1.22	6.0E-03	BF038198.1	EST_HUMAN	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
8734	22061	34990	7.06	6.0E-03	D10549.1	NT	h22c02.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW-R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
10070	22471		2.21	6.0E-03	AI432661.1	EST_HUMAN	Bacillus subtilis fenD gene
10157	22558	35526	1.04	6.0E-03	AJ011849.1	NT	Homo sapiens cdc42a acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10238	22639		0.98	6.0E-03	AF084555.1	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011). mRNA
10593	23038		1.89	6.0E-03	11545814	NT	Mus musculus zinc-finger protein mRNA, complete cds
10763	23201		6.04	6.0E-03	U14558.1	NT	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3899747 5'
10764	23202	36187	3.1	6.0E-03	BE737895.1	EST_HUMAN	Rhodobacter capsulatus strain SB1003, partial genome
11744	24029		1.89	6.0E-03	AF010498.1	NT	602161024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5'
11852	24784		1.49	6.0E-03	BF071185.1	EST_HUMAN	Methanobacterium thermoautotrophicum from bases 429192 to 450298 (section 39 of 148) of the complete genome
11878	24710		6.13	6.0E-03	AE000833.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds SYNAPTOMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
11958	24778		2.44	6.0E-03	U30790.1	NT	601492621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3895388 5'
12012	24191		1.4	6.0E-03	Q62209	SWISSPROT	Brassica napus slg gene for S-b locus glycoprotein, cultivar T2
12334	24402		1.46	6.0E-03	BE788019.1	EST_HUMAN	Chlamydia trachomatis partial ORF8; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
12356	24415		1.25	6.0E-03	AJ245480.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
688	13252	25668	2.31	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
688	13252	25669	2.31	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
689	13252	25668	4.36	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
689	13252	25669	4.36	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1139	13683	26123	1.29	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2623	15118	27631	10.54	5.0E-03	AB033008.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2889	16444	27867	0.69	5.0E-03	BE266057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538789 5'
3097	15651	28063	4.21	5.0E-03	T87623.1	EST_HUMAN	yc8108.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3113	15666		2.18	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3125	15678	28093	1.05	5.0E-03	R71794.1	EST_HUMAN	y88g02.s1 Soares breast 2N5HBst Homo sapiens cDNA clone IMAGE:155668 3'
3240	15791		0.89	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3665	16205	28610	3.46	5.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3696	16236	28644	4.59	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (pbmB) gene, complete cds
3759	16288	28689	0.7	5.0E-03	U38914.1	NT	Citrus shenshi seed storage protein cDNA, complete cds
3985	16320		1.95	5.0E-03	AA298675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4142	16370	29055	0.66	5.0E-03	AJ002125.1	NT	Natix domestica Zfx type gene
4323	16846	29234	0.74	5.0E-03	H78355.1	EST_HUMAN	y479g10.11 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:240068 5'
4325	16268	28696	0.9	5.0E-03	U39914.1	NT	Citrus shenshi seed storage protein cDNA, complete cds
4649	17165	29544	0.79	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4770	17284	29869	1.83	5.0E-03	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5013	17623	29898	0.99	5.0E-03	P16265	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5383	17880	30241	1.18	5.0E-03	AF171968.1	NT	Bos taurus acid alpha-glucosidase gene, exons 2 through 20 and complete cds
6078	18650	31344	5.29	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6350	18908	31641	2.63	5.0E-03	O00507	SWISSPROT	Chlamydomonas reinhardtii AR39, section 62 of 94 of the complete genome
6387	18944		1	5.0E-03	AE002234.2	NT	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860871 3'
6949	19486		7.32	5.0E-03	BE300091.1	EST_HUMAN	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
7243	18017	30431	8.07	5.0E-03	AB025024.1	NT	Turlelops truncatus mRNA for p40-phox, complete cds
7469	19673		0.91	5.0E-03	AB038267.1	NT	Mus musculus dynein, axon, heavy chain 11 (Dnaho11), mRNA
7526	19977	32812	0.52	5.0E-03	6753551	NT	EST03012 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HFBCR93 similar to EST containing Alu repeat
7988	20421	33288	0.57	5.0E-03	T05124.1	EST_HUMAN	RC5-CT0255-031099-011-07 CT0255 Homo sapiens cDNA
8123	20547		1.43	5.0E-03	AW854327.1	EST_HUMAN	Homo sapiens MASL1 mRNA, complete cds
8323	20738	33633	8.85	5.0E-03	AB016816.1	NT	

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8390	20804	33701	0.58	5.0E-03	Q6R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8390	20804	33702	0.58	5.0E-03	Q6R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8806	21240	34147	2.58	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9078	21510		6.8	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
9219	21651	34563	1.42	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA. (19.1 - 19.4 min)
9923	22325	35273	0.98	5.0E-03	L21710.1	NT	Plasmodium berghei 68 kDa phosphoprotein mRNA, partial cds
10506	22955		3.45	5.0E-03	T18596.1	EST_HUMAN	684F Heart Homo sapiens cDNA clone 684
10718	23166	36140	3.97	5.0E-03	AW170334.1	EST_HUMAN	xr59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1,L2 L1 repetitive element;
10718	23166	36141	3.97	5.0E-03	AW170334.1	EST_HUMAN	xr59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1,L2 L1 repetitive element;
11093	23517		3.58	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.yt NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2281622 5'
11898	24925		6.15	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12036	24207		10.47	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12147	24278		1.63	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12181	24301		1.9	6.0E-03	AA456597.1	EST_HUMAN	zx75a03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14885 PROBABLE DIPHECOL OXIDASE A2 COMPONENT;
12210	24720		4.87	5.0E-03	BF572332.1	EST_HUMAN	602077774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
12410	24442	30864	2.34	5.0E-03	AW449109.1	EST_HUMAN	UHL-B13-ekf-08-0-J.J.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
12434	24797		1.24	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
244	12845	25259	1.74	4.0E-03	AW500186.1	EST_HUMAN	UHF-BN0-akc-h-04-0-J.L.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078831 5'
335	12928	25344	2.33	4.0E-03	R46482.1	EST_HUMAN	y951e04.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
460	13034	25458	0.67	4.0E-03	P64975	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
620	13188	25692	2.63	4.0E-03	AA93939.1	EST_HUMAN	nt75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
900	13464	25904	2.03	4.0E-03	R46482.1	EST_HUMAN	y951e04.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
934	13488		4.11	4.0E-03	AW748101.1	EST_HUMAN	RC3-BT0333-110100-012-01 BT0333 Homo sapiens cDNA
1178	13720	26161	28.86	4.0E-03	AA099777.1	EST_HUMAN	z181e08.1 Strategene colon (#837204) Homo sapiens cDNA clone IMAGE:510968 5'
1200	13741	26185	1.93	4.0E-03	AW794740.1	EST_HUMAN	RC9-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1335	13871	26322	1.25	4.0E-03	AA284374.1	EST_HUMAN	ze59a01.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1604	14135		0.95	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1736	14263	28749	1.15	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-48 mRNA, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1955	14473	26979	8.7	4.0E-03	AA099777.1	EST_HUMAN	281a08.r1 Stragene cdon (#937204) Homo sapiens cDNA clone IMAGE:510988 5'
2155	14688		1.05	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2176	14887	27211	1.08	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2489	14990	27504	1.74	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2489	14990	27505	1.74	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2639	15134	27644	2.34	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2639	15134	27646	2.34	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2645	15139	27648	1.05	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3184	15737	28157	1.11	4.0E-03	BE154134.1	EST_HUMAN	PM1-H70340-151299-003-H08 HT0340 Homo sapiens cDNA
3184	15737	28158	1.11	4.0E-03	BE154134.1	EST_HUMAN	PM1-H70340-151299-003-H08 HT0340 Homo sapiens cDNA
3512	16055	28478	0.78	4.0E-03	AW188426.1	EST_HUMAN	X9804.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3512	16055	28477	0.78	4.0E-03	AW188426.1	EST_HUMAN	X9804.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3620	16160	28570	0.77	4.0E-03	Q13608	SWISSPROT	OLFACTORY RECEPTOR 5H1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3633	16173	28583	0.66	4.0E-03	AV646253.1	EST_HUMAN	AV646253 GLC Homo sapiens cDNA clone GLCALD02 3'
3942	16477	28887	0.67	4.0E-03	AF060968.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
4009	16542		2.02	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4654	17170	29552	1.16	4.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Abu repetitive element
5348	17845	30203	0.59	4.0E-03	AA699955.1	EST_HUMAN	z189b01.s1 Soares_fetal_liver_spleen_1NFLS_ST Homo sapiens cDNA clone IMAGE:436009 3'
5417	17913		6.61	4.0E-03	AW816104.1	EST_HUMAN	MR3-ST0220-110100-026-d05 ST0220 Homo sapiens cDNA
5464	17959	30307	2.2	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5527	18117	30474	1.87	4.0E-03	AF005959.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5655	18241	30638	26.17	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
6077	18848	31343	2.96	4.0E-03	P04198	SWISSPROT	(HPRG)
6081	18852	31345	1.85	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
6171	18739	31440	0.78	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7611014.1 r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611014 5'
6392	18949		4.05	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6554	19108	31850	1.02	4.0E-03	AW590572.1	EST_HUMAN	hg46cd7.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2948552 3'
6637	19185	31936	1.24	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
7038	19573	32304	1.26	4.0E-03	AA813222.1	EST_HUMAN	q32f1.s1 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7169	19872	32695	1.61	4.0E-03	U76408.1	NT	Lycopodium esculentum knotted 3 protein (TKn3) mRNA, complete cds
7503	19707	32508	1.14	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7503	19707	32507	1.14	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7642	20089	32941	4.11	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7918	20354	33221	1.05	4.0E-03	AI681483.1	EST_HUMAN	b37g12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7918	20356	33223	0.61	4.0E-03	BE070170.1	EST_HUMAN	7c31b02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
8031	20463		0.78	4.0E-03	X92109.1	NT	H. sapiens hcgIX gene
8668	21101	34005	5.26	4.0E-03	AF111944.1	NT	Dicotyledonum discolorum AX4 development protein DG1122 (DG1122) gene, partial cds
8780	21214	34117	1.16	4.0E-03	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9144	21576	34482	7.22	4.0E-03	AI653983.1	EST_HUMAN	te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2060013 3' similar to contains Alu repetitive element
9269	21701		3.92	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9277	21709	34619	3.77	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10805	23241	36222	2.51	4.0E-03	4759101	NT	Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) (SFRS8) mRNA
10807	23339	36345	3.84	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
11862	24942		3.5	4.0E-03	BE815173.1	EST_HUMAN	PM4-BND138-180600-002-508 BND138 Homo sapiens cDNA
11888	24122		1.55	4.0E-03	BE298280.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
11967	24164		2.16	4.0E-03	AW504273.1	EST_HUMAN	UI-HF-BND-01p-g-04-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12224	24335		2.91	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12273	24843		1.94	4.0E-03	AW614598.1	EST_HUMAN	h102c07.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element;
12288	24377		1.67	4.0E-03	AW810141.1	EST_HUMAN	RC3-ST0281-240400-015-003 ST0281 Homo sapiens cDNA
386	12973	26395	2.22	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
802	13456	26905	8.27	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1661	14192	26663	2.52	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2189	14700		3.33	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2180	14701	27219	4.82	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2180	14701	27220	4.82	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2303	14810	27328	1.61	3.0E-03	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2947	15502		0.65	3.0E-03	Y09006.1	NT	Arabidopsis thaliana tpoMt gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3045	15599	28010	4.43	3.0E-03	BE378286.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3110	15663	28075	2.91	3.0E-03	AW802887.1	EST_HUMAN	IL2-UM0076-240300-066-D03 UM0076 Homo sapiens cDNA
3395	15941	28363	2.1	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3404	15949		7.99	3.0E-03	Y12600.1	NT	C.elegans samdc gene
3991	16525	28928	8.66	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3991	16525	28930	8.66	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4049	16581	28970	1.89	3.0E-03	A1792278.1	EST_HUMAN	af0409.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4419	16940	29331	4.21	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4493	17011		0.8	3.0E-03	BE348739.1	EST_HUMAN	h89g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151834 3'
4555	17072	29456	5.48	3.0E-03	A1536141.1	EST_HUMAN	xb18a08.x6 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4890	17402	29773	1.77	3.0E-03	A1732754.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
4911	17422	29794	11	3.0E-03	BE787945.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5516	18106	30350	4.24	3.0E-03	8922499	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5920	18400	31084	1.3	3.0E-03	AJ249981.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
5994	18473	31163	1.03	3.0E-03	U35323.1	NT	aa13f10.r1 Soares_NhrMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
6908	19445	32223	10.19	3.0E-03	AA466701.1	EST_HUMAN	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7452	19955	32789	0.61	3.0E-03	D37977.1	NT	Kluyveromyces marxianus pop3 gene for purine-cytosine permease
7650	20096	32948	1.35	3.0E-03	AJ011419.1	NT	Oryza sativa gene for bZIP protein, complete cds
8029	20481	33336	3.98	3.0E-03	AB021738.1	NT	DNA REPAIR HELICASE RAD16 (RHP3)
8467	20880	33778	0.6	3.0E-03	P26659	SWISSPROT	Claviceps purpurea DNA for mitochondrial plasmid pCIK1
8487	20899	33793	0.42	3.0E-03	X15948.1	NT	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8590	21025	33926	0.86	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8590	21026	33927	0.86	3.0E-03	BF333058.1	EST_HUMAN	2b27004.s1 Soares_parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8741	21175	34078	1.64	3.0E-03	N62580.1	EST_HUMAN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8973	21408	34321	1.29	3.0E-03	P51989	SWISSPROT	Homo sapiens chromosome 21 segment HS21C068
8980	21423	34335	1.48	3.0E-03	AL163268.2	NT	NONSTRUCTURAL PROTEIN V
9058	21490		1.43	3.0E-03	Q8QM81	SWISSPROT	h80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.11 L1 repetitive element
9336	21768		10.63	3.0E-03	AW613774.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, config fragment No. 85
9374	21806	34716	3.98	3.0E-03	AL161589.2	NT	ov03d12.x1 NCI_CGAP_Kd3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X67138_ma1
9389	21821	34738	7.61	3.0E-03	A1016731.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9826	22041		0.91	3.0E-03	D90801.1	NT	Synechocystis sp. PC6803 complete genome, 3127, 271600-402289
9840	22243		7.21	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
9868	22368	35317	1.28	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10030	22432	35378	1.3	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10144	22545	35514	3.71	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10624	23068		1.73	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
10955	20461	33336	2.88	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11198	22848	35821	2.54	3.0E-03	AF268285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11235	23503	36847	3.16	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11235	23503	36848	3.16	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11619	24734		2.77	3.0E-03	AI525058.1	EST_HUMAN	promna-5.E07.7 b/tumor Homo sapiens cDNA 5'
11658	23973	36549	1.82	3.0E-03	AA933154.1	EST_HUMAN	ct77b10.s1 Soares fetal_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER28 repetitive element :
11717	24875		1.6	3.0E-03	AB009568.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
11808	24132	30866	1.73	3.0E-03	AJ298282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
533	13105	25515	0.85	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
533	13105	25516	0.85	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
808	15284		13.28	2.0E-03	T70874.1	EST_HUMAN	y415h03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108341 5'
1395	13929	26387	2.76	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1398	13932	26389	1.33	2.0E-03	AA661605.1	EST_HUMAN	nu86f01.s1 NCL_CGAP_A1v1 Homo sapiens cDNA clone IMAGE:1217563
1408	13942	26398	9.89	2.0E-03	AF264446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1518	14050	26514	1.17	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1543	14074	26534		2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1543	14074	26535	1.9	2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1608	14139		5.72	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 6(V) CHAIN PRECURSOR
1638	14457	26960	0.9	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2294	14801		5.91	2.0E-03	7662325	NT	Homo sapiens KIAA0831 protein (KIAA0831), mRNA
2466	14967	27478	3.37	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2466	14967	27479	3.37	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2499	15000		9.26	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B1-adl-g-10-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3394	16940	28352	6.14	2.0E-03	AA450138.1	EST_HUMAN	z642a10.t1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3401	15946	28358	0.91	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3666	18208	28611	5.57	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
3964	18499	28907	2.83	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4130	16658	29044	2.48	2.0E-03	P03374	SWISSPROT	ENV POLYPEPTIDE CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36
4191	18718	29107	0.97	2.0E-03	AA178693.1	EST_HUMAN	zp13h01.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
4236	18761		14.17	2.0E-03	U68491.1	NT	Rattus norvegicus 6-hydroxytryptamine7 receptor gene, partial cds
4438	16958		1.25	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4456	18978		1.12	2.0E-03	AW297380.1	EST_HUMAN	U1H-BW0-aii-g-03-0-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'
4582	17098	29486	1.94	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4582	17098	29487	1.94	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4761	17275		1.68	2.0E-03	R87773.1	EST_HUMAN	yc45e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
5123	17630	29991	0.91	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5302	17802		0.59	2.0E-03	AJ245187.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
5443	17938		3.72	2.0E-03	AF205067.1	NT	Desulfovibrio desulfuricans cytochrome c3 precursor (cycA) gene, complete cds
5747	18329	30768	1.53	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5895	24595	31154	1.36	2.0E-03	AB014583.1	NT	Homo sapiens mRNA for KIAA0683 protein, partial cds
5981	18557	31241	0.61	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
5981	18557	31242	0.61	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
5983	18559	31244	2.02	2.0E-03	U63711.1	NT	Xenopus laevis xefitin mRNA, complete cds
6421	18978	31710	3.73	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6421	18978	31711	3.73	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6676	19224	31972	2.33	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XI)
6676	19224	31973	2.33	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XI)
6676	19228	31975	8	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6718	19284	32021	2.47	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6719	19265	32022	0.65	2.0E-03	AV709076.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6753	19296	32061	1.72	2.0E-03	X94451.1	NT	L. seculentum mRNA for lysyl-IRNA synthetase (LysRS)
6958	19495		1.46	2.0E-03	AI91089.1	EST_HUMAN	wu36h09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element MSR1 repetitive element ;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7001	19537	32321	0.72	2.0E-03	AA877831.1	EST_HUMAN	213a1.1 s1 Soares fetal liver spleen 1NfLS_S1 Homo sapiens cDNA clone IMAGE:430652 3'
7374	18044	30428	0.77	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7518	19768	32574	4.25	2.0E-03	BE087888.1	EST_HUMAN	CNM4-BT0368-081299-064-001 BT0368 Homo sapiens cDNA
7694	20033	32880	0.76	2.0E-03	AI298883.1	EST_HUMAN	gm99d11.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1896885 3'
7751	20195	33057	0.79	2.0E-03	T86560.1	EST_HUMAN	yd77g10.f1 Soares fetal liver spleen 1NfLS_Homo sapiens cDNA clone IMAGE:114308 5'
8126	20550		0.43	2.0E-03	AF207550.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, plm-2 protooncogene homolog plm-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown gp
8148	20569	33445	1.24	2.0E-03	P07364	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8669	21104	34007	2.78	2.0E-03	AW592004.1	EST_HUMAN	h137b08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2894035 3' similar to TR-Q60976 Q60976 JERKY.
8792	21228	34132	5.44	2.0E-03	N20287.1	EST_HUMAN	yx42g08.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element
8792	21228	34133	5.44	2.0E-03	N20287.1	EST_HUMAN	yx42g08.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element
8841	21275	34185	1.08	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8882	21316	34227	0.85	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8882	21316	34228	0.85	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8904	21338	34252	1	2.0E-03	AU136678.1	EST_HUMAN	AU136678 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
9504	21935	34859	0.93	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9738	22065	34982	3.85	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEI) (JI)
9808	22211	35147	1.05	2.0E-03	P48982	SWISSPROT	(MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9808	22211	35148	1.05	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9880	22382	35331	1.01	2.0E-03	AW884289.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10069	22470		6.89	2.0E-03	AA251376.1	EST_HUMAN	QV3-OT0084-080400-144-e01 OT0084 Homo sapiens cDNA
10794	23232		3.03	2.0E-03	M86524.1	NT	zs10a08.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:684784 3'
11243	20569	33445	2.4	2.0E-03	P07364	SWISSPROT	Human dystrophin gene
11297	23662		2.77	2.0E-03	BF330909.1	EST_HUMAN	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11303	23668	36716	6.74	2.0E-03	Z11740.1	NT	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11600	23834		3.28	2.0E-03	AI625745.1	EST_HUMAN	H.sapiens variable number tandem repeat (VNTR) locus DNA
							ly65h03.x1 NCI CGAP K1d11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW-VATG_MANSE Q25632 VACUOLAR ATP SYNTHASE SUBUNIT G

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11618	23949	37008	3.25	2.0E-03	AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds
11642	23965	37011	1.44	2.0E-03	AJ084325.1	EST_HUMAN	oy43g06.a1 Soares parathyroid tumor NhHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to
11667	17802		8.69	2.0E-03	AJ245167.1	NT	TR:P07535 P07535 PS-PLA1 PRECURSOR.;
11891	24919		2.37	2.0E-03	AV697968.1	EST_HUMAN	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
11986	24179	30946	1.44	2.0E-03	Y00508.1	EST	AV697968 GKC Homo sapiens cDNA clone GKCGXD05 5'
12112	24256		1.42	2.0E-03	AL163203.2	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12172	24764		1.3	2.0E-03	AJ375037.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12253	24354		1.35	2.0E-03	AL163280.2	NT	ta6602.x1 Soares fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element
						NT	Homo sapiens chromosome 21 segment HS21C080
12306	24386		1.22	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12494	24712		-2.73	2.0E-03	AV697968.1	EST_HUMAN	AV697968 GKC Homo sapiens cDNA clone GKCGXD05 5'
456	13031	25463	1.34	1.0E-03	H89471.1	EST_HUMAN	y98c08.r1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
852	13408	25853	2.08	1.0E-03	AJ720263.1	EST_HUMAN	as70b08.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
852	13408	25854	2.08	1.0E-03	AJ720263.1	EST_HUMAN	as70b08.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
1122	13666	26105	2.61	1.0E-03	AI865788.1	EST_HUMAN	wk86a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422259 3'
1142	13666	26126	1.43	1.0E-03	AI854572.1	EST_HUMAN	wx03e10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1198	13737	26180	1.42	1.0E-03	AI892616.1	EST_HUMAN	wd86a01.x1 NCI_CGAP_Ju24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element
1862	14480	26989	3.34	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
2065	14580	27098	16.69	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
2484	14985		5.91	1.0E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2835	15480	27911	1.29	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3148	15701	28119	3.38	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3148	15701	28120	3.38	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3265	15816	28233	0.86	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3527	16070	28491	0.68	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3527	16070	28492	0.68	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3684	16204		1.29	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
3947	16482	28892	1.01	1.0E-03	Z49649.1	NT	S. cerevisiae chromosome X reading frame ORF YJR149w
4464	16984	28367	2.73	1.0E-03	BE939162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4511	17029	29408	5.27	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4707	17223	28607	0.79	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4880	17392	29762	2.94	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3'
4880	17392	29763	2.94	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3'
4881	17393		5.82	1.0E-03	BE154067.1	EST_HUMAN	PMO-H10339-200400-010-D02 HT0339 Homo sapiens cDNA
5192	17696	30058	4.43	1.0E-03	BE154941.1	EST_HUMAN	PM3-HT0344-181199-002-008 HT0344 Homo sapiens cDNA
5192	17698	30059	4.43	1.0E-03	BE154941.1	EST_HUMAN	PM3-HT0344-181199-002-008 HT0344 Homo sapiens cDNA
5208	17709	30073	10.78	1.0E-03	O49409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5386	17883		1.27	1.0E-03	AW440280.1	EST_HUMAN	hb7g08.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:2889370 3'
5471	17966	30313	2.45	1.0E-03	BE549156.1	EST_HUMAN	601076482F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3462116 5'
5561	18150	30512	2.2	1.0E-03	AA280951.1	EST_HUMAN	ze4401.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5658	18244	30642	3.67	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQ11 gene
5713	18298	30723	2.11	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5713	18298	30724	2.11	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5837	18417	31087	0.89	1.0E-03	BE796491.1	EST_HUMAN	601689941F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5843	18423	31092	1.84	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5901	18479	31160	0.7	1.0E-03	N41974.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2NbhHM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element:
5901	18479	31161	0.7	1.0E-03	N41974.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2NbhHM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element:
6183	18750	31460	0.66	1.0E-03	AA773352.1	EST_HUMAN	ab85g12.s1 Stratiogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:845734 3'
6206	18772		0.51	1.0E-03	BF941039.1	EST_HUMAN	602068042F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066907 5'
6324	18884		2.81	1.0E-03	X07699.1	NT	Mouse nucleolin gene
6365	18923	31658	0.96	1.0E-03	BE963939.2	EST_HUMAN	601657519R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875693 3'
6508	19060		9.39	1.0E-03	11528178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6664	19212	31960	1.19	1.0E-03	T87761.1	EST_HUMAN	yd93a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5'
6747	19281		1.74	1.0E-03	AW902596.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
7136	19668	32463	1.54	1.0E-03	L71570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7593	20042	32891	3.15	1.0E-03	D18826.1	NT	Human gene for fourth somatostatin receptor subtype
7988	20423		0.76	1.0E-03	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8170	20592	33475	1.81	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
8252	20689	33559	3.71	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
8311	20726	33619	0.93	1.0E-03	BE88044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 5'
8697	21032	33935	4.84	1.0E-03	AJ261973.1	NT	Homo sapiens partial stefin-1 gene
8733	21187	34072	1.15	1.0E-03	AA122270.1	EST_HUMAN	z07c09.s1 Soares_pregnant_uterus_NibHPU Homo sapiens cDNA clone IMAGE:460768 3' similar to contains L1.1f L1 repetitive element:
8811	21245	34150	1.48	1.0E-03	AF153980.1	NT	Homo sapiens exocyst-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
9303	21735	34150	1.63	1.0E-03	Y11204.1	NT	V.cartel gene encoding volvoxpsin
9422	21864	34769	3.42	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH6) chl subunit mRNA, complete cds
9422	21854	34770	3.42	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH6) chl subunit mRNA, complete cds
9770	22173	35104	1.85	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9770	22173	35105	1.95	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9807	22309	35253	0.88	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10251	22652	35616	0.95	1.0E-03	A024350.1	EST_HUMAN	ov7508.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1
10458	22809	35888	2.71	1.0E-03	AW362383.1	EST_HUMAN	MER39 MER39 repetitive element;
10458	22809	35889	2.71	1.0E-03	AW362383.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10532	22879	35959	4.93	1.0E-03	BE170859.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10605	23049		3.5	1.0E-03	A1583847.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
10935	23387		3.35	1.0E-03	AV759949.1	EST_HUMAN	tt73et12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248446 3' similar to TR:Q26195 Q26195
11595	23930	37006	3.69	1.0E-03	BE894488.1	EST_HUMAN	PVA1 GENE.;
12073	24227	30958	1.47	1.0E-03	8907208	NT	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
12102	24899		3.69	1.0E-03	A1347355.1	EST_HUMAN	601493087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12222	24923	30481	6.45	1.0E-03	BE780572.1	EST_HUMAN	Rattus norvegicus transformation related protein 63 (Trp63), mRNA
5449	17944	30295	3.02	9.0E-04	AJ277661.1	NT	tc05h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element
5951	18527		2.2	9.0E-04	P06727	SWISSPROT	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
6581	19132		0.68	9.0E-04	AJ006345.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
6834	19376	32163	1.17	9.0E-04	P02381	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
9794	22197		1.59	9.0E-04	AB037203.1	NT	Homo sapiens KVLQ11 gene MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1 Glycerhiza glabra GpbA51 mRNA for beta-amylin synthase, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1516	14048		0.94	8.0E-04	X98499.1	NT	X laevis mRNA for C4SR protein
4197	18722		6.41	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4817	17329	28709	2.37	8.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
5427	17822	30273	3.24	8.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11065	23491		2.87	8.0E-04	AJ571099.1	EST_HUMAN	h85a08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
12437	24469	30873	1.43	8.0E-04	AW578954.1	EST_HUMAN	PM2-HT0353-130100-002-f10 HT0353 Homo sapiens cDNA
2886	15159	27870	3.8	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3242	15783	28211	1.04	7.0E-04	4886170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6404	18961	31698	0.76	7.0E-04	AA516212.1	EST_HUMAN	hg65g12.s1 NCI_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.B3 L1 L1 repetitive element ;
6622	19171	31924	0.42	7.0E-04	AJ333875.1	EST_HUMAN	qq08h05.x1 Soares_NhMMP_u_S1 Homo sapiens cDNA clone IMAGE:1931961 3' similar to gb:X57025_ma1
6863	19403		2.11	7.0E-04	AJ769331.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN); contains Alu repetitive element; contains element MIR repetitive element ;
7676	20122		0.83	7.0E-04	AK024445.1	NT	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
11341	23705	36759	3.1	7.0E-04	Z40581.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone o-28a07 3'
12151	24281		4.11	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0814-110300-142-bt2 BT0614 Homo sapiens cDNA
12409	24441		3.84	7.0E-04	R17338.1	EST_HUMAN	y913c06.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32288 5'
12441	24471		4.66	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2644	15138		1.21	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4149287 5'
3973	16508	28914	1.66	6.0E-04	AJ882525.1	EST_HUMAN	w15a11.x1 NCI_CGAP_Kld12 Homo sapiens cDNA clone IMAGE:2402876 3'
4105	16635	29022	0.73	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHF1) gene, 5' flanking region
4105	16635	28023	0.73	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHF1) gene, 5' flanking region
4201	18728	29114	3.69	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4473	16993	29375	0.94	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-f09 HT0560 Homo sapiens cDNA
4473	16993	29376	0.94	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-f09 HT0560 Homo sapiens cDNA
8095	20522	33402	0.47	6.0E-04	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
8537	20972		3.98	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
10018	22420		3.94	6.0E-04	AL048507.2	EST_HUMAN	DKFZp566M2024_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp566M2024
10100	22501	35484	2.62	6.0E-04	BE005850.1	EST_HUMAN	RC2-BND120-250400-012-h11 BN0120 Homo sapiens cDNA
11240	23608	36653	2.33	6.0E-04	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11318	23682	36732	4.99	6.0E-04	AW013847.1	EST_HUMAN	UI-HB10-ab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11790	24784		2.59	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-261199-012-d08 HT0269 Homo sapiens cDNA
670	13235	25647	8.03	6.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1529	14081		2.03	6.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3391	15937	28349	1.3	6.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCL_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014784 3' similar to contains Alu repetitive element;
3713	16253	28657	5.19	5.0E-04	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6322	17822		8.38	5.0E-04	AW194050.1	EST_HUMAN	xm11d10.x1 NCL_CGAP_Uk4 Homo sapiens cDNA clone IMAGE:2683891 3' similar to gb:X58431_ma2 HOMEBOX PROTEIN HOX-56 (HUMAN);
5732	18314	30747	2.91	6.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6890	19527	32311	6.07	5.0E-04	AA156080.1	EST_HUMAN	z033b08.s1 Stratiogene cdon (#337204) Homo sapiens cDNA clone IMAGE:588663 5'
7850	20280	33163	10.79	5.0E-04	M23604.1	NT	Gorilla gorilla invaductin gene medium allele, complete cds
							q013106.x1 Soares_placenta_8169weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1
8601	21038	33939	5.96	6.0E-04	AI188382.1	EST_HUMAN	(HUMAN) contains Alu repetitive element;
8853	21287	34198	1.04	5.0E-04	AA814519.1	EST_HUMAN	ob96e02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element;
9534	21949	34872	1.68	6.0E-04	AA846545.1	EST_HUMAN	aj96h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394957 3'
9772	22176	35108	4.78	5.0E-04	AW270938.1	EST_HUMAN	xe06e02.x1 NCL_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:2768858 3'
10757	23195		1.74	5.0E-04	AL048507.2	EST_HUMAN	DKFZp566M2024_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586M2024
11435	18314	30747	14.01	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
11722	24721		3.11	5.0E-04	AA568813.1	EST_HUMAN	nt15h02.s1 NCL_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:913875
407	12983		1.04	4.0E-04	BF241482.1	EST_HUMAN	801876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4704897 6'
692	13255	25672	2.55	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
870	13426	25873	3.62	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barslead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
870	13425	25874	3.62	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barslead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1494	14026	28459	3.54	4.0E-04	AW753356.1	EST_HUMAN	RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA
2008	14524	27038	1.06	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment H821C078
2558	15057	27572	2.41	4.0E-04	O96916	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3123	15676	28050	2.54	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3288	15837	28256	0.62	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barslead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3335	15882	28303	0.7	4.0E-04	AV696624.1	EST_HUMAN	AV696624 GKC Homo sapiens cDNA clone GKCFH07 5'
3874	18410		0.99	4.0E-04	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4345	16867	28249	3.42	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL_CGAP_Co1 Homo sapiens cDNA clone IMAGE:961930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4345	16867	29250	3.42	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL_CGAP_Co1 Homo sapiens cDNA clone IMAGE:961930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4573	17080	29477	1.7	4.0E-04	AA086324.1	EST_HUMAN	zn61c08.s1 Stratiotes musclic 937209 Homo sapiens cDNA clone IMAGE:562670 3'
5221	17723	30090	3.04	4.0E-04	BE560680.1	EST_HUMAN	601345896F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
5332	17831		0.61	4.0E-04	BE178680.1	EST_HUMAN	PM4-HT0806-030400-001-h11 HT0808 Homo sapiens cDNA EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7722	20167	33025	1.36	4.0E-04	P48442	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8045	20477		0.79	4.0E-04	AL161966.2	NT	AUI22079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
8264	20861	33576	0.72	4.0E-04	AU122079.1	EST_HUMAN	601876985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5'
9025	21458	34387	0.98	4.0E-04	BF240712.1	EST_HUMAN	y339e12.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:284142 5'
9032	21464	34372	1.86	4.0E-04	N25507.1	EST_HUMAN	ov87h03.s1 Soares testis NIH Homo sapiens cDNA clone IMAGE:1644341 3'
9828	22231	35167	2.95	4.0E-04	A025689.1	EST_HUMAN	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
9924	22326		1.27	4.0E-04	AF022855.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
12113	24692		1.7	4.0E-04	AF254822.1	NT	FORMIN (LIMB DEFORMITY PROTEIN)
12284	24693		1.35	4.0E-04	Q05860	SWISSPROT	DKFZp761J221.1 761 (synonym: haryn2) Homo sapiens cDNA clone DKFZp761J221 5'
160	12765	25181	3.41	3.0E-04	AL119428.1	EST_HUMAN	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
201	12804	25221	1.84	3.0E-04	P49259	SWISSPROT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
603	13467	25906	1.7	3.0E-04	U83991.1	NT	q228d03.y1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1813	14336	26830	0.88	3.0E-04	AI262100.1	EST_HUMAN	h23a02.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2119082 3'
1825	14347		0.9	3.0E-04	AI999874.1	EST_HUMAN	INTERALIN B PRECURSOR
3273	15823	28240	3.86	3.0E-04	P25147	SWISSPROT	z558a04.r1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA clone IMAGE:446478 5'
3278	15827	28245	0.65	3.0E-04	AA203342.1	EST_HUMAN	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
3977	16512	28918	3.46	3.0E-04	P49448	SWISSPROT	Homo sapiens Xq pseudautosomal region, segment 1/2
4068	16599		1.28	3.0E-04	AI271735.1	NT	RCO-HT0014-310598-028 HT0014 Homo sapiens cDNA
4109	16639		1.15	3.0E-04	BE140809.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
4873	17365		5.5	3.0E-04	BE163778.1	EST_HUMAN	QV3-DT0045-221289-048-809 DT0045 Homo sapiens cDNA
4947	17458	29834	0.82	3.0E-04	AW937723.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
6456	19012		7.6	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C078
7211	19823	32637	1.63	3.0E-04	AL163278.2	NT	RC4-NN0027-060400-011-b08 NN0027 Homo sapiens cDNA
7408	18077	30371	0.98	3.0E-04	AW953981.1	EST_HUMAN	

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8113	20539	33418	0.64	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8820	21254	34160	5.33	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9983	22385	35335	1.27	3.0E-04	AA454055.1	EST_HUMAN	z48408.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:785471 5' similar to gb:M62762
10348	22748	35715	3.52	3.0E-04	AA781201.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); aj24905.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 603
11671	24943	30485	3.01	3.0E-04	AA228301.1	EST_HUMAN	nc38604.1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element;
12064	24772	30681	4.28	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
12510	24512		3.67	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185.1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547L185 5'
180	12783	25198	1.54	2.0E-04	AF217798.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
498	13068	25488	2.82	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001263 3'
930	13484	25930	7.59	2.0E-04	M86524.1	NT	Human dystrophin gene
930	13484	25931	7.59	2.0E-04	M86524.1	NT	Human dystrophin gene
1210	13751		4.58	2.0E-04	AI286021.1	EST_HUMAN	q988e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1217	13757		2.51	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2491	14992	27507	2.18	2.0E-04	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
2842	15497	27917	0.91	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3306	15954	28273	0.6	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3413	15958	28369	2.05	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-507 BT0636 Homo sapiens cDNA
3924	16459	28887	0.94	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4162	16689		5.78	2.0E-04	U01029.1	NT	Phasodius vulgaris nitrate reductase (PVNR2) gene, complete cds
4712	17228	28612	1.4	2.0E-04	H86266.1	EST_HUMAN	y001e11.1 Soares_pineal_gland_N3-HPG Homo sapiens cDNA clone IMAGE:232596 5'
4712	17228	28613	1.4	2.0E-04	H96265.1	EST_HUMAN	y001e11.1 Soares_pineal_gland_N3-HPG Homo sapiens cDNA clone IMAGE:232596 5'
4850	17362		1.33	2.0E-04	U09228.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4946	17457		0.98	2.0E-04	Z73018.1	NT	S.cerevisiae chromosome VII reading frame ORF YGR233c
5177	17681	30041	1.54	2.0E-04	AB037997.1	NT	Danio rerio hageroma gene, exons 1 to 6, partial cde
5253	17754	30123	1.05	2.0E-04	AF057019.1	NT	Dicotylellum discoidium Interaplin (abpD) gene, complete cds
5808	18388	31049	1.18	2.0E-04	AV654362.1	EST_HUMAN	AV654362 GLC Homo sapiens cDNA clone GLCDU10 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5821	18401	31065	2.04	2.0E-04	AI690862.1	EST_HUMAN	IQ03b11.x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:2207709 3'
6028	18502	31289	0.81	2.0E-04	AA286562.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' and similar to EST containing O family repeat
6246	18809	31523	1.01	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6560	19111	31855	0.85	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7678	20124		2.61	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000788 5'
7789	20231		0.87	2.0E-04	AY860983.1	EST_HUMAN	QV0-CT0387-180300-167-a10 CT0387 Homo sapiens cDNA
8161	20574		15.46	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8161	20583	33482	1.18	2.0E-04	P54298	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8518	20930	33826	0.43	2.0E-04	AL043272.2	EST_HUMAN	DKFZp434L2023_j1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L2023 5'
8518	20930	33827	0.43	2.0E-04	AL043272.2	EST_HUMAN	DKFZp434L2023_j1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L2023 5'
8800	21035	33937	1.03	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8800	21035	33938	1.03	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8839	21273	34182	1.27	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8839	21273	34183	1.27	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9047	21479	34392	2.01	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10014	22416	35364	0.98	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151099-011-b05 HT0254 Homo sapiens cDNA
10046	22448	35396	2.17	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742364 5'
10627	23089	36054	4	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
11074	23499	36527	1.98	2.0E-04	AI440282.1	EST_HUMAN	g01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140288 3' similar to contains Alu repetitive element;
11178	23594	36635	2.76	2.0E-04	AW138740.1	EST_HUMAN	UI-H-B11-adm-o-04-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
769	13347	25781	1.37	1.0E-04	H08648.1	EST_HUMAN	YK26c09.s1 Soares_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.11 L1 repetitive element;
874	13527	25969	0.61	1.0E-04	P48725	SWISSPROT	PERICENTRIN
1101	13846	26086	2.86	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1141	13895	26124	4.78	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1141	13895	26125	4.78	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708826 3'
1364	13898		4.47	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1637	14169	26638	2.6	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1637	14169	26639	2.6	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1833	14366	26865	1.3	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
2574	15071	27588	2.02	1.0E-04	AF195863.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2574	15071	27589	2.02	1.0E-04	AF195863.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2635	15130	27841	6.45	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2635	15130	27842	6.45	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3248	15797	28215	0.88	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPlicing FACTOR 3A SUBUNIT 2) (SF3A66)
3734	16274	28878	0.88	1.0E-04	A140282.1	EST_HUMAN	q011f1.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element
4073	16604	28994	1.99	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4098	16829	29018	1.39	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB004 3'
5233	17735	30104	0.93	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5233	17735	30105	0.93	1.0E-04	7662016	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
6147	18715	31417	1.74	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6221	18787	31493	0.63	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6221	18787	31494	0.63	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6779	19322	32088	0.88	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCL CGAP_P33 Homo sapiens cDNA clone IMAGE:252
7230	19842	32860	0.67	1.0E-04	AA584581.1	EST_HUMAN	n125a04.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb:M97252
7630	20078	32831	14.24	1.0E-04	A1251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
8087	20078	32931	14.81	1.0E-04	A1251980.1	EST_HUMAN	qv57d10.x1 NCL CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985883 3'
8031	21068	33975	1.11	1.0E-04	AA630463.1	EST_HUMAN	qv57d10.x1 NCL CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985883 3'
9575	21998	34928	2.8	1.0E-04	A1808220.1	EST_HUMAN	ab94g08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854654 3'
9592	22006	34932	1.5	1.0E-04	O88969	SWISSPROT	wf26c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9637	22052		1.2	1.0E-04	T77163.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9788	22189	35135	1.6	1.0E-04	10863876	NT	y072c08.1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 5'
10162	22563		4.94	1.0E-04	P08547	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10188	22589	35555	0.94	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11099	23523		2.14	1.0E-04	M28597.1	NT	Mouse alpha leukocyte interferon gene, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11445	23805	36863	3.39	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11445	23805	36864	3.39	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11494	23852	36922	2.82	1.0E-04	AA602845.1	EST_HUMAN	np20c02.s1 NCL CGAP_B3 Homo sapiens cDNA clone IMAGE:1116868 3'
11494	23852	36923	2.82	1.0E-04	AA602845.1	EST_HUMAN	np20c02.s1 NCL CGAP_B3 Homo sapiens cDNA clone IMAGE:1116868 3'
11583	23923		1.31	1.0E-04	BE686768.1	EST_HUMAN	CMO-GT0404-130700-475-h03 CT0404 Homo sapiens cDNA
11842	24741		2.13	1.0E-04	BE676399.1	EST_HUMAN	772Ba10.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296058 3' similar to contains L1.13 L1
718	13278	25701	2.6	9.0E-05	AA718933.1	EST_HUMAN	repetitive element;
9408	17904	30287	7.14	9.0E-05	AF166168.1	NT	ah45c11.s1 Soares, testis, NHT Homo sapiens cDNA clone 1292468 3'
6263	18827	31541	1.43	9.0E-05	Q60716	SWISSPROT	Homo sapiens putative tumor suppressor mRNA
8093	20520	33398	0.74	9.0E-05	AW204958.1	EST_HUMAN	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
8093	20520	33400	0.74	9.0E-05	AW204958.1	EST_HUMAN	U-H-B11-aer-d-05-0-UI.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9675	22022		2.73	9.0E-05	D85606.1	NT	U-H-B11-aer-d-05-0-UI.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9677	22024	34953	3.3	9.0E-05	AF120982.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
10914	23348	36354	2.21	9.0E-05	AW073078.1	EST_HUMAN	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11010	23437	38454	1.82	9.0E-05	AI287878.1	EST_HUMAN	xa34g05.x1 NCL CGAP_B18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1
11363	18927	31541	4.39	9.0E-05	Q60716	SWISSPROT	repetitive element;
11898	24805		5.71	9.0E-05	AF129756.1	NT	q23100.x1 NCL CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
844	13401	25842	1.78	8.0E-05	AJ251646.1	NT	MIR repetitive element;
887	13442		6.07	8.0E-05	AJ251646.1	NT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
2804	15459		0.67	8.0E-05	M83575.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G8b, G8c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
4517	17035	28412	0.83	8.0E-05	AW044605.1	EST_HUMAN	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
10930	23362	36374	4.43	8.0E-05	M69197.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
12555	24787		3.35	8.0E-05	AA279333.1	EST_HUMAN	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
361	12951	25365	4.11	7.0E-05	AW847445.1	EST_HUMAN	wy78a04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2564838 3'
381	12951	25366	4.11	7.0E-05	AW847445.1	EST_HUMAN	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
584	13155	25559	1.16	7.0E-05	L49075.1	EST_HUMAN	zs88h01.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu
584	13155	25560	1.16	7.0E-05	L49075.1	EST_HUMAN	repetitive element; contains element MSR1 repetitive element;
							RC3-CT0208-220899-011-E04 CT0208 Homo sapiens cDNA
							RC3-CT0208-220899-011-E04 CT0208 Homo sapiens cDNA
							HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
							HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1081	13627	26087	0.8	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYL TRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2871	15164	27674	9.28	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3117	15870	28083	6.22	7.0E-05	AB009080.1	NT	Dicotyledon discoidium gene for TRFA, complete cds
3697	16237		8.54	7.0E-05	AI432413.1	EST_HUMAN	ig73c08.x1 Scars_NhrHPu_S1 Homo sapiens cDNA clone IMAGE:2114416 3'
4394	16916	29301	1.23	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5005	17515	29889	0.77	7.0E-05	9845300	NT	Rat cytomegalovirus Mastricht, complete genome
8798	21230	34137	1.49	7.0E-05	AA505582.1	EST_HUMAN	nh83gd1.s1 NC1_GGAP_B2 Homo sapiens cDNA clone IMAGE:988086 3'
9733	22060	34889	3.09	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stragena (cat#938206) Homo sapiens cDNA clone HFBED60
10839	23371		9.49	7.0E-05	10835048	NT	Homo sapiens seroglycan, epsilon (SGOE), mRNA
1981	14479	29887	0.93	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1981	14479	29888	0.93	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2509	15010	27522	12.23	6.0E-05	AI655241.1	EST_HUMAN	w64h06.x1 NC1_GGAP_GC8 Homo sapiens cDNA clone IMAGE:2309631 3' similar to gb:J03250 DNA TOPOISOMERASE 1 (HUMAN);
2831	15126	27638	1.3	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA28B10
2831	15126	27639	1.3	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA28B10
2772	13281	26677	3.06	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5181	17695	30056	1.55	6.0E-05	AV722942.1	EST_HUMAN	AV722942 HTB Homo sapiens cDNA clone HTBBED12 5'
5191	17695	30057	1.55	6.0E-05	AV722942.1	EST_HUMAN	AV722942 HTB Homo sapiens cDNA clone HTBBED12 5'
6207	18773	31477	3.53	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6207	18773	31478	3.53	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6741	19286	32047	1.45	6.0E-05	N72829.1	EST_HUMAN	w50g1.1.1 Scars_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246212 5'
7343	19766	32560	0.93	6.0E-05	AA897880.1	EST_HUMAN	q80a03.s1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8694	21129	34029	1.03	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8694	21129	34030	1.03	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8982	21396	34307	2.69	6.0E-05	AW886829.1	EST_HUMAN	PM4-NN0050-310300-001-410 NN0050 Homo sapiens cDNA
9514	21877	34903	1.4	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9514	21877	34904	1.4	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9708	22131	35057	1.23	6.0E-05	T94149.1	EST_HUMAN	ye28c12.1 Stragena lung (#937210) Homo sapiens cDNA clone IMAGE:119082 5'
10530	22977	35958	3.24	6.0E-05	RT5639.1	EST_HUMAN	y59c03.s1 Scars_placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element, contains LTR7 repetitive element;
11271	23637	36888	1.68	6.0E-05	AA044015.1	EST_HUMAN	Z65802.1 Scars_pregnant uterus_NhrHPU Homo sapiens cDNA clone IMAGE:487035 5'
12121	24785	30687	11.24	6.0E-05	AW890110.1	EST_HUMAN	MR0-NT0038-250400-001-408 NT0038 Homo sapiens cDNA
1436	13968	28423	8.42	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241189-040-h11 ST0234 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3993	16527	28931	3.55	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5787	18368	30830	13.78	5.0E-05	X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6285	18857	31578	4.22	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCMA06 3'
6482	18037	31777	1.1	6.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7787	20239		1.17	5.0E-05	AB037864.1	NT	Mus musculus gene for calretinin, exon 1
11895	24300		3.58	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12180	24300		6.77	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2765	12838		3.72	4.0E-05	U12821.1	NT	Human renin (REN) gene, 6' flanking region
4518	17036	29413	0.8	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4518	17038	29414	0.8	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
5121	17828	29990	0.95	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
7351	19762	32569	0.69	4.0E-05	U01947.1	NT	Macaca mulatta heptoglobin (HP) gene, 5' region
8491	20903	33797	0.46	4.0E-05	AA574391.1	EST_HUMAN	nt48d01.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:3916801 similar to contains Alu repetitive element; contains L1.t1 L1 repetitive element;
8495	20907	33802	0.45	4.0E-05	P41315	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN B
9710	22133		7.27	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
10551	22988	35981	4.31	4.0E-05	AW627948.1	EST_HUMAN	h136c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element;
11768	24044	31022	1.54	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
11853	24101		1.75	4.0E-05	AW117580.1	EST_HUMAN	xd83409.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
12584	24662		1.28	4.0E-05	AA417786.1	EST_HUMAN	z01e11.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746252 3'
700	13262	25879	0.7	3.0E-05	A1248061.1	EST_HUMAN	qh64c10.x1 Soares_fejal_liver_spleen_1NFL.S_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains KER repetitive element;
1085	13631	26071	1.49	3.0E-05	AW273851.1	EST_HUMAN	x24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1158	13701	26139	1.28	3.0E-05	BF037898.1	EST_HUMAN	601481463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1158	13701	26140	1.28	3.0E-05	BF037898.1	EST_HUMAN	601481463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
2673	15168	27676	2.47	3.0E-05	Q62234	SWISSPROT	SKLELEMIN
3255	16806		0.91	3.0E-05	A1288919.1	EST_HUMAN	q91g11.x1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1876748 3' similar to TR:O08632
4404	16928	26313	7.59	3.0E-05	BE169211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN.;
4404	16928	26314	7.59	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4500	17018	28400	1.12	3.0E-05	AA368878.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4500	17018	28401	1.12	3.0E-05	AA368878.1	EST_HUMAN	EST79988 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4629	17145		0.69	3.0E-05	AL163302.2	NT	EST79988 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4663	17170	29558	0.59	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4895	13262	25679	0.7	3.0E-05	AJ248061.1	EST_HUMAN	qf64c10.x1 Soares_fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to, contains Alu repetitive element; contains element KER repetitive element;
5922	18402	31066	2.05	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2pl), mRNA
7138	18669	32484	0.95	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7138	18669	32495	0.95	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8561	20998	33893	2.34	3.0E-05	BE733157.1	EST_HUMAN	601597451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8892	21328	34238	1.07	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
9272	21704	34615	1.85	3.0E-05	AW770982.1	EST_HUMAN	h194e08.x1 NCL_CGAP_L124 Homo sapiens cDNA clone IMAGE:3009838 3'
9275	21707	34617	1.88	3.0E-05	6912431	NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9565	21988	34914	1.41	3.0E-05	AA372582.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9808	22209	34914	3.66	3.0E-05	A1769331.1	EST_HUMAN	wg36709.x1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10395	22795	35787	0.97	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
10395	22795	35788	0.97	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
11778	24052		3.25	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
2219	14729	27250	4.42	2.0E-05	A1286021.1	EST_HUMAN	q198e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
2503	15004	27515	0.89	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2665	15158		15.71	2.0E-05	AA160582.1	EST_HUMAN	zq46a12.r1 Stratagene hNT neuron (#37233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3098	15652	28084	1.59	2.0E-05	BE06036.1	EST_HUMAN	RC3-B10319-120200-014-108 BT0319 Homo sapiens cDNA
3321	15868	28287	0.97	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3346	15892	28315	1.07	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3470	16014		0.86	2.0E-05	X95455.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3814	16351		0.86	2.0E-05	AL039107.1	EST_HUMAN	DKFZp5681064_r1 586 (synonym: hfxd2) Homo sapiens cDNA clone DKFZp5681064 5'
4943	17454	29831	0.7	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5433	17928	30280	1.22	2.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5433	17928	30281	1.22	2.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6038	18812	31300	1.98	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6212	18778		0.77	2.0E-05	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
6272	18856	31549	0.97	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE CO-TRANSPORTER (NA+/D/CARBOXYLATE CO-TRANSPORTER)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6272	18835	31550	0.97	2.0E-05 Q13183		SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA+/D)DICARBOXYLATE COTRANSPORTER
6471	19028	31783	0.78	2.0E-05 A1149272.1		EST_HUMAN	qz72a02.x1 Soares_placenta_8to9weeks_2NblHP8to9W Homo sapiens cDNA clone IMAGE:1715114 3'
6548	19100	31842	0.49	2.0E-05 P35085		SWISSPROT	similar to contains L1.13 L1 repetitive element;
6984	19521	32303	2.41	2.0E-05 AA714330.1		EST_HUMAN	CALCIUM-BINDING PROTEIN
7309	19721	32523	1.84	2.0E-05 Y08928.1		NT	mw06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
7322	19734	32537	1.2	2.0E-05 A1492860.1		EST_HUMAN	P. falciparum mRNA for AAP1 protein, partial
7332	19744		8.77	2.0E-05 A1891025.1		EST_HUMAN	qz47d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:O02711
7594	20043	32892	2.07	2.0E-05 AF224282.1		NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
							wu35h07.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2622077 3'
							Heterodonthus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7594	20043	32893	2.07	2.0E-05 AF224282.1		NT	
7840	20280		0.94	2.0E-05 AF128847.1		NT	Heterodonthus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
							Homo sapiens Indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
8488	20900	33784	0.49	2.0E-05 U66061.1		NT	Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
8551	20986	33885	1.81	2.0E-05 A1981040.1		EST_HUMAN	ig20h05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108369 3'
10140	22541	35509	1.03	2.0E-05 BF055939.1		EST_HUMAN	775g09.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
10425	22825	35786	2.61	2.0E-05 N41751.1		EST_HUMAN	yw91a08.r1 Soares_placenta_8to9weeks_2NblHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
10425	22825	35797	2.61	2.0E-05 N41751.1		EST_HUMAN	yw91a08.r1 Soares_placenta_8to9weeks_2NblHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
10440	19744		3.45	2.0E-05 A1891025.1		EST_HUMAN	wu35h07.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2622077 3'
11082	23507	36538	1.73	2.0E-05 A1493285.1		EST_HUMAN	ti30h09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN ;
11082	23507	36539	1.73	2.0E-05 A1493285.1		EST_HUMAN	ti30h09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN ;
11201	22853	35828	1.88	2.0E-05 BE175801.1		EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11804	24704		2.9	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kdrt11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
12014	24885		4.86	2.0E-05	AW074604.1	EST_HUMAN	Q12832 GLYCOPHORIN HEP2;
12068	24890		1.65	2.0E-05	AF275948.1	NT	xa89a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2873932 3' similar to contains L1.b3 L1 repetitive element;
12237	24344	30922	1.69	2.0E-05	AU131513.1	EST_HUMAN	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12601	24575		1.21	2.0E-05	AJ200970.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
2843	16344	27847	1.9	1.0E-05	AL163282.2	NT	qf68g11.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755238 3'
3649	16189	28598	1.88	1.0E-05	AF088273.1	NT	Homo sapiens chromosome 21 segment HS21C082
3981	16518	28921	12.68	1.0E-05	P81274	SWISSPROT	Drosophila melanogaster strain Lemito 120 Suppressor of Hairless (Su(H)) gene, partial cds
4189	18718	29104	1.68	1.0E-05	AL163203.2	NT	MOSAIC PROTEIN LGN
4293	16818	29201	1.87	1.0E-05	AA431119.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
4908	17419	29791	2.36	1.0E-05	AW419134.1	EST_HUMAN	zw68g04.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
5055	17565	29933	0.59	1.0E-05	AL163248.2	NT	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5389	17886		1.01	1.0E-05	AJ733566.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
7132	19665	32459	1.02	1.0E-05	AJ246003.1	NT	os64d07.x6 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1610125 3' similar to contains Alu repetitive element
7248	18022	30438	0.45	1.0E-05	P08548	SWISSPROT	Homo sapiens Spast gene for spastin protein
7517	19765	32573	3.36	1.0E-05	AA641846.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7519	19970	32804	6.78	1.0E-05	4505844	NT	ns18g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.k1 L1 L1 repetitive element;
8191	20913	33500	0.87	1.0E-05	BF222846.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
8338	20753		1.89	1.0E-05	P19474	SWISSPROT	7p57d01.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3 MER10 repetitive element;
8290	21722		1.32	1.0E-05	AL163227.2	NT	62 KD RO PROTEIN (SJOOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9385	21817	34793	2.63	1.0E-05	AA452578.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9541	21956	34878	12.39	1.0E-05	AA236110.1	EST_HUMAN	z35h12.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb1.02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9922	22324	35271	0.87	1.0E-05	AW510902.1	EST_HUMAN	z505e11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element/contains element TAR1 repetitive element;
9922	22324	35272	0.87	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element;
9981	22383	35332	1.3	1.0E-05	AW291521.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element;
							UI-H-B12-egk-e-09-Q-UJ.e1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9981	22383	35333	1.3	1.0E-05	AW291521.1	EST_HUMAN	U1H-B12-agk-a-08-Q-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10168	22667		1.89	1.0E-05	AW466995.1	EST_HUMAN	ha07c10.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element:
12427	24879	30575	1.22	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2611	15108	27625	15.15	9.0E-06	AI583811.1	EST_HUMAN	h73a06.x1 NCL_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3057	15811	28020	5.89	9.0E-06	AI218883.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to9weeks_2NbHP8b0W Homo sapiens cDNA clone IMAGE:1759191 3'
3604	16144		3.25	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6175	17979	30040	2.46	9.0E-06	AI984806.1	EST_HUMAN	wr85a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
5231	17733	30102	1.48	9.0E-06	Q03385	SWISSPROT	GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF)
6186	18762	31465	2.88	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7268	19771	32578	0.97	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7925	20362	33229	1.02	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8933	20748	33845	14.93	9.0E-06	AI034370.1	EST_HUMAN	alpha20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1666912 3' similar to contains Alu repetitive element;
8976	21409	34324	1.16	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9329	21761	34687	3.72	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9329	21761	34688	3.72	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9492	21923	34847	4.7	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10717	23165	36139	3.12	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2435	15337	27453	0.93	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
1004	13555		2.12	7.0E-06	AA689728.1	EST_HUMAN	ab00f10.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.11 MER20 repetitive element:
1467	14000	28465	3.59	7.0E-06	7682177	NT	Homo sapiens KIA0555 gene product (KIA0555), mRNA
2826	15382		8.15	7.0E-06	AB688252.1	EST_HUMAN	qwr16g09.x1 NCL_CGAP_U18 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;
3551	16093		0.78	7.0E-06	AA385542.1	EST_HUMAN	EST198205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5224	17726	30094	2.1	7.0E-06	AB032604.1	NT	Mus musculus mRNA for MIWI (pml), complete cds
5966	18542		5.74	7.0E-06	AV983141.1	EST_HUMAN	QV2-OT0082-250400-173-h01 OT0082 Homo sapiens cDNA
6088	18658	31351	0.91	7.0E-06	N98845.1	EST_HUMAN	yw65c07.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278412 5'
11622	24914	30456	2.18	7.0E-06	BF216972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2871	15426	27845	1.33	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4807	15450	27875	2.08	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4814	17326	29705	2.34	6.0E-06	A1040099.1	EST_HUMAN	α08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element;
5603	18191	30556	1.48	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5685	18250	30651	1.22	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
9935	22337		1.82	6.0E-06	AW801812.1	EST_HUMAN	IL5-JM0070-110400-063-g02 UM0070 Homo sapiens cDNA
12543	24532	30863	2.2	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
6367	18925	31660	2.2	6.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6667	19215	31983	2.12	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7479	19683	32480	0.62	5.0E-06	BE145171.1	EST_HUMAN	CM2-HT0193-191099-022-f06 HT0193 Homo sapiens cDNA
7682	20127	32980	1.21	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
10118	22519	35484	4.01	5.0E-06	AA313620.1	EST_HUMAN	EST185498 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
12417	24457	30870	4.53	5.0E-06	A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
666	13231	25842	6.92	4.0E-06	R16267.1	EST_HUMAN	ya48c03.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element;
869	13424	25872	13.15	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element;
1366	13900	26356	5.72	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1366	13900	26357	5.72	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1502	14034	26498	1.7	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
3024	15579	27990	0.85	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3903	18438	28844	1.28	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4865	17377	29753	1.9	4.0E-06	A1889939.1	EST_HUMAN	wf94c10.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
9214	21846	34555	3.81	4.0E-06	AF009860.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9841	22244	35180	1.13	4.0E-06	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11199	22851	35924	4.62	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2072	14587	27105	2.2	3.0E-06	AA700562.1	EST_HUMAN	z134b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element;
2072	14587	27106	2.2	3.0E-06	AA700562.1	EST_HUMAN	z134b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element;
2169	14680		1.72	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2876	15431	27849	1	3.0E-06	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3227	16779		2.31	3.0E-06	A1857779.1	EST_HUMAN	w122a06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ;contains L1.12 L1 repetitive element;
3785	16322	28722	1	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3785	16322	28723	1	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4510	17028	29407	0.69	3.0E-06	T50286.1	EST_HUMAN	yp78b10.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4589	17115	29503	4.64	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
6474	19029	31768	0.92	3.0E-06	AU159412.1	EST_HUMAN	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7192	19903	32731	0.42	3.0E-06	Z79478.1	NT	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA8E5
7192	19903	32732	0.42	3.0E-06	Z79478.1	NT	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA8E5
7677	20123		1.94	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12077	24230		6.64	3.0E-06	AW355282.1	EST_HUMAN	RCOL10001-281199-011-A03 LT0001 Homo sapiens cDNA
208	12811		2.84	2.0E-06	P54386	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1587	14119		5.33	2.0E-06	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2272	14780	27302	4.42	2.0E-06	A1872138.1	EST_HUMAN	wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element;
2480	14981	27495	0.97	2.0E-06	P05719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3499	16042	28463	1.08	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone G1.CFDB05 3'
3762	16301	28702	1.78	2.0E-06	AA173518.1	EST_HUMAN	zp02e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3770	16308	28709	0.8	2.0E-06	AW450215.1	EST_HUMAN	UH-BB-aky-g-05-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736178 3'
3777	16315	28715	1.51	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A18, complete cds
6397	18954		0.89	2.0E-06	AA974832.1	EST_HUMAN	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1668609 3' similar to contains Alu repetitive element;
6431	18987	31718	1.05	2.0E-06	AI539448.1	EST_HUMAN	ts61f05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537 Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
6781	19324	32091	5.63	2.0E-06	AI819424.1	EST_HUMAN	wj90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7984	20400	33270	0.67	2.0E-06	AA888423.1	EST_HUMAN	nv68a08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234090 3' similar to contains L1.13 L1 repetitive element;
8573	21008		0.89	2.0E-06	AW869223.1	EST_HUMAN	MR3-SN0087-120400-002-f02 SN0067 Homo sapiens cDNA
9240	21672		0.99	2.0E-06	AA772497.1	EST_HUMAN	zh27c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:PT0487 PT0487 REVERSE TRANSCRIPTASE;

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9252	21684	34595	1.9	2.0E-06	H62051.1	EST_HUMAN	YU37604.f1 Soares ovary tumor NIHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929
9489	21920	34844	1.02	2.0E-06	AF003529.1	NT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9489	21920	34845	1.02	2.0E-06	AF003529.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
11974	24915	30457	1.66	2.0E-06	P23249	SWISSPROT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
12139	24272		3.63	2.0E-06	BE328232.1	EST_HUMAN	PROTEIN MOV-10
35	12855	25045	1.37	1.0E-06	O76082	SWISSPROT	hs92902.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144899 3' similar to contains L1.12 L1 repetitive element;
676	13241	25856	1.88	1.0E-06	AF084364.1	NT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1480	14012	26477	1.81	1.0E-06	P09125	SWISSPROT	Mus musculus DENM5E protein (D6M5E) mRNA, complete cds
1548	14080	26941	1.08	1.0E-06	AL163278.2	NT	MEROZOITE SURFACE PROTEIN CMZ-8
1601	14133		0.98	1.0E-06	P27625	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
1837	14456	26958	3.9	1.0E-06	AF184614.1	NT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1937	14458	26959	3.9	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2310	14817	27335	1.99	1.0E-06	AL163285.2	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2310	14817	27336	1.99	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4391	16913	29297	14.86	1.0E-06	U07561.1	NT	Homo sapiens chromosome 21 segment HS21C085
5252	17763	30121	0.98	1.0E-06	AL163285.2	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5252	17753	30122	0.98	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5542	18132	30489	6.12	1.0E-06	BF333015.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
5568	18166	30519	1.08	1.0E-06	BE834518.1	EST_HUMAN	MR1-BT0800-030700-002-c08 BT0800 Homo sapiens cDNA
5568	18156	30520	1.08	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5735	18317	30751	1.39	1.0E-06	O60813	SWISSPROT	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
6078	18649		1.02	1.0E-06	BE083527.1	EST_HUMAN	15 KDA SELENOPROTEIN PRECURSOR
7276	19781	32581	6.92	1.0E-06	P02671	SWISSPROT	CMO-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
8286	24995		0.63	1.0E-06	BE185330.1	EST_HUMAN	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
8335	21070		1.34	1.0E-06	AA912623.1	EST_HUMAN	IL6-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8330	21284	34170	1.32	1.0E-06	AI347010.1	EST_HUMAN	α29c08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8994	21427	34337	1.21	1.0E-06	AI287878.1	EST_HUMAN	qp54402.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926842 3'
9555	22118	35046	0.91	1.0E-06	N74635.1	EST_HUMAN	q23f08.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
9821	22224	35159	3.63	1.0E-06	U82968.1	NT	MIR repetitive element;
						EST_HUMAN	zsf5501.e1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:286472 3'
						NT	Homo sapiens shox gene, alternatively spliced products, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9821	22224	35160	3.63	1.0E-06	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9853	22258	35193	5.53	1.0E-06	AA132611.1	EST_HUMAN	2017608.t1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:587174.5'
9890	22293		1.9	1.0E-06	AA449257.1	EST_HUMAN	2044d11.s1 Soares fetal N22HF8.9w Homo sapiens cDNA clone IMAGE:785493.3' similar to gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
10367	22767		1.74	1.0E-06	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11391	23753		3.74	1.0E-06	AW880941.1	EST_HUMAN	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
12011	24180	30948	4.23	1.0E-06	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
12123	14456	26958	1.59	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
12123	14456	26958	1.59	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
375	12963	26382	1.82	9.0E-07	AF003529.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
375	12963	25383	1.82	9.0E-07	AF003529.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
11013	23440	36458	4.83	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
2366	14890		5.16	8.0E-07	AF049259.1	NT	Homo sapiens keralin 13 gene, complete cds
4822	17334	29713	4.09	8.0E-07	A1288598.1	EST_HUMAN	q182g07.x1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1878876.3'
4822	17334	29714	4.09	8.0E-07	A1288598.1	EST_HUMAN	q182g07.x1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1878876.3'
6176	18744		9.8	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
6636	21071		9.01	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11370	23732		5.27	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBEN89
11603	23937		5.17	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5781	18362	30823	1.02	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5781	18362	30824	1.02	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1868	14390	26882	1.99	6.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221089-024-et1 CT0277 Homo sapiens cDNA
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes.>
2395	14999	27418	1.34	6.0E-07	AF019413.1	NT	
3886	16521		1.92	6.0E-07	P41476	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
6432	21884	34780	1.62	6.0E-07	BF001867.1	EST_HUMAN	7g94f07.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149.3' similar to TR:O75920 O75920 4F5L.;
11871	24857		2.22	6.0E-07	AW603222.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
340	12932		1.16	5.0E-07	A1831893.1	EST_HUMAN	W64410.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547.3'
1083	13629		3.41	5.0E-07	AA330630.1	EST_HUMAN	EST03616 Supt cells Homo sapiens cDNA 5' end
2493	14964		5.93	6.0E-07	AW771303.1	EST_HUMAN	h162f02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032476.3'
2990	15546		0.92	5.0E-07	A1831893.1	EST_HUMAN	W64410.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547.3'
4892	17208	28598	1.45	8.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds

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6432	18988	31718	1.26	5.0E-07	U65087.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
6522	19075	31816	0.45	5.0E-07	AA278183.1	EST_HUMAN	z08e09.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712552 5' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
7496	19700	32498	1.91	5.0E-07	A1393981.1	EST_HUMAN	tg66b05.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7496	19700	32499	1.91	5.0E-07	A1393981.1	EST_HUMAN	tg66b05.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7816	20258	33118	18.18	5.0E-07	AW070885.1	EST_HUMAN	xc31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:X16341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8832	21268	34172	0.94	5.0E-07	Q6WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8995	21428		0.96	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10282	22683	35845	4.88	5.0E-07	A1908587.1	EST_HUMAN	CM-B178-220498-014 BT178 Homo sapiens cDNA
11269	23635	36986	3.57	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11328	23682		2.13	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12325	24750		2.38	5.0E-07	AW882537.1	EST_HUMAN	QV60-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
4013	16548	28944	1.75	4.0E-07	AW009602.1	EST_HUMAN	ws84h05.x1 NCI_CGAP_G63 Homo sapiens cDNA clone IMAGE:2504697 3'
5402	17898		2.22	4.0E-07	A165089.1	EST_HUMAN	HA0900 Human fetal liver cDNA library Homo sapiens cDNA
7622	20071		0.77	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7721	20168	33023	1.16	4.0E-07	Q9Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7721	20168	33024	1.16	4.0E-07	Q9Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8378	21811	34724	5.44	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2858548 3'
10715	23153	36136	2.22	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
10715	23153	36137	2.22	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
458	13033	25455	7.23	3.0E-07	U19719.1	NT	Human microfilament-associated glycoprotein (MIFAP2) gene, putative promoter region and alternatively spliced untranslated exons
600	13169	25573	2.68	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1407	13941	26397	1.4	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1636	14168		2.04	3.0E-07	M64857.1	NT	Human IgK subgroup 1 germline gene, exons 1 and 2, V-region 018 allele
2364	14869	27389	4.94	3.0E-07	BE006077.1	EST_HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2364	14869	27390	4.94	3.0E-07	BE006077.1	EST_HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2993	15548	27860	0.83	3.0E-07	T84704.1	EST_HUMAN	y45012.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:111695 5'
3118	15671	28084	1.53	3.0E-07	P36739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4726	17242		0.81	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVOMACROGLOBULIN)

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4778	17292	29877	8.55	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3'
4816	17327	29708	33.48	3.0E-07	A197236.1	EST_HUMAN	we88b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347987 3'
5186	17690	30050	1.46	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratiagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5188	17690	30051	1.46	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratiagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5935	18513	31189	12.19	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6275	18838	31553	0.87	3.0E-07	O42280	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
7075	18609		5.56	3.0E-07	AA815176.1	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
8015	20447	33318	4.1	3.0E-07	AW797168.1	EST_HUMAN	cc04c10.s1 NCL_CGAP_Homo sapiens cDNA clone IMAGE:1339890 3'
8187	20618		1.21	3.0E-07	AI591065.1	EST_HUMAN	QV1-JM0038-200300-115-g02 UM0038 Homo sapiens cDNA
12587	24565		5.46	3.0E-07	AJ132352.1	NT	tw28f1.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
30	12650	25039	3.02	2.0E-07	AF262988.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
158	12763	25179	7.09	2.0E-07	L77589.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
158	12763	25180	7.09	2.0E-07	L77589.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
188	12788	25203	67.83	2.0E-07	U38849.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
769	13329	25760	1.98	2.0E-07	AF003530.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
769	13329	25761	1.98	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
781	13340		1.04	2.0E-07	P11369	SWISSPROT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
967	13520	25964	3.05	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stratiagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
968	13521	25965	5.49	2.0E-07	T83042.1	EST_HUMAN	yc15g04.s1 Stratiagene lung (#837210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ;
1193	13734	26177	1.15	2.0E-07	Q26788	SWISSPROT	IIG AUTOANTIGEN
1617	14148	26619	1.74	2.0E-07	Q09701	SWISSPROT	HYPOTHEICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I
3614	16154		0.65	2.0E-07	BF131397.1	EST_HUMAN	801818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3687	16227	28635	23.54	2.0E-07	AF126348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
6304	17804	30169	0.68	2.0E-07	AW070995.1	EST_HUMAN	xa08h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1 CE00923 PROBABLE RABGAP DOMAINS ;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5304	17804	30170	0.86	2.0E-07	AW070995.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2867485 3' similar to WP:C38H2.1
5598	18188	30550	1.43	2.0E-07	AW88066.1	EST_HUMAN	CE00923 PROBABLE RABGAP DOMAINS ;
6903	24817	32220	0.77	2.0E-07	AW448968.1	EST_HUMAN	RC3-NN0068-260400-021-g11 NN0068 Homo sapiens cDNA
7029	19585	32362	2.04	2.0E-07	AI208715.1	EST_HUMAN	UI-H-B13-ake-b-01-O-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 3'
7044	19578	32371	0.54	2.0E-07	AA572853.1	EST_HUMAN	cg56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8204	20625	33512	1.8	2.0E-07	X95169.1	NT	nm33a08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1081938 similar to contains Alu repetitive element
8978	21412	34469	3.97	2.0E-07	AV729390.1	EST_HUMAN	H.sapiens brca2 gene exon 9
9132	21584	34469	1.2	2.0E-07	AA035198.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAE G02 5'
9874	22277	35589	1.11	2.0E-07	AL16303.2	NT	zk27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
10221	22622	35589	6.05	2.0E-07	AW892507.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10368	22768	35734	0.92	2.0E-07	P00751	SWISSPROT	CM4-NN0003-280300-124-408 NN0003 Homo sapiens cDNA
10368	22768	35735	0.92	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
11656	24447		2.02	2.0E-07	BE163717.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11648	24751		1.28	2.0E-07	AI732462.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
1129	13673		0.89	1.0E-07	AL163282.2	NT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
2280	14788	27308	1.28	1.0E-07	P10263	SWISSPROT	PMO-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA
2360	14855	27375	2.74	1.0E-07	7549818	NT	zn88h11 x5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element ;
2785	14078	28539	2.83	1.0E-07	P08266	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
3743	13673		1.23	1.0E-07	AL163282.2	NT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
4311	16835	29223	3.03	1.0E-07	AV718662.1	EST_HUMAN	Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, mRNA
4311	16835	29224	3.03	1.0E-07	AV718662.1	EST_HUMAN	GLYCOPROTEIN GPV
4791	17305		1.29	1.0E-07	O75820	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
6853	19393	32169	1.53	1.0E-07	U82671.2	NT	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
7270	19775	32582	5.71	1.0E-07	BE047871.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
7270	19775	32583	5.71	1.0E-07	BE047871.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
7896	20430	33297	7.75	1.0E-07	N55081.1	EST_HUMAN	ZINC FINGER PROTEIN 189
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
							tz43d06.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5'
							tz43d06.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5'
							zy43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8178	20601	33487	0.84	1.0E-07	BF375908.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
8179	20601	33488	0.84	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
8216	20635	33524	2.19	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8790	21224	34129	3.42	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8790	21224	34130	3.42	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9311	21743	34651	2.68	1.0E-07	AA693576.1	EST_HUMAN	z151e10.s1 Scores fetal_liver spleen .1NFLS_S1 Homo sapiens cDNA clone IMAGE:494348 3'
9527	21942	34884	1.26	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9993	22395	35347	2.78	1.0E-07	BF674524.1	EST_HUMAN	602137171F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274428 5'
9997	22399	35350	1.24	1.0E-07	AA388311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
10362	22762		1.54	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
11993	24724	30873	3.87	1.0E-07	BE048770.1	EST_HUMAN	h183c11.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:095722 O95722
12079	24232		1.31	1.0E-07	X64487.1	NT	DJ116331.1 ;
12265	24361		2.88	1.0E-07	X51755.1	NT	H. sapiens ALAD gene for porphobilinogen synthase
7738	20182	33043	1.01	9.0E-08	AI539362.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
9860	22362	35312	1.96	9.0E-08	AV734819.1	EST_HUMAN	ts51b06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
11885	24121		3.89	9.0E-08	AJ251973.1	NT	AV734819 cDNA Homo sapiens cDNA clone cdABFB08 5'
626	18288		3.38	8.0E-08	AI911352.1	EST_HUMAN	Homo sapiens partial elastin-1 gene
1076	13622		1.57	8.0E-08	BE785469.1	EST_HUMAN	wd16b05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
3529	16072		1.72	8.0E-08	BE785469.1	EST_HUMAN	801690133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5'
9166	21598	34508	3.89	8.0E-08	AI752387.1	EST_HUMAN	801690133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5'
9166	21598	34509	3.89	8.0E-08	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH7BC_cn15c02 random
9782	22185	35121	3.28	8.0E-08	AW970693.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH7BC_cn15c02 random
83	12700	25114	2.86	7.0E-08	X02357	SWISSPROT	EST382776 MAGE resequences, MAGK Homo sapiens cDNA
1393	13927	26385	7.4	7.0E-08	X04809.1	NT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
3566	16108	28622	1.25	7.0E-08	P15305	SWISSPROT	Rat mRNA for ribosomal protein L31
3566	16108	28523	1.25	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10598	23041		2.63	7.0E-08	AI535743.1	EST_HUMAN	DYNEIN HEAVY CHAIN (DYHC)
11407	23768	36828	3.43	7.0E-08	U24070.1	NT	cong3.P11.A5 conorm Homo sapiens cDNA 3'
12388	16108	28522	3.32	7.0E-08	P15305	SWISSPROT	Rattus norvegicus Munc13-1 mRNA, complete cds
12388	16108	28523	3.32	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12468	24487		1.62	7.0E-08	AL131016.1	NT	Homo sapiens SCL gene locus
840	13397	25835	3.41	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
840	13397	25836	3.41	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2258	14784	27286	0.98	6.0E-08	BE144398.1	EST_HUMAN	MRO-HT0168-181199-004-g09 HT0168 Homo sapiens cDNA
3022	15577	27888	0.65	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4284	18789	29173	1.07	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8498	20910	33806	0.49	6.0E-08	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
87	12704	25118	3.24	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2143	14656	27180	1.2	5.0E-08	AA493851.1	EST_HUMAN	h03b09.g1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
2627	15122	27635	2.53	5.0E-08	Q02487	SWISSPROT	DESMOCOLLIN 2A/2B PRECURSOR (DESMOSOMAL GLYCOPROTEIN II AND III) (DESMOCOLLIN-3)
11605	23938		5.88	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
11809	24069	30985	2.45	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-412 CT0225 Homo sapiens cDNA
3927	18462	28970	2.64	4.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6743	19287	32048	1.08	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9213	21645	34554	0.85	4.0E-08	O16393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9431	21863	34779	1.2	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
10294	22895	35681	3.67	4.0E-08	A1050027.1	EST_HUMAN	an22d10.x1 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
10873	23306	36301	4.64	4.0E-08	BF682493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
10873	23306	36302	4.64	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
11610	24889		2.66	4.0E-08	W76159.1	EST_HUMAN	z085g03.r1 Soares_fetal_heart_NbhH19W Homo sapiens cDNA clone IMAGE:346558 5' similar to contains L1.1 L1 repetitive element;
12313	24390		2.41	4.0E-08	A1343353.1	EST_HUMAN	IB96a11.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3
5878	18457	31131	2.02	3.0E-08	BE018348.1	EST_HUMAN	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3046570 5' similar to TR:Q8Z158 Q8Z158 SYNTAXIN 17.;
7393	18082	30403	4.65	3.0E-08	A1792737.1	EST_HUMAN	qs76f11.y5 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:1944045 5'
8052	20484	33359	1.56	3.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8303	20718		2.75	3.0E-08	A1438352.1	EST_HUMAN	th93h09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
8452	20868		0.47	3.0E-08	AV731469.1	EST_HUMAN	AV731469 HTF Homo sapiens cDNA clone HTFABH01 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11397	23758	38817	2.71	3.0E-08	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11576	23919		18.8	3.0E-08	R18420.1	EST_HUMAN	ygo204.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
212	12815		11.88	2.0E-08	AW302988.1	EST_HUMAN	xc8700.x1 NCI CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
237	12839		10.83	2.0E-08	AA425598.1	EST_HUMAN	zw4807.r1 Soares total fetus Nb2HF8.9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element;
514	13087	25501	1.77	2.0E-08	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
679	13244	25658	13.26	2.0E-08	AW886438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
679	13244	25659	13.26	2.0E-08	AW886438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1016	13568		7.75	2.0E-08	BE280477.1	EST_HUMAN	601165321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 6'
1374	13909	26365	2.08	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1733	14260		1.16	2.0E-08	BE734871.1	EST_HUMAN	601670463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845193 5'
1826	14348		2.6	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCI CGAP_HNT11 Homo sapiens cDNA clone IMAGE:2743149 3'
2319	14826	27341	1.34	2.0E-08	AA731948.1	EST_HUMAN	nw64h01.s1 NCI CGAP_GC81 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L1.13 L1 repetitive element;
2454	14956		1.56	2.0E-08	K00216.1	NT	Sheep His-IRNA-GUG
3166	16719	28140	7.31	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3166	16719	28141	7.31	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3885	16401		1.67	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA
4092	16823	28012	0.6	2.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4430	16951		1.59	2.0E-08	AA459040.1	EST_HUMAN	aa28c07.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
5045	17555		3.47	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI CGAP_GML1 Homo sapiens cDNA clone IMAGE:2918327 3' similar to contains Alu repetitive element;
5904	18482	31164	0.82	2.0E-08	AA813204.1	EST_HUMAN	ai80h11.s1 Soares testis NHT Homo sapiens cDNA clone 1377189 3'
6119	18688	31368	0.98	2.0E-08	AW088924.1	EST_HUMAN	xd32cd4.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2695462 3' similar to contains MER18.b3
8638	21073	33981	1.14	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element;
8711	21146	34049	1.52	2.0E-08	AA490121.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9397	21829		1.02	2.0E-08	AU136078.1	EST_HUMAN	eb02g06.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
1537	18313	26828	1.12	1.0E-08	P31792	SWISSPROT	AU159978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
1978	14494		2.04	1.0E-08	BE141959.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
5866	18445	31120	4.21	1.0E-08	AJ010770.1	NT	PM2-HT0130-150999-001-412 HT0130 Homo sapiens cDNA
							Homo sapiens hypoxanthine gene, exons 1-50

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8325	20740	33635	1.1	1.0E-08	P19474	SWISSPROT	S2 KD RO PROTEIN (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9035	21467	34377	1.97	1.0E-08	A1015304.1	EST_HUMAN	cd35a05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
10008	22410	35359	0.87	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
11080	23505	36536	2.3	1.0E-08	AFO44083.1	NT	Homo sapiens major histocompatibility locus class III region
12008	24187		2.41	1.0E-08	X57155.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12538	24709		1.3	1.0E-08	BF375398.1	EST_HUMAN	MR4-ST0240-240700-013-g04 ST0240 Homo sapiens cDNA
4259	16784	29168	4.53	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4259	16784	29169	4.53	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
11500	23858	36933	1.78	9.0E-09	AW173008.1	EST_HUMAN	x82a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2663706 3' similar to contains L1.12
6829	19370		0.85	8.0E-09	A1270616.1	EST_HUMAN	qu86c11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978964 3' similar to contains L1.13 L1
7718	20163	33020	7.84	8.0E-09	A1183500.1	EST_HUMAN	qd42a07.x1 Soares_fetal_heart_NbH-H18W Homo sapiens cDNA clone IMAGE:1732164 3' similar to
8634	21069	33978	2.67	8.0E-09	AW900159.1	EST_HUMAN	contains MSR1.11 MSR1 repetitive element ;
9333	21786		2.63	8.0E-09	AA938892.1	EST_HUMAN	CMQ-NN1004-100300-273-e08 NN1004 Homo sapiens cDNA
3501	16141		2.05	7.0E-09	D86842.1	NT	op74408.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582576 3'
4022	16555		1.16	7.0E-09	U50871.1	NT	Homo sapiens DNA for 3-ketoadipyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
8665	21100		0.87	7.0E-09	AA256200.1	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
9521	21936	34850	2.65	7.0E-09	L09709.1	NT	zr80c05.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:681892 5' similar to contains L1.12 L1
10165	22568	35532	1.66	7.0E-09	BE254850.1	EST_HUMAN	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10463	22813		5.13	7.0E-09	T97950.1	EST_HUMAN	601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
4041	16573	28985	1.2	6.0E-09	AA557940.1	EST_HUMAN	y658a12.s1 Soares_fetal_liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:121918 3'
5078	17586	28954	6.22	6.0E-09	BE169421.1	EST_HUMAN	nl17a11.s1 NCI_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1
5217	17720	30086	3.48	6.0E-09	AW593471.1	EST_HUMAN	repetitive element ;
5217	17720	30087	3.48	6.0E-09	AW593471.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA
5638	18223	30623	7.94	6.0E-09	AW195784.1	EST_HUMAN	hg16f12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2845807 3' similar to gb:X63743 FIBULIN-1
8054	21466	34398	1.21	6.0E-09	BE161653.1	EST_HUMAN	hg16f12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2845807 3' similar to gb:X63743 FIBULIN-1
							1. ISOFORM C PRECURSOR (HUMAN);
							1. ISOFORM C PRECURSOR (HUMAN);
							xn85f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
							MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9458	21889	34810	2.55	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10230	22631		3.41	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase subunit (TSKS) gene, complete cds
1446	13978	28437	3.2	5.0E-09	BE149284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
6748	19292	32052	2.08	5.0E-09	AA359454.1	EST_HUMAN	EST168746 Fetal lung II Homo sapiens cDNA 5' end
7245	18018	30434	0.65	5.0E-09	U68059.1	NT	Human gamine T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV8S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
10112	22513	35478	2.83	5.0E-09	AW799687.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
639	13111		1.81	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
989	13541		2.25	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1498	14030	28493	1.22	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2329	14836	27351	10.88	4.0E-09	AA350878.1	EST_HUMAN	EST158385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
2247	14765	27275	3.83	3.0E-09	BE222239.1	EST_HUMAN	hu09a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2465	14866	27477	5.12	3.0E-09	BE222239.1	EST_HUMAN	hu09a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2566	15082	27696	3.62	3.0E-09	P23249	SWISSPROT	PROTEIN MOV-10
3299	15848	28268	1.01	3.0E-09	BE222239.1	EST_HUMAN	hu09a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3354	15900		0.62	3.0E-09	AA442272.1	EST_HUMAN	MER18 repetitive element;
4113	16843		0.71	3.0E-09	X16674.1	NT	z164a04.1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4455	16975	28382	4.08	3.0E-09	AF175325.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4549	17066	28448	2.66	3.0E-09	Q8Y3R5	SWISSPROT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
8562	20997	33894	1.14	3.0E-09	BE465780.1	EST_HUMAN	258.1 KDA PROTEIN C21ORF5 (K1AA0933)
10210	22811	35570	1.84	3.0E-09	AL183247.2	NT	hu08a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O65091
10798	23235	36217	2.71	3.0E-09	BF108943.1	EST_HUMAN	Q55091 IMPACT PROTEIN.;
10798	23236	36218	2.71	3.0E-09	BF108943.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
895	13392		0.75	2.0E-09	X16674.1	NT	7172e08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1291	13826	28277	6.5	2.0E-09	AL183284.2	NT	7172e08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1660	14191		8.76	2.0E-09	AL118573.1	EST_HUMAN	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
2221	14731	27251	1.68	2.0E-09	Q8Y3R5	SWISSPROT	Homo sapiens chromosome 21 segment HS21C084
							DKFZp761B1710_1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3950	18485	28894	3.97	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5994	18568	31254	0.61	2.0E-09	A1004082.1	EST_HUMAN	cd47b09.e1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1618897 3'
6463	19019		0.54	2.0E-09	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
7164	19877		0.77	2.0E-09	AA357407.1	EST_HUMAN	EST166142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7636	20373	33240	8.88	2.0E-09	AA461430.1	EST_HUMAN	z63h06.r1 Soares total_fetus_Nb2HF8 9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
8030	20482	33337	0.8	2.0E-09	W28834.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8357	20772	33669	0.54	2.0E-09	A1249732.1	EST_HUMAN	q888g10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854114 3'
8438	20850	33750	0.48	2.0E-09	AW862126.1	EST_HUMAN	MR1-CT0352-240200-105-b06 CT0352 Homo sapiens cDNA
8143	21575	34481	1.16	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11036	23483	36484	2.31	2.0E-09	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12166	13392		17.08	2.0E-09	X16674.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12242	24986		2.34	2.0E-09	AA226070.1	EST_HUMAN	nc11c02.r1 NCI CGAP_Prl Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element
12250	24802		1.24	2.0E-09	AW301637.1	EST_HUMAN	x89a02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2769234 3'
12558	24543		18.11	2.0E-09	AV767897.1	EST_HUMAN	AV757897 BM Homo sapiens cDNA clone BMFBFC12 5'
1021	13572		0.7	1.0E-09	W78192.1	EST_HUMAN	zdf0d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to gb1.02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1136	13680	26119	1.6	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1136	13680	26120	1.6	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2408	14912		0.99	1.0E-09	A1356088.1	EST_HUMAN	q64a11.x1 NCI CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12
2843	15389	27815	2.19	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
2880	15435	27853	3.6	1.0E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2880	15435	27854	3.6	1.0E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2897	15562	27964	0.8	1.0E-09	BE535440.1	EST_HUMAN	601056602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4853	17365		5.68	1.0E-09	AA718297.1	EST_HUMAN	zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414028 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
5765	18346	30802	0.72	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6116	18885	31383	1.33	1.0E-09	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
6457	19013	31746	3.41	1.0E-09	P26694	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8416	20830	33727	0.64	1.0E-09	AV728645.1	EST_HUMAN	AV728645 HTC Homo sapiens cDNA clone HTCBIG07 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8924	21358	34273	0.85	1.0E-09	AI688474.1	EST_HUMAN	w639b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains MER25.11 MER25 repetitive element;
10249	22650		2.82	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12059	24901	30579	2.77	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
1341	13877	26330	2.22	9.0E-10	AW867740.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2791	15348	27770	5.72	9.0E-10	AI870071.1	EST_HUMAN	w678h03.x1 Soares_Dieckgraefe_coton_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element PTR5 repetitive element ;
7227	19839	32686	6.36	9.0E-10	AI452982.1	EST_HUMAN	TR:O00372 O00372 PUTATIVE P160. ;
151	12756	25174	12.04	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3315	15863	28281	1	8.0E-10	BE080748.1	EST_HUMAN	QV1-B70631-160200-071-071 B70631 Homo sapiens cDNA
4217	16742	29130	4.42	8.0E-10	AA376832.1	EST_HUMAN	EST89564 Small intestine I Homo sapiens cDNA 5' end
10007	22409		2.93	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
721	13282	25706	24.08	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
721	13282	25707	24.08	7.0E-10	Q13342	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1633	14165	26636	2.1	7.0E-10	P08547	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2472	14973		13.63	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3050	15604	28013	2.73	7.0E-10	X00856.1	NT	H.sapiens DHFR gene, exon 3
6499	16053	31793	3.74	7.0E-10	AA345220.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
7998	20337	33205	1.28	7.0E-10	BF332883.1	EST_HUMAN	IL3-HT0619-110700-208-D12 HT0619 Homo sapiens cDNA
8187	20609		1.89	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8614	21049	33954	2.03	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8814	21049	33955	2.03	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
936	13490	25933	3	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2918	15113	27628	4.94	8.0E-10	AI424405.1	EST_HUMAN	h02a07.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4789	17303		2.66	8.0E-10	AW853719.1	EST_HUMAN	RC3-GT0254-031099-012-g12 GT0254 Homo sapiens cDNA
9202	21634	34542	1.09	8.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
9202	21634	34543	1.09	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
11643	23958		1.73	8.0E-10	AW971923.1	EST_HUMAN	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
782	13341		4.9	5.0E-10	AL046804.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
							EST384012 IMAGE resequences, MAGL Homo sapiens cDNA
							DKFZp434N219_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N219 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3451	15995	28414	0.96	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
5089	17599	28964	1.16	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7786	20228		1.76	5.0E-10	BF105159.1	EST_HUMAN	601822184Ft NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9720	22143	35069	2.1	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
9720	22143	35070	2.1	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
115	12727		1.08	4.0E-10	A1221083.1	EST_HUMAN	qg09009.x1 Soares_plicenta_8109weeks_2NbhP8to9W Homo sapiens cDNA clone IMAGE:1769049 3'
598	13167	26571	0.72	4.0E-10	AA515260.1	EST_HUMAN	similar to contains LTR8.b2 LTR8 repetitive element:
1939	14458	26961	1.03	4.0E-10	AW594709.1	EST_HUMAN	nt84a01.s1 NCL_CGAP_Oc3 Homo sapiens cDNA clone IMAGE:924648 3'
2490	14981	27506	16.31	4.0E-10	AL163303.2	EST_HUMAN	hg58g03.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2849844 3' similar to contains Alu repetitive element:
7620	20069	32821	16.34	4.0E-10	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C103
10336	22736	35704	0.84	4.0E-10	A1267342.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
838	13491	26935	1.55	3.0E-10	N36113.1	EST_HUMAN	ad63h1.1.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035553
1382	13917		8.38	3.0E-10	AY005150.1	NT	w3206.s1 Soares_melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.11 L1 repetitive element:
5712	18295	30722	0.79	3.0E-10	N50109.1	EST_HUMAN	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
6517	19070	31813	5.04	3.0E-10	P20350	SWISSPROT	yz11g08.s1 Soares_multiple_sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:282782 3'
9682	19230	31980	4.11	3.0E-10	BE302970.1	EST_HUMAN	RHOMBOLD PROTEIN (VEINLET PROTEIN)
8315	20730	33622	1.08	3.0E-10	AV743302.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5'
8315	20730	33623	1.06	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
9157	21589	34497	1.37	3.0E-10	H87208.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
9377	21809	34721	1.76	3.0E-10	AW850731.1	EST_HUMAN	ye74b12.s1 Soares_retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element:
9377	21809	34722	1.76	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
10350	22750		1.91	3.0E-10	T85891.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
10428	22828		1.13	3.0E-10	AA769294.1	EST_HUMAN	ye11e12.r1 Stragelone lung (#937210) Homo sapiens cDNA clone IMAGE:80398 5'
11485	23843	36911	2.29	3.0E-10	A1765528.1	EST_HUMAN	rz36g03.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1289908 3'
12552	24412	30893	2.5	3.0E-10	BE179517.1	EST_HUMAN	w181b08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389703 3'
37	12657	25047	1.67	2.0E-10	P48988	SWISSPROT	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
37	12657	25048	1.67	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1860	14382		1.25	2.0E-10	U80017.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) Homo sapiens basic transcription factor 2 p44 (btf2p-44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2941	15496		0.77	2.0E-10	BF675047.1	EST_HUMAN	602136940F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
6087	18657		2.37	2.0E-10	Q28640	SWISSPROT	(HPRG)
6572	19123	31865	1.71	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7853	20293	33156	6.32	2.0E-10	BE791082.1	EST_HUMAN	601566208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
9553	21987		0.97	2.0E-10	BF434565.1	EST_HUMAN	7078009.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3842303 3' similar to contains L1.13 L1 repetitive element;
1536	14068		1.71	1.0E-10	AW897787.1	EST_HUMAN	MRO-SN0038-290300-001-f01 SN0038 Homo sapiens cDNA
1823	14154	26624	2.49	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2498	14999		5.17	1.0E-10	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2502	15003		14.92	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA
3478	16021	28442	1.1	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3523	16066		0.67	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3851	16066		0.93	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
4028	16561		7.16	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4145	16673	29059	5.87	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4145	16673	29060	6.87	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4152	16680	29069	2.2	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4188	16713		2.48	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
7069	18623	32419	0.44	1.0E-10	AA631233.1	EST_HUMAN	nc81805.s1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:1158704 3'
7209	19920	32749	0.45	1.0E-10	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7975	20411		0.67	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8221	20640	33530	0.59	1.0E-10	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8807	21241	34148	1.15	1.0E-10	AW408990.1	EST_HUMAN	fb_6A4 Fetal brain library Homo sapiens cDNA
9107	21539		1.04	1.0E-10	AI268340.1	EST_HUMAN	qm04e10.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10178	22578		4.46	1.0E-10	AA081868.1	EST_HUMAN	zn23g06.r1 Stratiogene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548314 5'
10693	23132	36113	4.26	1.0E-10	AI038280.1	EST_HUMAN	cy85h03.x1 Soares fetal_liver_spleen_INFUS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
11585	18015		1.48	1.0E-10	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 8, 13 and 14 genes
11634	23959		1.26	1.0E-10	AA397885.1	EST_HUMAN	z86b10.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:729211 5'
275	12872	25289	1.14	9.0E-11	BE145600.1	EST_HUMAN	IL2-H10203-291089-018-c08 H10203 Homo sapiens cDNA
2025	14541	27054	3.97	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
2025	14541	27055	3.97	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3361	15907	28329	2.95	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3361	15907	28330	2.85	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
4537	17055	28438	1.05	9.0E-11	AA775885.1	EST_HUMAN	ae78f01.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:370297 3'
5058	17568	28834	1.23	9.0E-11	AL163246.2	NT	Homo sapiens chromosome 21 segment HS210046
5839	18419		3.76	9.0E-11	BE079780.1	EST_HUMAN	RC8-BT0627-140200-011-E08 BT0627 Homo sapiens cDNA
10152	22553	35520	1.18	9.0E-11	AA324980.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10152	22553	35521	1.18	9.0E-11	AA324980.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
11881	24174	30980	4.21	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-506B08 5'
3077	16631		9.75	8.0E-11	H19871.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element:
3978	16511	28918	0.65	8.0E-11	AI478617.1	EST_HUMAN	hm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
4055	16587	28977	6.29	8.0E-11	N23712.1	EST_HUMAN	yw46e08.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
5168	17672	30036	2.53	8.0E-11	P47884	SWISSPROT	OLFATORY RECEPTOR 1D4 (OLFATORY RECEPTOR 17-30) (OR17-30)
6078	18947	31342	0.64	8.0E-11	AW674316.1	EST_HUMAN	b660g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982 3'
7040	18575		0.6	8.0E-11	AW168158.1	EST_HUMAN	xf45h11.x1 NCI_CGAP_Bm50 Homo sapiens cDNA clone IMAGE:2821061 3' similar to contains MER10.11 MER10 repetitive element:
1477	14009	28475	2.06	7.0E-11	AA330842.1	EST_HUMAN	EST34392 Embryo, 8 week I Homo sapiens cDNA 5' end
2803	15099	27014	2.07	7.0E-11	AW692611.1	EST_HUMAN	GM3-NN0004-100300-111-h08 NN0004 Homo sapiens cDNA
6001	21434	34343	2.47	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10197	22598		1.52	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
12135	24268		1.53	7.0E-11	AV701656.1	EST_HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBAB008 5'
429	13003	25430	7.66	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
429	13003	25431	7.66	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7098	19831	32428	0.94	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
8232	20651	33543	3.76	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8902	21336	34260	8.91	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC08 5'
11	12631	25018	1.13	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3342	12631	25018	1.48	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6868	19408	32180	1.57	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
8038	20470	33344	16.18	5.0E-11	11416789	NT	Homo sapiens proteodherin beta 3 (PCDH3), mRNA
1433	13965		1.03	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2749	16239	27762	5.81	4.0E-11	BE885900.1	EST_HUMAN	801507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909285 5'
2923	16478	27901	1.1	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4682	17178	29557	1.21	4.0E-11	D44668.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6822	18363	32140	2.68	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
7422	18927	32758	0.7	4.0E-11	AA442630.1	EST_HUMAN	zv56f10.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757983 5' similar to TR:G1055230
7848	20288		4.29	4.0E-11	AF224689.1	NT	G1055250 PHEROMONE RECEPTOR VN4. ;
9616	22031		1.64	4.0E-11	BE149426.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9805	22208	35146	0.89	4.0E-11	AI609753.1	EST_HUMAN	RC1-HT0256-210100-013-08 HT0256 Homo sapiens cDNA
12204	24321	30917	1.83	4.0E-11	11545732	NT	h82g12.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP:ZK363.1
1520	14052	26516	2.18	3.0E-11	6879077	NT	CE00385 ;
4292	16917		1.34	3.0E-11	AA309248.1	EST_HUMAN	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
984	13537	25980	1.82	2.0E-11	AI150502.1	EST_HUMAN	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
1216	13758	26202	5.2	2.0E-11	R24807.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
1216	13758	26203	5.2	2.0E-11	R24807.1	EST_HUMAN	q36c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1627	14168	26827	5.41	2.0E-11	L17432.1	NT	MER10 repetitive element ;
1627	14158	26628	5.41	2.0E-11	L17432.1	NT	Y943e12.1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:35144 5'
3153	15708	28127	7.64	2.0E-11	P10283	SWISSPROT	Y943e12.1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:35144 5'
3294	15843	28281	1	2.0E-11	AI478617.1	EST_HUMAN	Y943e12.1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:35144 5'
							Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
							COR3 beta (COR3 beta) genes, complete cds
							Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
							COR3 beta (COR3 beta) genes, complete cds
							RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
							Im54c09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3340	16887	28308	0.71	2.0E-11	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1)
3473	16016		0.86	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4474	16894		1.3	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
4646	17162		0.67	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5016	17526		2.38	2.0E-11	BE062658.1	EST_HUMAN	QV2-BT0258-261099-014-e01 BT0258 Homo sapiens cDNA
5138	17642	30006	1.09	2.0E-11	AA307331.1	EST_HUMAN	EST178226 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2-
6448	18004	31738	1.09	2.0E-11	AW877806.1	EST_HUMAN	macroglobulin
6638	19186	31937	1.69	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.r1 NCL CGAP_GC1 Homo sapiens cDNA clone IMAGE:787433 5' similar to SW:PR16_YEAST
7639	20083	32940	0.72	2.0E-11	BF682945.1	EST_HUMAN	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16. ; 7/97c03.X1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442565 3'
9493	21924		0.98	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10234	22635	35598	5.25	2.0E-11	Q13606	SWISSPROT	OLFACTORY RECEPTOR G11 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10384	22784	35752	1.14	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10384	22784	35753	1.14	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10920	23352	36360	2.81	2.0E-11	AA281958.1	EST_HUMAN	Zs18b04.r1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:685519 5'
11718	24887		1.48	2.0E-11	AA704185.1	EST_HUMAN	477e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:480924 3'
11751	24033		1.75	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-e01 CN0027 Homo sapiens cDNA
11779	24053	31024	1.89	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-p01 TN0140 Homo sapiens cDNA
12058	24222		1.84	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12223	24334		1.95	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12577	24657		2.72	2.0E-11	11417966	NT	Homo sapiens SEG14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
695	13257	25674	1.99	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
806	13365	25800	1.03	1.0E-11	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
1248	13786	26232	4.05	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1527	14059		2.24	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2045	14561	27073	2.2	1.0E-11	AF000579.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3476	16018	28438	1.36	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-282-d12 BN0105 Homo sapiens cDNA
5487	17962	30310	3.76	1.0E-11	AV746904.1	EST_HUMAN	AV746904 NPC Homo sapiens cDNA clone NPOBK04 5'
5585	18173	30537	16.71	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descrip ^{tr}
6117	18886	31384	0.77	1.0E-11	BF222646.1	EST_HUMAN	7p57d01.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.53
8415	20829		0.46	1.0E-11	AB042297.1	NT	MER10 repetitive element;
8778	21213	34116	3.3	1.0E-11	4885546	NT	Homo sapiens PTS gene for 6-pyruvoyl-tetrahydropterin synthase, complete cds
9057	21489	34401	4.06	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9376	21808	34719	1.36	1.0E-11	BF365119.1	EST_HUMAN	y73d08.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28186 5'
9376	21808	34720	1.36	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
11057	23483	36510	1.81	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
12312	24669		1.21	1.0E-11	Z20377.1	EST_HUMAN	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4265977 5'
8894	22296	35236	1.22	9.0E-12	AL163300.2	NT	HSAACADH P. Human foetal Brain Whole tissue Homo sapiens cDNA
8894	22296	35237	1.22	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
11488	23846	36914	1.73	9.0E-12	AL046639.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
11512	23870	36948	2.49	9.0E-12	AI858300.1	EST_HUMAN	DKFZp586i0417 r1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp586i0417 5'
							w336a05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426960 3' similar to WP:F53F10.1
11512	23870	36949	2.49	9.0E-12	AI858300.1	EST_HUMAN	w336a05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426960 3' similar to WP:F53F10.1
							CE10980 ;
2630	15125		2.31	8.0E-12	AA016131.1	EST_HUMAN	2831c05.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1
9576	21899		0.91	8.0E-12	BE074720.1	EST_HUMAN	repetitive element ;
11634	24086		5.24	8.0E-12	AJ271736.1	NT	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
4705	17221	29604	1.77	7.0E-12	Q05904	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2
11107	23660	36601	5.38	7.0E-12	AA704735.1	EST_HUMAN	34 KD SPIGULE MATRIX PROTEIN PRECURSOR (LSM34)
3532	16075		0.68	6.0E-12	AV730554.1	EST_HUMAN	223g01.s1 Scores fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
							AV730554 HTF Homo sapiens cDNA clone HTFAWF08 5'
4370	16892	29273	9.98	6.0E-12	AA732516.1	EST_HUMAN	r288f11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu
							repetitive element;
6725	19271	32030	0.58	6.0E-12	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9338	21770	34673	1.08	6.0E-12	AF003249.1	NT	Marone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
							cd10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.12
9873	22020		1.28	6.0E-12	AA847898.1	EST_HUMAN	MER29 repetitive element ;
1088	13614	26056	2.88	5.0E-12	T08573.1	EST_HUMAN	EST044682 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HFBDV33
3368	15914	28335	1.09	5.0E-12	BE047778.1	EST_HUMAN	tz42b05.y1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291217 5'
3726	16266	28670	6.28	5.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6325	18885	31614	6.41	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Table 4

Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6325	18885	31615	6.41	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6840	19381	32156	12.28	5.0E-12	AW974760.1	EST_HUMAN	EST386850 IMAGE resequences, MAGN Homo sapiens cDNA
7460	19675	32471	1.03	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1616_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
7471	19675	32471	1.08	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1616_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8800	21234	34142	1.22	5.0E-12	AA033745.1	EST_HUMAN	Z01g12.s1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1 repetitive element;
9418	21848	34763	2.69	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9636	22051	34982	1.19	5.0E-12	P34692	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10229	22630		4.55	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
257	12858	25273	4.61	4.0E-12	AA700326.1	EST_HUMAN	Z174g11.s1 Soares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
258	12858	25273	5.04	4.0E-12	AA700326.1	EST_HUMAN	Z174g11.s1 Soares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
4664	17180	28559	1.03	4.0E-12	AI689984.1	EST_HUMAN	b26h05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
5388	17885		0.89	4.0E-12	U76377.1	NT	Human olfactory receptor 17-43 (OR17-43) and olfactory receptor 17-201 (OR17-201) genes, complete cds
8150	20573		0.77	4.0E-12	BF445140.1	EST_HUMAN	had21b03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2 MER7 repetitive element;
8810	21244		3.73	4.0E-12	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
10865	23298	36282	2.96	4.0E-12	AJ228043.1	NT	Homo sapiens 958 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
12106	24262		1.98	4.0E-12	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
635	13169	25606	3.32	3.0E-12	AW341693.1	EST_HUMAN	hd13a01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.;
635	13169	25607	3.32	3.0E-12	AW341693.1	EST_HUMAN	hd13a01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.;
5709	18283	30720	1.36	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
7449	19952	32766	0.5	3.0E-12	BE149692.1	EST_HUMAN	RC1-HT0256-280300-017-c09 HT0256 Homo sapiens cDNA
7910	20349		0.57	3.0E-12	AB042297.1	NT	Homo sapiens P1S gene for 6-pyruvoyltetrahydropterin synthase, complete cds
8308	20723		0.5	3.0E-12	AW864328.1	EST_HUMAN	RC3-CT0255-031098-011-h02 CT0255 Homo sapiens cDNA
10448	22899	35876	2.92	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10448	22899	35877	2.92	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
3443	15987	28405	1.11	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4131	16659	29045	1.05	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4131	16659	29046	1.05	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4449	16869		2.13	2.0E-12	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
4966	17477	29853	0.7	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
4968	17477	29854	0.7	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5499	18090	30331	0.79	2.0E-12	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
6823	19364		1.87	2.0E-12	AW971857.1	EST_HUMAN	EST383946 IMAGE resequences, MAGL Homo sapiens cDNA
7619	20068	32920	4.14	2.0E-12	T08169.1	EST_HUMAN	EST08060 Infant Brain, Benito Soares Homo sapiens cDNA clone HIBBA13 5' end
7811	20253	33114	1.44	2.0E-12	BE173035.1	EST_HUMAN	MRO-H0559-200400-015-e08 HT0559 Homo sapiens cDNA
8043	20475		0.57	2.0E-12	AW842798.1	EST_HUMAN	MR2-CN0037-210200-101-b02 CN0037 Homo sapiens cDNA
8192	20614	33501	2.42	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9558	22121		1.83	2.0E-12	AF168884.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10023	22425		10.27	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
11734	24023		3.31	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
11943	24150		1.36	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
127	12736	25153	2.36	1.0E-12	AW627674.1	EST_HUMAN	hh00a09.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element ;
1931	14450		1	1.0E-12	AI871726.1	EST_HUMAN	wnt5107.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element ;
3031	15586	27996	0.97	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3031	15586	27997	0.97	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3982	16417	28820	45.05	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3982	16417	28821	45.05	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6267	18830		1.83	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6347	18905		1.73	1.0E-12	Q9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6467	19022	31756	0.52	1.0E-12	BF642800.1	EST_HUMAN	EST000008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6467	19022	31757	0.52	1.0E-12	BF642800.1	EST_HUMAN	EST000008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6983	19423	32197	0.54	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative enkerin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7070	19604		0.44	1.0E-12	BE018794.1	EST_HUMAN	bb55a11.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049148 5' similar to TR:Q63291 Q63291 L1
7555	20005	32847	2.18	1.0E-12	AF198864.1	NT	RETROPOSON, ORF2 MRNA ; Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7691	20040	32888	12.45	1.0E-12	AJ248533.1	EST_HUMAN	qh66a04.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
7691	20040	32889	12.45	1.0E-12	AJ248533.1	EST_HUMAN	qh66a04.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
9139	21571	34478	1.35	1.0E-12	AA782323.1	EST_HUMAN	ac26a05.s1 Stralagene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3'
11835	23960	37010	2.01	1.0E-12	AW982184.1	EST_HUMAN	EST374237 MAGG Homo sapiens cDNA
11865	24110		1.19	1.0E-12	AJ738592.1	EST_HUMAN	w33h09.x1 NCI CGAP_Cov18 Homo sapiens cDNA clone IMAGE:2392095 3'
12022	24858		1.75	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
12362	24453		1.74	1.0E-12	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3625	16165		2.39	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3959	16494	28904	0.83	9.0E-13	AB028900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
7736	20180	33041	0.43	9.0E-13	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
9765	22168		2.39	9.0E-13	N60953.1	EST_HUMAN	za26h06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283651 3'
737	13298	25722	7.01	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
737	13298	25723	7.01	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1812	14935	26829	1.15	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nabp) and survival motor neuron protein (smn) genes, complete cds
10148	22549		2.13	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8437	20851	33751	0.56	7.0E-13	AI884398.1	EST_HUMAN	wm31h09.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
8437	20851	33752	0.56	7.0E-13	AI884398.1	EST_HUMAN	wm31h09.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
12141	24273		18.78	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866613 5'
12366	24428		1.44	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP
2023	14539	27052	2.86	6.0E-13	AL163207.2	NT	ACETYL GALACTOSAMINYL TRANSFERASE (UDP-GALNAc:POLYPEPTIDE, N-
3280	15839		0.76	6.0E-13	R78338.1	EST_HUMAN	ACETYL GALACTOSAMINYL TRANSFERASE (GALNAc-T1)
3375	16922		1.66	5.0E-13	AA435773.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
7280	19785	32594	0.95	5.0E-13	P08983	SWISSPROT	repetitive element; contains element MER22 repetitive element;
10641	23092	36066	2.51	5.0E-13	P07313	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
							MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1837	14369		1.94	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
2357	14862		1.01	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4800	17314		1.22	4.0E-13	AA454054.1	EST_HUMAN	z48d07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795469 5'
9853	18432	31104	4.78	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7651	20097	32949	1.48	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
8139	20562	33439	0.99	4.0E-13	AA431529.1	EST_HUMAN	z476g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763
8267	20884		2.05	4.0E-13	N44291.1	EST_HUMAN	y33g05.r1 Soares_melanocyte_ZNblHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32985
9245	21877	34586	1.24	4.0E-13	AL043810.1	EST_HUMAN	A32995 t complex sterility protein - mouse ; DKFZp434A0128_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5'
10049	22451	35399	4.57	4.0E-13	AI289831.1	EST_HUMAN	q132a05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:189945 3' similar to contains Alu repetitive element ; Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
184	12786		5.76	3.0E-13	AF003528.1	NT	z468g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'
888	13443		2.44	3.0E-13	AA430310.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
2376	14881		1.69	3.0E-13	AL163210.2	NT	CM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA
2601	15097	27612	8.48	3.0E-13	BF372962.1	EST_HUMAN	cb18402.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
3144	15697		2.95	3.0E-13	AA745844.1	EST_HUMAN	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3482	16025	28446	3.2	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3482	16025	28447	3.2	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5803	18383	31043	0.83	3.0E-13	AA134017.1	EST_HUMAN	z188h10.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element ;
5803	18383	31044	0.83	3.0E-13	AA134017.1	EST_HUMAN	z188h10.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element ;
6294	18856	31577	0.86	3.0E-13	AW005639.1	EST_HUMAN	wz8bc02.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:25668890 3' similar to TR:O75139
8549	20884	33883	7.91	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
10468	22918		5.09	3.0E-13	AI084788.1	EST_HUMAN	HA0538 Human fetal liver cDNA library Homo sapiens cDNA
10828	23262	36247	3.86	3.0E-13	BE083509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11347	23711	36768	2.1	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048

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Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
154	12759	25177	2.82	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
252	12852	25270	1.61	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1303	13838	26287	6.78	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
2983	15518	27898	0.88	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
2983	15518	27899	0.88	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3243	16704	28212	0.65	2.0E-13	BF431899.1	EST_HUMAN	mab7805.x1 Source_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3486	18029	28451	1.82	2.0E-13	AF109907.1	NT	Homo sapiens S104 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4125	18854		1.81	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6435	18991	31722	4.65	2.0E-13	Q08852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6521	19074		0.57	2.0E-13	X79417.1	NT	S. sacchari rps12 mRNA for ribosomal protein S12
7205	19916	32744	6.43	2.0E-13	X16912.1	NT	Human PKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7485	19889	32485	0.74	2.0E-13	10835072	NT	Homo sapiens N-myristyltransferase 1 (NMT1), mRNA
7485	19889	32486	0.74	2.0E-13	10835072	NT	Homo sapiens N-myristyltransferase 1 (NMT1), mRNA
10347	22747	35714	2.78	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
11815	24072		10.86	2.0E-13	AW892155.1	EST_HUMAN	GM0-NK001-100300-274-e11 NN0001 Homo sapiens cDNA
305	12900	25319	1.46	1.0E-13	S74129.1	NT	FGF-1= fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
911	13485	25913	4.84	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1368	13902	26359	1.21	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
1958	14476	26983	1.94	1.0E-13	AA720574.1	EST_HUMAN	hw21g02.e1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
4632	17148	29528	1.38	1.0E-13	BF340987.1	EST_HUMAN	THR repetitive element;
6785	18928	32066	0.52	1.0E-13	AA090732.1	EST_HUMAN	602038009F1 NCI_CGAP_Brt64 Homo sapiens cDNA clone IMAGE:4185866 5'
8569	21004	33902	0.92	1.0E-13	AA577812.1	EST_HUMAN	y1535.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8569	21004	33903	0.92	1.0E-13	AA577812.1	EST_HUMAN	m24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
10107	22508		1.21	1.0E-13	O15481	SWISSPROT	m24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
							MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11134	23586	36827	7.81	1.0E-13	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3624443 3' similar to contains MER29.b2 MER29 repetitive element;
11626	23964		1.85	1.0E-13	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
12327	24396		2.08	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12483	24486		1.3	1.0E-13	X87579.1	NT	H. sapiens CD4 gene
347	12837	25352	3.18	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element;
348	12938	25353	4.22	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element;
2407	14911		2.74	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-409 CT0322 Homo sapiens cDNA
2513	15014	27628	4.85	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2513	15014	27527	4.85	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2711	15201	27717	6.08	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3072	15628	28032	6.78	9.0E-14	AW513296.1	EST_HUMAN	xs54h05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'
3197	12937	25352	1.01	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element;
3801	16338	28740	7.69	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4811	17323	29702	1.93	9.0E-14	AJ002153.1	NT	Segulus oedipus gene for seminal vesicle secreted protein semenogelin I
3474	16017		1.53	8.0E-14	BE468263.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
3969	16504		3.67	8.0E-14	R76269.1	EST_HUMAN	yf72e03.t7 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144798 3'
8952	20843	33843	7.14	8.0E-14	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9740	22067	34594	4.56	8.0E-14	AA216316.1	EST_HUMAN	zq17c10.s1 Stralagene fetal retina 037202 Homo sapiens cDNA clone IMAGE:628970 3'
12031	24203	30955	2.05	8.0E-14	AI688118.1	EST_HUMAN	wc92h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328143 3'
1638	15316		3.26	7.0E-14	AW151673.1	EST_HUMAN	x87e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823148 3' similar to contains MER10.t2 MER10 repetitive element;
382	12969	25389	14.45	8.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
8909	22311	35255	2.22	8.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
8909	22311	35256	2.22	8.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
637	13201	25609	5	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5167	17671	30035	1.08	5.0E-14	AW073791.1	EST_HUMAN	x003605.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1 L2 L1 repetitive element ;
5785	18378	31034	5.13	6.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1160	16302		2.13	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1848	14370	28865	6.48	4.0E-14	AJ007793.1	NT	Homo sapiens LGMD2B gene
3753	16292		0.87	4.0E-14	AA046502.1	EST_HUMAN	z667a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487868 5'
4310	16834	28222	0.98	4.0E-14	N46328.1	EST_HUMAN	y773c12.e1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:278190 3' similar to contains L1 L3 L1 repetitive element ;
12395	24978		5.89	4.0E-14	AI886224.1	EST_HUMAN	wm08c03.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2495332 3' similar to contains Alu repetitive element
973	13528	25888	2.14	3.0E-14	X05466.1	NT	Rnonvegicus mRNA for GPG2 protein
5004	17614	28888	1.15	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element ;
7113	18846	32441	0.95	3.0E-14	AI420786.1	EST_HUMAN	ta91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
7113	18846	32442	0.95	3.0E-14	AI420786.1	EST_HUMAN	ta91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
7239	24628		0.67	3.0E-14	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7457	19980	32794	0.76	3.0E-14	AA386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
9204	21636	34545	0.93	3.0E-14	N42165.1	EST_HUMAN	y07b10.r1 Soares_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:270523 5'
10774	23212	36195	3.15	3.0E-14	BE886016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11003	17514	29888	4.41	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element ;
12302	24831		1.52	3.0E-14	AL183285.2	NT	Homo sapiens chromosome 21 segment HS21C085
405	12981	25403	3.04	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
405	12981	25404	3.04	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
710	15280	25680	8.94	2.0E-14	AL183303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2286	14793		7.41	2.0E-14	AW372868.1	EST_HUMAN	RC6-BT0377-081289-031-D12 BT0377 Homo sapiens cDNA
2361	14886		2.45	2.0E-14	7657529	NT	Homo sapiens ribosomal tumor deletion region protein 1 (RTDR1), mRNA
2431	14934	27448	5.31	2.0E-14	AL183209.2	NT	Homo sapiens chromosome 21 segment HS21C099
2451	14952		2.41	2.0E-14	BE222432.1	EST_HUMAN	hy80g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.H1 OFR repetitive element ;
2614	15109		3.63	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5786	18367	30829	1.09	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6888	18487	31145	0.91	2.0E-14	A1312351.1	EST_HUMAN	ta78n01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1
5995	18569	31255	4.58	2.0E-14	U01317.1	NT	repetitive element 1
7288	19763		1.16	2.0E-14	BE000550.1	EST_HUMAN	Human beta globin region on chromosome 11
7521	19872	32808	0.41	2.0E-14	4585709	NT	RC3-BN0072-240200-011-a08 BN0072 Homo sapiens cDNA
7742	20186	33048	1.04	2.0E-14	P56163	SWISSPROT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAMT1) mRNA
8013	20445	33315	26.21	2.0E-14	BE168761.1	EST_HUMAN	ZINC-FINGER PROTEIN NEURO-D4
8013	20445	33316	26.21	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
10563	23010	36097	6.56	2.0E-14	AW139800.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
12298	24834		1.37	2.0E-14	AF008191.1	NT	UI-H-BH-adw-a-10-Q-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
1093	19638	26077	1.68	1.0E-14	AL163248.2	NT	Homo sapiens putative G6 protein (G6P) gene, complete cds
1438	13970	28426	9.11	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C046
1438	13970	28426	9.11	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1944	14463	26987	12.23	1.0E-14	L44140.1	NT	Homo sapiens chromosome 21 segment HS21C103
2091	14805	27122	3.66	1.0E-14	AL163303.2	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2307	14814	27331	9.37	1.0E-14	AF001689.1	NT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
2898	15463	27879	1.1	1.0E-14	P05227	SWISSPROT	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3126	15878	28094	3.65	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3126	15878	28095	3.65	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3895	16430	28836	2.38	1.0E-14	AA682894.1	EST_HUMAN	ae89a12.61 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4508	17028	28405	1.89	1.0E-14	AW278862.1	EST_HUMAN	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2763059 3'
6093	18662	31356	2.05	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
7043	24822	32359	12.58	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
7043	24822	32370	12.58	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1593	14125	28590	1.47	9.0E-15	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2080	14594		4.81	9.0E-15	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
5078	17588	29856	6.03	9.0E-15	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
8000	20434	33299	4.55	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8644	21079	33886	1.5	9.0E-15	BE903559.1	EST_HUMAN	60167750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980168 5'
2769	13071		1.12	8.0E-16	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3184023 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7625	20073	32928	1.28	7.0E-15	BF05327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882086 5'
10328	22728		2.43	7.0E-15	AW241988.1	EST_HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element;
1020	13671	26016	9.64	6.0E-15	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6215	18781	31485	1.35	6.0E-15	X73482.1	NT	O arles mRNA for hair keratin cysteine-rich protein
6215	18781	31486	1.35	6.0E-15	X73492.1	NT	O arles mRNA for hair keratin cysteine-rich protein
427	13001	25427	7.7	6.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2719	15209	27725	6.07	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10467	22817		2.34	5.0E-15	AV730058.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE08 5'
444	12622	25009	2.58	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4149	16677	29065	0.87	4.0E-15	AL118598.1	EST_HUMAN	DKFZp761C0810_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761C0810 5'
7032	19568	32355	0.96	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
8475	20888	33785	0.55	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
8475	20888	33786	0.55	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10844	20888	33785	2.87	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10844	20888	33786	2.87	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4231	16758		8.05	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5006	17516		0.9	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
5134	17639	30001	0.73	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5134	17639	30002	0.73	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
7204	19815		1.34	3.0E-15	Q64825	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7734	20178	33038	4.02	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7734	20178	33039	4.02	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6987	22389		1.97	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11
10576	23023	36008	2.67	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12039	24868		1.59	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
263	12861	25279	5.75	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
383	12970	26390	4.4	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
383	12970	25391	4.4	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3489	16032	28453	1.02	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3489	16032	28454	1.02	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4666	17182		2.64	2.0E-15	AI808335.1	EST_HUMAN	wf07f06.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN.
6496	19050	31790	1.1	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6496	19050	31791	1.1	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7553	20003		1.7	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7725	20169	33029	2.76	2.0E-15	AA704195.1	EST_HUMAN	z177e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7874	20313	33179	5.35	2.0E-15	W05064.1	EST_HUMAN	z177e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
8420	20834	33730	0.55	2.0E-15	AL163247.2	NT	WP:F44F4.8 CE02227 TRANSPOSASE ;
9283	21716	34626	2.59	2.0E-15	D14547.1	NT	Homo sapiens chromosome 21 segment HS21C047
9391	21823	34759	0.85	2.0E-15	AA397758.1	EST_HUMAN	Human DNA, SINE repetitive element
9391	21823	34740	0.85	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9822	22037	34969	1.21	2.0E-15	AW379465.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9822	22037	34970	1.21	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201098-078-a12 HT0244 Homo sapiens cDNA
10817	23080		2.2	2.0E-15	AJ271735.1	NT	CM0-HT0244-201098-078-a12 HT0244 Homo sapiens cDNA
12422	16032	28453	3.31	2.0E-15	AF223391.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12422	16032	28454	3.31	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2733	15223		2.49	1.0E-15	AI889984.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2970	15525	27847	1.23	1.0E-15	BE043584.1	EST_HUMAN	bc28f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
3102	15656	28087	1.08	1.0E-15	P08547	SWISSPROT	MARINER TRANSPOSASE ;
4381	16903	29288	1.19	1.0E-15	BE182898.1	EST_HUMAN	hk40e02.y1 NCI_CGAP_OY34 Homo sapiens cDNA clone IMAGE:2899162 5'
5314	17814	30178	3.26	1.0E-15	AI884928.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							RC3-HT0649-100500-022-505 HT0649 Homo sapiens cDNA
							wf86e04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494590 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6705	19252	32004	1.85	1.0E-16	T85763.1	EST_HUMAN	ye40e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MERB repetitive element;
7430	19835		2.44	1.0E-16	BE074217.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
7468	19872	32468	0.7	1.0E-16	P39057	SWISSPROT	DYNEIN BETA CHAIN, CILIARY
8803	21237	34144	1.1	1.0E-16	AL163280.2	NT	Homo sapiens chromosome 21 segment H521C080
8946	21379	34292	5.13	1.0E-16	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8946	21379	34293	5.13	1.0E-16	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9371	21803	34712	1.25	1.0E-16	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9510	21973	34806	0.99	1.0E-16	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9785	22188	35125	0.88	1.0E-16	AA884653.1	EST_HUMAN	dh37c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.3 L1 repetitive element;
10800	23045	36031	3.06	1.0E-16	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
12503	24679	30772	4.41	1.0E-16	AI783944.1	EST_HUMAN	tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive element
2625	15120	27633	5.26	9.0E-16	Q39910	SWISSPROT	DYNEIN ALPHA CHAIN, FLAGELLAR OUTER ARM
4541	17058	28441	1.01	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
10775	23213	36196	1.66	9.0E-16	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone o-23f05
5972	18548	31233	0.81	7.0E-16	4885120	NT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7808	20250	33110	1.29	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7808	20250	33111	1.29	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
12446	24780		11.24	7.0E-16	T94149.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
2054	14589		11.35	6.0E-16	AW972611.1	EST_HUMAN	EST384702 MAGe resequences, MAGL Homo sapiens cDNA
1521	14053	28517	0.92	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2622	15117	27630	11.58	5.0E-16	AA992176.1	EST_HUMAN	cd80c04.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element;
11273	23639	36691	1.92	5.0E-16	BF217368.1	EST_HUMAN	60185734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
12546	24534		9.53	5.0E-16	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2146	14659		1.06	4.0E-16	AB001523.1	NT	Homo sapiens gene for TMEH1 and PWP2, complete and partial cds
2274	14782	27303	3.8	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
2274	14782	27304	3.8	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3434	15978	28392	4.44	4.0E-16	Q16953	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4161	16688	29074	6.99	4.0E-16	BE083876.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4161	16688	29075	6.99	4.0E-16	BE083876.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5033	17543		4.81	4.0E-16	AV730833.1	EST_HUMAN	AV730833 HTF Homo sapiens cDNA clone HTFAXE09 5'
8257	20674	33564	47.86	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
11714	24013		2.02	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11808	24068		7.92	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
11820	24076	30987	2.16	4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
137	12743	25163	1.17	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
137	12743	25164	1.17	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
483	13057		1.7	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'
483	13066		1.54	3.0E-16	AF135448.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1481	14013	26478	1.72	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2930	15485	27905	4.48	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3946	16481	28891	0.71	3.0E-16	T08169.1	EST_HUMAN	EST08060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
3971	16508		4.18	3.0E-16	U03887.1	NT	Human BXP20 gene
5024	17534	29906	1.02	3.0E-16	AV661393.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3'
5529	18119		0.91	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5884	18463	31139	1.5	3.0E-16	AF003629.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9110	21542	34448	3.58	3.0E-16	AI002836.1	EST_HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;
9663	22365		1.01	3.0E-16	BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10130	22531	35499	4.57	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
996	13548		0.98	2.0E-16	AL103279.2	NT	Homo sapiens chromosome 21 segment HS21C078
2284	14761		5.54	2.0E-16	AA621761.1	EST_HUMAN	af06d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2837	15132		9.97	2.0E-16	J03061.1	NT	Human SSAY-related endogenous retroviral LTR-like element
4195	16720	29108	1.68	2.0E-16	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
7121	18654	32450	0.83	2.0E-16	Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
8261	20676	33570	1.06	2.0E-16	AK470723.1	EST_HUMAN	tt16e11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element;
8607	21042	33947	1.88	2.0E-16	A1732837.1	EST_HUMAN	nz4708.x5 NCI_CGAP_Prl12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:054849 054849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:008905 contains MER7.1 MER7 repetitive element;
8743	21177	34080	0.84	2.0E-16	BE848026.1	EST_HUMAN	782h09.x1 NCI_CGAP_Prl28 Homo sapiens cDNA clone IMAGE:3303521 3'

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8743	21177	34081	0.84	2.0E-16	BE858026.1	EST_HUMAN	7182h08.x1 NCL_CGAP_P228 Homo sapiens cDNA clone IMAGE:3303521 3'
9017	21450	34380	1.07	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-508-e01 PT0034 Homo sapiens cDNA
9017	21450	34381	1.07	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-508-e01 PT0034 Homo sapiens cDNA
189	12791	25204	2.28	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
397	13013		38.45	1.0E-16	AA628592.1	EST_HUMAN	af39g11.e1 Soares_tetrahymena_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element :
1916	14435	26938	2.83	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5996	18570	31256	0.76	1.0E-16	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6774	19317		20.82	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6927	19466	32244	3.33	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
8088	19317		6.05	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
3737	16277	28680	2.44	9.0E-17	AW900048.1	EST_HUMAN	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
7100	19633		2.3	9.0E-17	AB392964.1	EST_HUMAN	tg22c11.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12 MER28 repetitive element ;
8709	21144		3.19	9.0E-17	AW150267.1	EST_HUMAN	xq49g12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR repetitive element ;
10194	22595		2.24	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1044	13580		1.48	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3901	16436		0.74	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5848	24594	31098	4.45	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7729	20173		1.72	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
8297	20712	33804	0.56	8.0E-17	6763651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahtc11), mRNA
1487	14019		2.89	7.0E-17	6763097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5576	18164		3.76	7.0E-17	AF216650.1	NT	Homo sapiens putative MITAP (MITAP) mRNA, partial cds, alternatively spliced
7057	19591	32386	8.19	7.0E-17	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
209	12812	25230	7.78	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
6641	19189	31940	2.57	6.0E-17	AW662772.1	EST_HUMAN	h181d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12 L1 repetitive element ;
438	12818	25003	3.68	5.0E-17	T94110.1	EST_HUMAN	yc05h08.r1 Stragogene lung (#937210) Homo sapiens cDNA clone IMAGE:70639 5'
5059	17569	29837	3.1	5.0E-17	Q06278	SWISSPROT	ALDEHYDE OXIDASE
8106	20632	33409	2.04	5.0E-17	T81043.1	EST_HUMAN	yd26b04.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:109927 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3635	16175	26584	0.72	4.0E-17	AA643697.1	EST_HUMAN	n19605.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058528 3'
9593	22073	34998	1.13	4.0E-17	AW129165.1	EST_HUMAN	x20604.x1 NCL_CGAP_Ku8 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element ;
11249	23615	36661	2.29	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11729	24021		3.19	4.0E-17	AI073548.1	EST_HUMAN	ov45e04.x1 Soares_testis_NH7 Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530
2020	14536	27048	0.99	3.0E-17	AW119123.1	EST_HUMAN	Q16530 PMS3 MRNA, contains MER10.12 MER10 repetitive element ;
3190	16703		1.25	3.0E-17	P36410	SWISSPROT	xd89c09.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3641	16181	28589	1.29	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3641	16181	28590	1.29	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
8827	21261	34167	1.34	3.0E-17	N88451.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
9835	22238	35173	4.94	3.0E-17	AB028898.1	NT	zat14b02.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.13 PTR5 repetitive element ;
11690	23996		3.02	3.0E-17	11417896	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes; complete cds)
12562	24539		4.72	3.0E-17	AV720204.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
367	12957	25374	4.08	2.0E-17	AI270080.1	EST_HUMAN	AV720204 GLO Homo sapiens cDNA clone GLCDIF08 5'
368	12957	25374	2.86	2.0E-17	AI270080.1	EST_HUMAN	q163a06.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
1014	13588		1.42	2.0E-17	AA722832.1	EST_HUMAN	q163a06.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
2345	14851	27369	3.61	2.0E-17	Q28983	SWISSPROT	zg81d04.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:399751 3'
2345	14851	27370	3.61	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2884	15439	27860	7.37	2.0E-17	P12098	SWISSPROT	ZONADHESIN PRECURSOR
5622	18209	30908	1.91	2.0E-17	M27685.1	NT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5622	18209	30909	1.91	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6588	19139		1.89	2.0E-17	AF055063.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6839	18380		1.38	2.0E-17	AL134881.1	EST_HUMAN	Homo sapiens MHC class 1 region
8446	20860	33761	0.74	2.0E-17	AB037839.1	NT	DKFZ762J0610_r1 762 (synonym: hne12) Homo sapiens cDNA clone DKFZp762J0610 5'
8693	21128	34028	1.37	2.0E-17	Q95156	SWISSPROT	Homo sapiens mRNA for KIAA1418 protein, partial cds
8970	21403	34317	1.05	2.0E-17	AA300940.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
9945	22347	35237	2.26	2.0E-17	BE29888.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to glycogenin
9972	22374	35322	3.67	2.0E-17	AL163247.2	NT	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860616 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9972	22374	35323	3.67	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10216	22817	35585	4.53	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10308	22708	35673	0.85	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10308	22708	35674	0.85	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
771	13331	25764	5.04	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1706	14234		1.09	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1755	14282	26766	3.04	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2036	14552	27063	1.28	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2230	14739	27259	1.85	1.0E-17	U78410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3556	16098		1.3	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4155	16882		8.67	1.0E-17	R08942.1	EST_HUMAN	yf30e07.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 6'
6901	19344		0.45	1.0E-17	AW468488.1	EST_HUMAN	he38e05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element; contains LTR8.1 LTR8 repetitive element;
7018	19554	32339	1.89	1.0E-17	A185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7018	19554	32341	1.99	1.0E-17	A185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7527	19978	32813	1.05	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9063	21495	34404	0.85	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0263-101299-072-407 BT0263 Homo sapiens cDNA
10038	22440	35387	1.15	1.0E-17	AW999538.1	EST_HUMAN	QV3-BN0046-220300-129-610 BN0046 Homo sapiens cDNA
11170	23550	36592	2.19	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2366	14871	27391	0.89	9.0E-18	AA174078.1	EST_HUMAN	zp18g12.s1 Siratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:609892 3'
9691	22103		2.91	9.0E-18	AA172167.1	EST_HUMAN	j36d03.x1 Soares_NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3788	16325	28726	1.44	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
363	12953	25368	25.97	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
363	12953	25369	25.97	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
7928	20365	33230	1.17	7.0E-18	AW887542.1	EST_HUMAN	RC3-OT0091-170300-011-d03 OT0091 Homo sapiens cDNA
12239	12953	25368	4.4	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
12239	12953	25369	4.4	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
3258	15800	28225	1.32	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdnf/Pn-1 gene for glia-derived neurotrophic protease nectin 1, enhancer region

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4789	17313		4.25	6.0E-18	P62181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8812	21246		2.81	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8888	21322	34233	0.89	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11980	24161	30976	2.1	6.0E-18	U87929.1	NT	Human aconitase hydratase (ACO2) gene, exon 4
1176	13717	26158	14.14	6.0E-18	AI280214.1	EST_HUMAN	qm65g11.X1 Soares_placenta_8to9weeks_2NblHP8b9W Homo sapiens cDNA clone IMAGE:1893688 3'
4338	16858	29244	0.73	5.0E-18	10946865	NT	similar to contains Alu repetitive element;
5524	18114	30471	1.33	5.0E-18	AF087913.1	NT	Mus musculus gasdermin (Gsdm), mRNA
9150	21582	34488	4.53	6.0E-18	BE143312.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
10760	23198	36183	3.99	5.0E-18	10242378	NT	MRO-HT0181-221099-002-c08 HT0181 Homo sapiens cDNA
10760	23198	36184	3.99	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12086	24245		7.65	6.0E-18	AW867182.1	EST_HUMAN	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12473	24490		18.7	5.0E-18	AV650547.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
129	12737	25154	1.42	4.0E-18	BE044076.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
129	12737	25155	1.42	4.0E-18	BE044076.1	EST_HUMAN	h036h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
1714	14242	26726	5.56	4.0E-18	AA621814.1	EST_HUMAN	h024f11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
2106	14620	27140	2.01	4.0E-18	Q06430	SWISSPROT	N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYLTRANSFERASE (N- ACETYL GLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2106	14620	27141	2.01	4.0E-18	Q06430	SWISSPROT	N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYLTRANSFERASE (N- ACETYL GLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
3794	16331	28732	0.63	4.0E-18	AI581586.1	EST_HUMAN	ar93b09.x1 Bareillead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
5619	18206	30603	2.48	4.0E-18	AI017565.1	EST_HUMAN	cu23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5619	18206	30604	2.48	4.0E-18	AI017565.1	EST_HUMAN	cu23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
10785	23223	36207	3.63	4.0E-18	AA371807.1	EST_HUMAN	EST183633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
872	13427	25876	5.69	3.0E-18	AA814196.1	EST_HUMAN	db23h11.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5;
954	13506	25950	3.03	3.0E-18	BE088634.1	EST_HUMAN	CM0-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3982	16497	28906	1.4	3.0E-18	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7222	19834	32651	3.7	3.0E-18	BE001671.1	EST_HUMAN	PMO-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
12245	24348		4.23	3.0E-18	AW022016.1	EST_HUMAN	d31h12.y1 Marton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
264	12892	25280	3.62	2.0E-18	AW836820.1	EST_HUMAN	QV1-LT0038-150200-070-007 LT0036 Homo sapiens cDNA
1180	13722		137.43	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
3084	15638	28045	1.13	2.0E-18	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5687	18252		1.9	2.0E-18	AA888610.1	EST_HUMAN	ak53a07.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1409892 3' similar to TR:O14577
6768	18349	30806	3.8	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A08 FROM 7Q31, COMPLETE SEQUENCE. ;
5768	18349	30807	3.8	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
6166	18734		1.78	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6479	18034	31772	0.87	2.0E-18	X60459.1	NT	602021164F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
6479	18034	31773	0.87	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6602	19183	31901	0.9	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6846	19194	31946	1.88	2.0E-18	AW665953.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
7921	20359	33228	0.71	2.0E-18	AA457618.1	EST_HUMAN	h194g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979894 3' similar to contains
10074	22475	35432	1.15	2.0E-18	AW151673.1	EST_HUMAN	MER19.12 MER19 repetitive element ;
10074	22475	35433	1.15	2.0E-18	AW151673.1	EST_HUMAN	aa89d11.r1 Strabagene fetal retina 637202 Homo sapiens cDNA clone IMAGE:838485 5' similar to
10755	23193	36178	1.76	2.0E-18	AW470791.1	EST_HUMAN	TR:G61634 G61634 POLYPEPTIDE PR77 ;
11451	23810	36869	3.14	2.0E-18	AW151299.1	EST_HUMAN	x187e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
11894	13722		7.52	2.0E-18	BE256097.1	EST_HUMAN	MER10 repetitive element ;
4443	18683		1.01	1.0E-18	TG5408.1	EST_HUMAN	x187e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
5611	18189	30565	3.05	1.0E-18	AV653405.1	EST_HUMAN	MER10 repetitive element ;
5835	18415	31085	2.69	1.0E-18	D00099.1	NT	h333d06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
5835	18415	31086	2.69	1.0E-18	D00099.1	NT	xq47e09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
6797	18340	32111	1.47	1.0E-18	AL163290.2	NT	MER8 repetitive element ;
							601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
							ye43g05.r1 Soares fetal liver spleen TNF1LS Homo sapiens cDNA clone IMAGE:120538 5' similar to contains
							L1 repetitive element ;
							AV653405 GLC Homo sapiens cDNA clone GLCCKE11 3'
							Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
							Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
							Homo sapiens chromosome 21 segment HS21C080

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8958	21391	34303	0.99	1.0E-18	AI148288.1	EST_HUMAN	α26k09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.1 L1 repetitive element;
9969	22371	35319	3.01	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11841	24092	30992	2.53	1.0E-18	AF003529.1	NT	Homo sapiens glycylproline 3 (GPC3) gene, partial cds and flanking repeat regions
582	13134	25546	4.33	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
583	13134	25546	3.6	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
8527	20982		3.85	9.0E-19	FO8688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
9127	21559	34465	2.52	9.0E-18	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9127	21559	34465	2.52	9.0E-19	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10806	23338	36344	3.96	9.0E-19	AB032999.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11591	13134	25546	12.69	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
1074	13620		1.4	8.0E-19	AW974902.1	EST_HUMAN	EST387007 IMAGE resequences, MAGN Homo sapiens cDNA
4429	10850		1.05	8.0E-19	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8735	21169	34074	1.15	8.0E-19	BE158936.1	EST_HUMAN	MRO-HIT0404-210200-001-g08 HT0404 Homo sapiens cDNA
2154	14687	27180	1.12	7.0E-19		NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kd) (DDX6) mRNA
6789	19342	32113	2.08	7.0E-19	AF092090.1	NT	Rattus norvegicus cp161 mRNA, partial cds
7761	20205	33067	1.03	7.0E-19	P28444	SWISSPROT	BETA CRYSTALLIN A2
11738	24958		2.96	7.0E-19	AA705684.1	EST_HUMAN	z16b01.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3780	16318		1.44	6.0E-19	AW852830.1	EST_HUMAN	PMO-CT0248-131089-001-g01 CT0248 Homo sapiens cDNA
4486	17013	29397	1.81	6.0E-19	P34988	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4495	17013	29398	1.81	6.0E-19	P34988	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4855	17367		1.14	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
6145	18713	31416	4.73	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC95)
6534	19086	31827	0.59	5.0E-19	AW663302.1	EST_HUMAN	hh77b06.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
8484	24998		0.6	5.0E-19	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
10320	22720	35688	0.88	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11292	23697	39703	7.05	5.0E-19	AW183725.1	EST_HUMAN	x187b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2694171 3' similar to contains element MSR1 repetitive element ;
571	13142	25550	43.52	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2824	15119	27632	9.56	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287874 5'
5652	18238	30637	1.15	4.0E-19	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4302	16827	29215	1.43	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4302	16827	29216	1.43	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4477	16907	29378	1.4	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
5531	18121		0.67	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7860	20299		2.25	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9662	20963	33851	1.27	3.0E-19	X89885.1	NT	M.musculus mRNA for TPCR33 protein
11988	24181		18.09	3.0E-19	AF165520.1	NT	Homo sapiens phorbol [protein (PBI) mRNA, complete cds
2473	14974	27488	19.45	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4478	16996		1.05	2.0E-19	AI311783.1	EST_HUMAN	q691602.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916898 3' similar to TR:Q69388 Q69388 POL/ENV GENE ;
6360	18918	31653	1.04	2.0E-19	AV731392.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'
7805	20247	33107	0.71	2.0E-19	7667288	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8876	21309	34222	10.76	2.0E-19	AA012854.1	EST_HUMAN	z634609.t1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
9976	22378	35329	0.87	2.0E-19	Q85155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
499	13073		1.86	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2870	15163		1.21	1.0E-19	D38044.1	NT	Human gene for A1H-receptor, exon 7-9
2803	15360		6.43	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3379	15925	28341	1.28	1.0E-19	AA834667.1	EST_HUMAN	al49b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MIER37.12 MER37 repetitive element ;
5590	18178	30543	0.62	1.0E-19	AI890869.1	EST_HUMAN	wm91b08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443287 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;
6382	18939	31676	2.93	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6525	24985		0.57	1.0E-19	AA595527.1	EST_HUMAN	nh22d03.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:853093 similar to contains L1.t1 L1 repetitive element ;
8159	20582	33460	1.13	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
8159	20582	33461	1.13	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
8372	24648		0.75	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8963	21396	34308	1.89	1.0E-19	M64657.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
9168	21600		3.07	1.0E-19	T98920.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains ORF repetitive element;
10168	22569	35535	22.59	1.0E-19	AW812259.1	EST_HUMAN	RCO-ST0174-191089-031-b05 ST0174 Homo sapiens cDNA
10175	22576	35544	1.53	1.0E-19	N44631.1	EST_HUMAN	ya31e09.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:272872 5'
7010	18546	32331	2.52	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7010	18546	32332	2.52	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8024	20458	33328	1.39	8.0E-20	A1221371.1	EST_HUMAN	qg8f09.x1 Soares NFL_T GBC S1 Homo sapiens cDNA clone IMAGE:1842089 3'
8024	20458	33329	1.39	8.0E-20	A1221371.1	EST_HUMAN	qg8f09.x1 Soares NFL_T GBC S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3238	16789	28208	0.79	7.0E-20	BF328455.1	EST_HUMAN	PM4-AN0088-050900-003-c04 AN0088 Homo sapiens cDNA
7413	18082	30376	7.12	7.0E-20	AL139120.1	EST_HUMAN	DKFZp547D092.r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D092 5'
8402	20818	33714	0.41	7.0E-20	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
8899	21432	34341	10.42	7.0E-20	AA557657.1	EST_HUMAN	n46c04.s1 NCL CGAP_P44 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
8999	21432	34342	10.42	7.0E-20	AA557657.1	EST_HUMAN	MER29 repetitive element;
11436	23788		1.63	7.0E-20	8912633	NT	MER29 repetitive element;
3541	16083	28502	3.84	6.0E-20	P39188	SWISSPROT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
4289	16814	29198	3.67	6.0E-20	BE622434.1	EST_HUMAN	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
7554	20004	32848	1.25	5.0E-20	AF075301.1	EST_HUMAN	601447231F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3916231 5'
8595	21030	33032	5.17	5.0E-20	W90525.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0260
8595	21030	33033	5.17	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
8705	21140	34043	0.91	5.0E-20	BE165980.1	EST_HUMAN	zh78d08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
9239	21671	34581	1.38	5.0E-20	AB028174.1	NT	MIR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9239	21671	34582	1.38	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9650	20941		1.13	5.0E-20	O60809	SWISSPROT	Mus musculus MMAN-g mRNA, complete cds
5917	19495		0.92	4.0E-20	Q99880	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
8580	21015		5.79	4.0E-20	A1874382.1	EST_HUMAN	HISTONE H2B C (H2B/C)
10374	22774	35743	1.84	4.0E-20	AW837489.1	EST_HUMAN	tb84g03.x1 NCL CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2283396 3'
4224	18749	29140	1.32	3.0E-20	P23273	SWISSPROT	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
4698	17184	29562	0.87	3.0E-20	AA037616.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN 114
							z368b12.s1 Soares pregnant uterus_NblFPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9298	21730		2.7	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
11265	23631	36680	2.74	3.0E-20	A1284244.1	EST_HUMAN	q70402.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
11265	23631	36681	2.74	3.0E-20	A1284244.1	EST_HUMAN	q70402.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
11754	24035	31018	9.34	3.0E-20	BE889422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
853	13409		7.61	2.0E-20	AW303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
1138	13682	26121	2.67	2.0E-20	AA516335.1	EST_HUMAN	p97461.40S RIBOSOMAL PROTEIN S5;
1138	13682	26122	2.67	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:3940097 similar to TR:G1224066
2776	13409		6.78	2.0E-20	AW303868.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN. ;
5029	17539	28911	4.95	2.0E-20	Q28983	SWISSPROT	ng69h09.s1 NCI_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:3940097 similar to TR:G1224066
5029	17539	28912	4.95	2.0E-20	Q28983	SWISSPROT	G1224066 ORF2: FUNCTION UNKNOWN. ;
5319	17819		1.26	2.0E-20	5174538	NT	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
8716	21151	34058	0.95	2.0E-20	AA309457.1	EST_HUMAN	p97461.40S RIBOSOMAL PROTEIN S5;
9468	21899	34821	0.89	2.0E-20	D10083.1	NT	ZONADHESIN PRECURSOR
9468	21899	34822	0.89	2.0E-20	D10083.1	NT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
12164	24668	30769	1.63	2.0E-20	H55371.1	EST_HUMAN	EST180328 Liver III Homo sapiens cDNA 5' and
1952	15268	26975	3.15	1.0E-20	AA281961.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
4468	16988	28371	1.18	1.0E-20	BF115158.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
6278	17779	30145	3.27	1.0E-20	Q95155	SWISSPROT	CHIR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
7300	19804	32616	0.68	1.0E-20	AF049567.1	EST_HUMAN	z11406.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
9448	21879	34797	2.62	1.0E-20	11418491	NT	MER19 repetitive element ;
11308	23671	36720	1.73	1.0E-20	AF223391.1	NT	hr84b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element ;
11890	24124		3.93	1.0E-20	AA420453.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
2867	15422		1.01	9.0E-21	AJ003514.1	EST_HUMAN	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
11594	23629		3.38	9.0E-21	AW898189.1	EST_HUMAN	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							nc60g08.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1 repetitive element ;
							AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MIP12-BJ21
							RC3-NN0068-090500-021-003 NN0068 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9222	21654		1.28	8.0E-21	AW674891.1	EST_HUMAN	b330a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW.NIAM_HUMAN
11293	23658	38704	7.88	8.0E-21	AA809411.1	EST_HUMAN	O85169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR;
11768	24046		2.35	8.0E-21	O21330	SWISSPROT	d571108.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338835 3'
1993	14509	27017	1.46	7.0E-21	P15800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 8)
1993	14509	27018	1.46	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3699	16239	28645	0.71	7.0E-21	AL163300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4271	16796		6.22	7.0E-21	AA046502.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
6773	19316	32083	0.78	7.0E-21	AL163218.2	NT	z687a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
							Homo sapiens chromosome 21 segment HS21C018
8922	21356	34270	1.61	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
9118	21650	34455	6.97	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10125	22526	35493	0.97	7.0E-21	AW856922.1	EST_HUMAN	RC0-GT0301-271189-031-F03 GT0301 Homo sapiens cDNA
4120	16650	29038	1.14	6.0E-21	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
947	13499	25942	1.39	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4384	16906	29290	2.9	5.0E-21	BE968839.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4735	13499	25942	1	6.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4857	17369	29750	5.51	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEG1), mRNA
7144	19857		0.9	5.0E-21	AW440884.1	EST_HUMAN	he05e10.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:29718154 3'
							783411.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3903573 3' similar to contains OFR.11
7439	19943	32777	1.23	5.0E-21	BE856505.1	EST_HUMAN	OFR repetitive element;
11690	23999		1.64	5.0E-21	AA393574.1	EST_HUMAN	z672c04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
1728	14255	26740	1.12	4.0E-21	AA970743.1	EST_HUMAN	o086608.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16630 Q16630
7275	19780	32590	2.81	4.0E-21	AB019576.1	NT	PMS3 MRNA ;contains OFR.11 OFR repetitive element;
2174	14695	27209	1.28	3.0E-21	AL163201.2	NT	Rattus norvegicus mRNA for rTIM, complete cds
3042	16598	28007	3.68	3.0E-21	AJ007673.1	NT	Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens LGM228 gene
5761	18342	30798	0.76	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5761	18342	30789	0.76	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
6014	16598		0.78	3.0E-21	AV681044.1	EST_HUMAN	AV681044 GLC Homo sapiens cDNA clone GLCGOA10 3'
6493	19047		2.61	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_94 Homo sapiens cDNA clone IMAGE:4064945 5'
7501	19705	32504	8.05	3.0E-21	BF361093.1	EST_HUMAN	RC1-O10083-100800-019-g08 O10083 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9829	22232	35168	0.85	3.0E-21	AW697760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
12282	24881	30576	3.12	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
150	12755		21.81	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
959	13511	25952	0.79	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
958	13511	25953	0.79	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1245	13763		2.71	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2573	15070	27589	18.89	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2573	15070	27587	18.89	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5744	18326	30763	1.94	2.0E-21	AI824582.1	EST_HUMAN	ts30103.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5841	18421	31089	0.77	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN ;
5841	18421	31080	0.77	2.0E-21	AA027211.1	EST_HUMAN	zs97a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
6337	18895	31627	0.51	2.0E-21	W44483.1	EST_HUMAN	zs97a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8901	21335	34248	5.34	2.0E-21	BE141785.1	EST_HUMAN	z228102.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323667 5'
9232	21664	34573	3.42	2.0E-21	AU136778.1	EST_HUMAN	QV0-HT10103-091199-050-g11 HT10103 Homo sapiens cDNA
10840	23274		2.24	2.0E-21	BE350127.1	EST_HUMAN	AU136778 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11997	24186		5.05	2.0E-21	AF176816.1	NT	h09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
1288	13823	26276	1.99	1.0E-21	AA557657.1	EST_HUMAN	MER29 repetitive element ;
1435	13957		3.38	1.0E-21	AI601264.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
6835	18376		2.84	1.0E-21	AL079752.1	EST_HUMAN	n146c04.s1 NCI CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
7636	20083	32937	5.17	1.0E-21	AI223104.1	EST_HUMAN	MER29 repetitive element ;
10421	22821		1.68	1.0E-21	5730038	NT	ar8841.2.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2162343 3'
12420	24458		1.83	1.0E-21	AF046133.1	NT	DKFZp434I0830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I0830 5'
4436	16986	29346	3.02	9.0E-22	AI702438.1	EST_HUMAN	qg47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M84241 QM
9073	21505	34413	0.94	9.0E-22	AL163201.2	NT	PROTEIN (HUMAN);
9073	21505	34414	0.94	9.0E-22	AL163201.2	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10573	23020	36006	2.4	9.0E-22	AV781874.1	EST_HUMAN	Homo sapiens chromosome Xp22 410-8
972	13525		5.44	8.0E-22	BE144748.1	EST_HUMAN	ts29403.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408
6749	19293	32053	0.44	8.0E-22	BF373321.1	EST_HUMAN	NEUTRAL PROTEASE LARGE SUBUNIT ;
6749	19293	32054	0.44	8.0E-22	BF373321.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens chromosome 21 segment HS21C001
							AV781874 MDS Homo sapiens cDNA clone MDSGCG05 5'
							CM0-HT0179-281089-076-h05 HT0179 Homo sapiens cDNA
							MRO-FT0144-120800-006-d06 FT0144 Homo sapiens cDNA
							MRO-FT0144-120800-006-d06 FT0144 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8559	20994		3.28	8.0E-22	AA046502.1	EST_HUMAN	zh67a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 6'
884	13248	28683	7.05	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
4300	16825	28211	2.94	7.0E-22	Q81838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5145	17649	30015	0.94	7.0E-22	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
9129	21661		1.31	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
9238	21670	34580	2.27	7.0E-22	M78590.1	EST_HUMAN	EST00738 Fetal brain, Striatum (cat#806206) Homo sapiens cDNA clone HFBCF07
9768	22189	35101	2.18	7.0E-22	AF009650.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
4074	16505	28995	3.07	8.0E-22	AA040504.1	EST_HUMAN	zu65d10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742867 5'
8809	21243		2.22	8.0E-22	AA028123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
6867	19407	32181	4.02	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10254	22856	35617	3.99	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12247	24350		3.09	5.0E-22	BF476511.1	EST_HUMAN	naa27b08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element;
3636	16176		0.67	4.0E-22	AL271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7213	19825	32640	0.45	4.0E-22	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
7213	19825	32641	0.45	4.0E-22	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8940	24898		3.74	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10508	22857	35038	3.17	4.0E-22	BF216030.1	EST_HUMAN	607882873F7 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4089434 5'
12426	24462		1.31	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
983	13538		1.21	3.0E-22	AI469979.1	EST_HUMAN	hm14h10.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:2156811 3' similar to gb:U19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.1 L1 repetitive element;
2486	14887	27500	0.99	3.0E-22	AI859038.1	EST_HUMAN	w166b04.x1 NCI_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2428639 3' similar to SW:RL21_HUMAN
3672	16212		1.73	3.0E-22	D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21.;
4856	17368	29749	3.01	3.0E-22	AI090125.1	EST_HUMAN	Human chromosomal protein HMGT1 related gene
8801	21235		1.16	3.0E-22	BE156613.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
8805	21239	34146	2.59	3.0E-22	BE089841.1	EST_HUMAN	QV0-HT0368-080200-099-f12 HT0368 Homo sapiens cDNA
8898	21332	34243	1.17	3.0E-22	X60860.1	NT	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8898	21332	34244	1.17	3.0E-22	X60860.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
1803	14422		2.32	2.0E-22	N24842.1	EST_HUMAN	R.rattus RY2G5 mRNA for a potential ligand-binding protein
3398	15644	28356	4.23	2.0E-22	8394043	NT	Yw73d05.s1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
							Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4243	16768	29154	1.64	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0262-281199-001-d12 ST0262 Homo sapiens cDNA
6138	24600	31405	1.1	2.0E-22	W39456.1	EST_HUMAN	zcd201.1.1 Soares senescent fibroblasts_NHSEF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:XT2308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6491	18045	31785	4.09	2.0E-22	BF092116.1	EST_HUMAN	RCO-TN0078-150900-026-h12 TN0078 Homo sapiens cDNA
6836	22239	35174	1.1	2.0E-22	A1276522.1	EST_HUMAN	q17h06.x1 Soares_NhHMP_u_S1 Homo sapiens cDNA clone IMAGE:1878289 3' similar to contains MER28.t3 MER28 repetitive element:
11558	24449	30887	1.67	2.0E-22	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1849	14371	28886	1.03	1.0E-22	AW665517.1	EST_HUMAN	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
2504	15005	27516	2.23	1.0E-22	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3388	15934	28348	1.42	1.0E-22	D14547.1	NT	Human DNA: SINE repetitive element
8283	20709	33602	0.9	1.0E-22	BE084687.1	EST_HUMAN	MRO-BT0658-220200-002-h07 BT0659 Homo sapiens cDNA
12484	24497		6.78	9.0E-23	AW802801.1	EST_HUMAN	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA
3560	16102	28516	0.7	8.0E-23	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
5551	18141	30500	0.43	8.0E-23	AI133716.1	EST_HUMAN	HA2340 Human fetal liver cDNA library Homo sapiens cDNA
5551	18141	30501	0.43	8.0E-23	AI133716.1	EST_HUMAN	HA2340 Human fetal liver cDNA library Homo sapiens cDNA
3275	15824		1.89	7.0E-23	AV647246.1	EST_HUMAN	AV647246 GLC Homo sapiens cDNA clone GLCAW.C07 3'
10816	23282	38237	4.07	7.0E-23	5031952	NT	Homo sapiens Not56 (D. melanogaster)-like protein (NOT56L) mRNA
3411	15956		1.54	6.0E-23	AF198333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4285	16810	29194	1.02	6.0E-23	AL183249.2	NT	Homo sapiens chromosome 21 segment HS21C049
7440	18944	32778	0.44	6.0E-23	AF056181.1	NT	Homo sapiens TPA inducible protein mRNA, complete cds
11547	23904	36988	2.55	6.0E-23	X66687.1	NT	H. sapiens mRNA for autogenous NOR-80
11704	24006	31005	3.17	6.0E-23	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11704	24006	31006	3.17	6.0E-23	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11810	24134	30887	2.51	6.0E-23	AI209130.1	EST_HUMAN	qg59c03.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW:MV10_MOUSE P23249 PROTEIN MOV-10.1
5701	18285	30710	4.53	6.0E-23	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
6560	24611	31856	5.04	6.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
7922	24611	31856	3.23	6.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6780	19323	32089	0.91	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6780	19323	32090	0.91	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8522	20857	33859	2.83	3.0E-23	AA130185.1	EST_HUMAN	z35g09.t1 Soares_pregnant_uterus_NH1PU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER28.12 MER29 repetitive element;
9512	21875	34899	2.86	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
9512	21875	34900	2.86	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
10252	22853		1.74	3.0E-23	AW897927.1	EST_HUMAN	RC3-NN0066-270400-011-h01 NN0066 Homo sapiens cDNA
685	13249	25684	4.85	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1170	15281		3.4	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2754	15244	27757	4.58	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2754	15244	27758	4.88	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3348	15894		1.32	2.0E-23	AI201458.1	EST_HUMAN	qs7311.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:1943787 3' similar to TR:Q13537 Q13537
3714	16254		3.54	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
3980	16524	28927	3.45	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3980	16524	28928	3.45	2.0E-23	H59931.1	EST_HUMAN	yr16a02.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:205418 5'
5131	17636	28988	0.94	2.0E-23	D14547.1	NT	yr16a02.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:205418 5'
							Human DNA, SINE repetitive element
8543	20878		4.81	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
9247	21879	34588	1.01	2.0E-23	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11687	23994		3.82	2.0E-23	M32658.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12260	24357		1.85	2.0E-23	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12392	24884		1.81	2.0E-23	AU139931.1	EST_HUMAN	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4565	17082	29468	1.69	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4818	17330		6.72	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7098	19829		2.31	1.0E-23	BE378471.1	EST_HUMAN	601238495F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
8895	21329	34240	6.1	1.0E-23	AA448097.1	EST_HUMAN	zw82c08.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782688 5' similar to contains PTR5.12 PTR5 repetitive element ;
589	13140		1.7	9.0E-24	AA663213.1	EST_HUMAN	ab75a08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852788 3' similar to
4694	17210	29588	1.1	8.0E-24	P23269	SWISSPROT	TR-E19822 E19822 CA PROTEIN ;
4694	17210	29589	1.1	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
5791	18334	32104	0.83	8.0E-24		SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
8486	20898	33792	0.63	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3880	18415		1.49	7.0E-24	AW937954.1	EST_HUMAN	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
							QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5335	17834		1.01	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A2311 5'
728	13287		2.98	6.0E-24	AB001421.1	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY); complete cds
891	13417	25862	11.19	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
3984	16518	28923	8.84	5.0E-24	AL229043.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8312	20727	33620	1.27	5.0E-24	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6227	18792	31500	2.89	4.0E-24	AA594178.1	EST_HUMAN	nm31h05.s1 NCL CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVK
9123	21555	34459	1.2	4.0E-24	AW813711.1	EST_HUMAN	P31795 POL POLYPROTEIN ;
10954	23384	36394	1.85	4.0E-24	BE544822.1	EST_HUMAN	RC3-ST0197-130100-014-06 S10187 Homo sapiens cDNA
12090	24241	30963	3.54	4.0E-24	AB029018.1	NT	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464498 5'
12280	24697	30768	4.95	4.0E-24	M20707.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
5391	17898	30246	2.57	3.0E-24	P11369	SWISSPROT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II) RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
7516	19764	32571	0.84	3.0E-24	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV19S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
7516	19764	32572	0.84	3.0E-24	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
8948	21381		2.87	3.0E-24	AW614871.1	EST_HUMAN	h168608.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2987950 3' similar to contains MER28.b2
8980	21419		0.84	3.0E-24	AW662078.1	EST_HUMAN	MER28 repetitive element ;
9867	22014	34944	4.05	3.0E-24	AL163262.2	NT	EST374149 MAGG resequences, MAGG Homo sapiens cDNA
12178	24298	30941	1.64	3.0E-24	BF127762.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C062
2241	14760	27270	3.39	2.0E-24	AA167559.1	EST_HUMAN	601810449F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053396 5'
3802	16339		1.16	2.0E-24	AW688189.1	EST_HUMAN	zp1109.r1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
7831	24891		0.62	2.0E-24	AL163209.2	NT	RC3-NN0068-080500-021-503 NN0068 Homo sapiens cDNA
7974	20410	33280	0.99	2.0E-24	AF086824.1	NT	Homo sapiens chromosome 21 segment HS21C009
7979	20415	33283	0.49	2.0E-24	AJ003536.1	EST_HUMAN	Mus musculus rho/rao-interacting citron kinase (Crik) mRNA, complete cds
9167	21599	34510	2.84	2.0E-24	AL119156.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP1p12-5H13
							DKFZp761L1712_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9197	21829		1.05	2.0E-24	H88214.1	EST_HUMAN	y92b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element ;
9833	22335	35283	1.01	2.0E-24	AI521769.1	EST_HUMAN	U77609.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
9933	22335	35284	1.01	2.0E-24	AI6221769.1	EST_HUMAN	U77609.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
12005	24934		8.88	2.0E-24	M28877.1	NT	Human O family dispersed repeat element
1694	14223	28703	2.42	1.0E-24	7706340	NT	Homo sapiens CGI-127 protein (LOC51846), mRNA
2812	15107		7.62	1.0E-24	AW820194.1	EST_HUMAN	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
2980	15535	27952	0.93	1.0E-24	D86423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4287	16812		1.9	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
8739	19284	32045	1.76	1.0E-24	7106338	NT	Mus musculus keratin complex-1, gene C29 (Krt1-c29), mRNA
8062	20493	33371	5.12	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8278	20696	33587	0.9	1.0E-24	BE144526.1	EST_HUMAN	MRO-HT0166-271199-005-008 HT0168 Homo sapiens cDNA
8594	21028	33931	1.98	1.0E-24	AW907184.1	EST_HUMAN	GMN-N1010-130300-281-d07 NN1010 Homo sapiens cDNA
6828	18367	32144	0.48	9.0E-25	11420402	NT	Homo sapiens helicase-like protein NHL (LOC51750), mRNA
5098	17608	29869	2.8	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.s1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
8763	21227	34134	5.33	7.0E-25	AA488846.1	EST_HUMAN	MER1 repetitive element ; na06a09.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element ;
11427	23768	36849	3.72	7.0E-25	AA683540.1	EST_HUMAN	n28h08.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST
7409	18078		6.02	6.0E-25	W87623.1	EST_HUMAN	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA ;
8269	20866	33579	12.43	6.0E-25	7305360	NT	z165h07.r1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
11081	23506	36537	1.68	6.0E-25	AW879107.1	EST_HUMAN	Mus musculus otogelin (Otog), mRNA
1478	14008	26474	2.34	4.0E-25	T88107.1	EST_HUMAN	EST391217 MAGP resequences, MAGP Homo sapiens cDNA
3380	15926		3.05	4.0E-25	AW887671.1	EST_HUMAN	y566h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
3916	16460	28857	1.22	4.0E-25	AF000368.1	NT	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
4339	16881		4.22	4.0E-25	BE170957.1	EST_HUMAN	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
2090	14604	27121	1.8	3.0E-25	BE088922.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
3287	15836	28254	3.99	3.0E-25	8923321	NT	RC6-BT0377-131299-031-F02 BT0377 Homo sapiens cDNA
3287	15836	28255	3.99	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
4960	17471	29848	0.71	3.0E-25	P29622	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
6083	18635	31329	0.61	3.0E-25	U53212.1	NT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
6973	19510	32291	0.59	3.0E-25	AA603590.1	EST_HUMAN	Human degenerate channel MDEG mRNA, partial cds np27b02.s1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb:M61866 ZINC FINGER PROTEIN 86 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8980	21314	34225	4.23	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1378	13914	26370	4.74	2.0E-25	5032158	NT	Homo sapiens transudh (beta)-like 1 (TBL1) mRNA
2203	14713	27235	7.45	2.0E-25	BE88018.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2788	14955	27469	12.57	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4206	16731	29120	2.12	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4206	16731	29120	2.12	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
9877	22280	35220	0.93	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Slavides GS) Homo sapiens cDNA
378	12986	25386	0.8	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434H0313_1 434 (synonym: hss3) Homo sapiens cDNA clone DKFZp434H0313 5'
1281	13817		1.35	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome
2333	14840	27355	2.19	1.0E-25	Q08065	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4918	17429	29802	2.99	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-009 HT0454 Homo sapiens cDNA
6920	19459		0.94	1.0E-25	AA189080.1	EST_HUMAN	z445b08.s1 Striatum hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element
7183	24629	32722	2.92	1.0E-25	AA582690.1	EST_HUMAN	nm54h11 s1 NCL CGAP_K16 Homo sapiens cDNA clone IMAGE:1087749 3'
8229	20648	33540	0.58	1.0E-25	Q8JUL58	SWISSPROT	ZINC FINGER PROTEIN 276 (BWSR2 ASSOCIATED ZINC-FINGER PROTEIN BAZ2)
8571	21006	33906	4.09	1.0E-25	AA709079.1	EST_HUMAN	z196g04.s1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.13 PTR5 repetitive element
10750	23188	36174	2.58	1.0E-25	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11701	24004	36563	2.03	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
11701	24004	36564	2.03	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
12560	24544		1.3	1.0E-25	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
2383	14897	27408	1.41	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11559	24688		2.16	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5480	17975	30319	11.1	8.0E-26	11560136	NT	Rattus norvegicus synaptotagmin interacting protein 1 (STIP1), mRNA
5994	18540		1.78	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1594	14126	26591	1.65	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3994	16528	28932	1.46	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4176	16703	29091	2.16	7.0E-26	AW340153.1	EST_HUMAN	h002e12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2908366 3'
5906	18484	31166	0.71	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11403	23764		7.72	7.0E-26	AA116895.1	EST_HUMAN	zn30d08.r1 Striatum neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12310	24388		2.04	7.0E-26	AW954559.1	EST_HUMAN	EST366829 MAGE resequences, MAGEC Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2131	14844	27168	1.63	6.0E-26	AF028908.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinase gene families
3319	15868	28285	0.97	8.0E-26	AA206131.1	EST_HUMAN	z352h04.r1 Stratiene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
1208	13749	26194	1.84	6.0E-26	A1708235.1	EST_HUMAN	as38h08.x1 Barsblad aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
1208	13749	26195	1.64	6.0E-26	A1708235.1	EST_HUMAN	as38h08.x1 Barsblad aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
9828	22044		3.13	4.0E-26	7657870	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10454	22905	35884	4.26	4.0E-26	BE266187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
1968	14484		3.89	3.0E-26	AA115895.1	EST_HUMAN	z330408.r1 Stratiene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3779	16317	28717	1.3	3.0E-26	AA152484.1	EST_HUMAN	z330f10.r1 Stratiene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3779	16317	28718	1.3	3.0E-26	AA152484.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
7319	19731	32535	3.81	3.0E-26	BF245488.1	EST_HUMAN	z330f10.r1 Stratiene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
11351	23715	36774	3.84	3.0E-26	AA583173.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
701	13283	25680	6.91	2.0E-26	AL163282.2	NT	z330f10.r1 Stratiene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
1838	14380		2.49	2.0E-26	AL038099.2	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
3180	15743	28185	5.5	2.0E-26	X86694.1	NT	601884963F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4083278 5'
10992	23421	38438	3.78	2.0E-26	AI801412.1	EST_HUMAN	nm37405.at NCL_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains ORF.11
11171	23561		1.78	2.0E-26	AF056066.1	NT	ORF repetitive element ;
11816	24073		2.12	2.0E-26	AB037859.1	NT	Homo sapiens chromosome 21 segment HS21C082
12026	24873	30571	1.19	2.0E-26	11435947	NT	DKFZp568L171_s1 568 (synonym: hfkid2) Homo sapiens cDNA clone DKFZp568L171 3'
141	12747	25166	9.83	1.0E-26	BE170371.1	EST_HUMAN	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
2476	14977	27491	18.08	1.0E-26	BE814995.1	EST_HUMAN	to89a01.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element; contains element MER20 MER20 repetitive element ;
2834	15129		4.33	1.0E-26	AF261085.1	NT	Homo sapiens MHC class 1 region
7234	19846		2.64	1.0E-26	BE168980.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
12076	24953		2.76	1.0E-26	H55093.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
8102	20528		1.08	9.0E-27	BF371227.1	EST_HUMAN	GV4-HT0538-020300-123-e02 HT0538 Homo sapiens cDNA
9554	22117		4.65	9.0E-27	U93183.1	NT	MR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA
							Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
							MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
							CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
							RC8-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
							Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11459	23818		2.17	9.0E-27	BE207127.1	EST_HUMAN	ba17e04.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2824062 5'
11562	23912		3.5	9.0E-27	BF445556.1	EST_HUMAN	naa03c07.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3253844 3' similar to contains OFR.H
10	12630	25017	3.17	8.0E-27	AI631462.1	EST_HUMAN	OFR repetitive element ;
574	13145		4.44	8.0E-27	AL163227.2	NT	W49-04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
1447	13979	28438	14.36	8.0E-27	AW162737.1	EST_HUMAN	THR repetitive element ;
1447	13979	28439	14.36	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
2075	14589	27109	2.2	8.0E-27	AW884776.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
3142	15895	28114	1.98	8.0E-27	P12236	SWISSPROT	TUBULIN ALPHA-1 CHAIN (HUMAN);
3326	15873	28295	0.71	8.0E-27	AF181897.1	NT	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
5956	18541	31228	0.78	8.0E-27	AV732214.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
7395	18094		2.5	8.0E-27	BE926560.1	EST_HUMAN	PM2-SN0018-220300-002-407 SN0018 Homo sapiens cDNA
7477	19681	32477	2.46	8.0E-27	N84970.1	EST_HUMAN	ADP.ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE
9482	21813	34836	1.73	8.0E-27	AW857579.1	EST_HUMAN	NUCLEOTIDE TRANSLATOR 3) (ANT 3)
9482	21813	34837	1.73	8.0E-27	AW857579.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
703	13265		1.18	7.0E-27	Z70684.1	NT	AV732214 HTF Homo sapiens cDNA clone HTFBC806 5'
5225	17727		2.58	7.0E-27	AW629172.1	EST_HUMAN	MR4-BT0398-250800-204-406 BT0398 Homo sapiens cDNA
5458	17963	30303	7.95	7.0E-27	5032158	NT	J1761F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1761 5' similar to
5458	17963	30304	7.95	7.0E-27	5032158	NT	REPETITIVE ELEMENT L1
6381	18938	31675	0.81	7.0E-27	X65747.1	NT	GM1-CT0315-091299-063-407 CT0315 Homo sapiens cDNA
9259	21691		1	7.0E-27	D86984.1	NT	GM1-CT0315-091299-063-407 CT0315 Homo sapiens cDNA
10531	22978		4.6	7.0E-27	AJ271735.1	NT	Human endogenous retroviral element HC2
12228	24337		2.04	7.0E-27	AV723365.1	EST_HUMAN	h15h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2976879 3' similar to TR:O76040
10511	22960	35940	4.55	6.0E-27	M26697.1	NT	O76040 ORF2: FUNCTION UNKNOWN. ;
8338	20751		0.7	6.0E-27	AL163303.2	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
10203	22604	35568	3.38	5.0E-27	BF666814.1	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
10203	22604	35569	3.38	5.0E-27	BF666814.1	EST_HUMAN	R.norvegicus gnat-3 mRNA for gustducin
2279	14787	27307	1.02	4.0E-27	D26303.1	NT	Human mRNA for KIAA0231 gene, partial cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7124	19857	32452	1.84	4.0E-27	8910569	NT	Mus musculus sperm tail associated protein (Slap), mRNA
8591	21028		0.92	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
8621	21056		1.25	4.0E-27	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
1972	14490	26999	3.17	3.0E-27	XG0658.1	NT	Rattus RYA3 mRNA for a potential ligand-binding protein
4288	16813	29187	1.73	3.0E-27	BE071924.1	EST_HUMAN	PMO-BT0527-090100-001-411 BT0527 Homo sapiens cDNA
5600	18188	30553	7.66	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
8380	20784	33692	0.98	3.0E-27	BE070351.1	EST_HUMAN	7633102.X1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284283 3'
9558	22119	35047	4.36	3.0E-27	BF036327.1	EST_HUMAN	601458631F1.NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
43	12663	25055	14.02	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1858	14380		22.35	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3070	15624		12.87	2.0E-27	AW629172.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); hi61h12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
3183	15736	28155	1.24	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3183	15736	28166	1.24	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
7045	19579	32372	0.78	2.0E-27	H02655.1	EST_HUMAN	X36601.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
8688	21131	34032	1.09	2.0E-27	AI868347.1	EST_HUMAN	SP-HMGC_MOUSE Q02691 HOMEBOX PROTEIN ; w128g07.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2426268 3'
9526	21941		2.67	2.0E-27	AA551527.1	EST_HUMAN	nk08h05.s1 NCL CGAP_Tny1 Homo sapiens cDNA clone IMAGE:B43737 similar to contains L1.13 L1
10062	22463	35416	1.18	2.0E-27	M78590.1	EST_HUMAN	repetitive element ; EST00738 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBCF07
10062	22463	35417	1.18	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBCF07
10734	23172	36155	2.07	2.0E-27	AU121685.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
11242	14380		6.64	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
453	13028		1.37	1.0E-27	AL163246.2	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); Homo sapiens chromosome 21 segment HS21C048
1023	13574	26016	1.46	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DEC1 to ORCTL4 gene region, section 1/2 (DEC1, ORCTL3, ORCTL4 genes, complete cds)
4097	16828		1.03	1.0E-27	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Ktd13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MEF2a.b3
6895	19435	32211	6.14	1.0E-27	6005855	NT	MER28 repetitive element ; Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7274	19779	32588	1.68	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s400095C10

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7274	19779	32599	1.68	1.0E-27	F30168.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
8077	21609	34419	0.97	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8331	21763		1.21	1.0E-27	BE079780.1	EST_HUMAN	RC8-BT0827-140200-011-E08 BT0827 Homo sapiens cDNA
8950	22253	35189	2.76	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
11428	23780	36851	4.38	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant bhah mRNA, complete cds
146	12760		2.44	9.0E-28	BE348399.1	EST_HUMAN	hwl7c11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
325	12918	25336	2.68	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313
11644	23967		3.98	9.0E-28	BF377859.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
11990	24789		2.22	8.0E-28	AW167671.1	EST_HUMAN	GM2-TN0140-070800-372-g01 TN0140 Homo sapiens cDNA
1212	13753	28198	15.71	7.0E-28	AU142750.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:O60302 O60302 KIAA0555 PROTEIN. contains element MER22 repetitive element
10982	23991	38402	2.11	7.0E-28	11417668	NT	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
11801	23935		2.5	7.0E-28	AV735348.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
4093	16624	29013	1.43	6.0E-28	AB020673.1	NT	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
4093	16824	29014	1.43	6.0E-28	AB020673.1	NT	Homo sapiens mRNA for KIAA0868 protein, complete cds
9292	21724		1.27	6.0E-28	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
12279	24372		5.1	6.0E-28	AA504562.1	EST_HUMAN	aa60a03.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:823340 5' similar to contains Alu repetitive element:contains element PTR5 repetitive element
332	12925		2.33	6.0E-28	AI921003.1	EST_HUMAN	w018c07.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element
4023	16556	28952	1.46	5.0E-28	R79762.1	EST_HUMAN	y89f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'
2556	15055	27571	1.58	4.0E-28	AW195066.1	EST_HUMAN	xt33c09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN
2931	15486	27906	0.8	4.0E-28	4505316	NT	Q08379 GOLGIN-95 ;
3069	15623	28030	3.27	4.0E-28	BE409100.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
7795	20237	33097	2.07	4.0E-28	AI198941.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
10647	23087		2.74	4.0E-28	AF029308.1	NT	qf66f10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M18503 LINE-1
10786	23224		11.33	4.0E-28	AB038241.1	NT	REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
10802	20237	33097	4.03	4.0E-28	AI198941.1	EST_HUMAN	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
12041	24210		1.3	4.0E-28	AW854244.1	EST_HUMAN	qf66f10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M18503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1310	13651		2.53	3.0E-28	AF156382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5283	17784		0.85	3.0E-28	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9235	21667	34577	2.14	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-09 HT0713 Homo sapiens cDNA
10712	23150	36133	2.5	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
12071	24225		3.38	3.0E-28	AI831891.1	EST_HUMAN	wf88f07.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element ;
12211	24326		1.22	3.0E-28	BE082801.1	EST_HUMAN	RC2-BT0842-210200-013-f03 BT0842 Homo sapiens cDNA
91	12708	25122	8.3	2.0E-28	BE092167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1071	13617	26059	1.09	2.0E-28	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
1185	13736	26179	11.65	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2373	14878	27398	1.61	2.0E-28	AI348634.1	EST_HUMAN	qc35b06.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element ;
3338	15885	28306	1.06	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6635	19183	31935	1.88	2.0E-28	BF224402.1	EST_HUMAN	hr76d03.x1 NCL CGAP_Kld11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element ;
6660	19208		2.67	2.0E-28	BF212905.1	EST_HUMAN	601814186F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
9755	22168		3.57	2.0E-28	AW972305.1	EST_HUMAN	EST384394 MAGE resequences, MAGL Homo sapiens cDNA
11360	23723	36783	1.89	2.0E-28	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1507	14039	26504	3.01	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2126	14638	27163	2.75	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-380-503 BT0821 Homo sapiens cDNA
2628	16121	27634	2.03	1.0E-28	AF000995.1	NT	Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds
5034	17544	29815	0.61	1.0E-28	AV732194.1	EST_HUMAN	AV732194 HTF Homo sapiens cDNA clone HTFBIH05 5'
8533	20988		5.84	1.0E-28	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC630091), mRNA
8646	21081		2.87	1.0E-28	8922793	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
9635	21950	34873	3.91	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
9949	22351	35300	4.79	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9949	22351	35301	4.78	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
11606	23939		6.86	1.0E-28	AA054182.1	EST_HUMAN	z51c01.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
12419	24671		2.76	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12536	24904	30451	3.86	9.0E-28	AW66987.1	EST_HUMAN	hr76g08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12175	24295		4.87	8.0E-28	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1619	14150	26621	0.97	7.0E-29	AW969447.1	EST_HUMAN	EST378521 IMAGE resequences, MAGI Homo sapiens cDNA
12591	24567		5.81	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
612	13180	25584	8.5	6.0E-29	AI938748.1	EST_HUMAN	vp98b01.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
11921	24140		5.95	6.0E-29	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN :contains LTR7.b1 LTR7 repetitive element ;
12010	24189		1.71	6.0E-29	BF588097.1	EST_HUMAN	RC3-UT0082-210800-021-c05 UT0082 Homo sapiens cDNA
5098	17608		1.04	6.0E-29	AL163203.2	NT	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
9158	21580		8.44	5.0E-29	AW987541.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
3191	15744		2.04	4.0E-29	A1752367.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
6313	18874		8.38	4.0E-29	BE164930.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_on15c02 random
9171	21603	34513	4.27	4.0E-29	JO4988.1	NT	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
4442	16962	28349	1.59	3.0E-29	AB042287.1	NT	Human 80 kD heat shock protein gene, complete cds
4763	17297	29681	1.35	3.0E-29	BF333236.1	EST_HUMAN	Homo sapiens PTS gene for 8-pyruvyltetrahydropterin synthase, complete cds
6228	18793	31501	1.16	3.0E-29	BE314018.1	EST_HUMAN	QV1-B10821-120900-360-003 B10821 Homo sapiens cDNA
9160	21592	34499	2.23	3.0E-29	D38044.1	NT	601152657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5'
9551	21995	34888	1.23	3.0E-29	AW303317.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
9718	22139		1.69	3.0E-29	AL163246.2	NT	xv1703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element:contains MER19.12 MER19 repetitive element ;
11812	24070		1.71	3.0E-29	D63982.1	NT	Homo sapiens chromosome 21 segment HS21C048
510	13083	25496	1.11	2.0E-29	AF084699.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
510	13083	25497	1.11	2.0E-29	AF084699.1	NT	Homo sapiens envelope protein RIG-6 (env) gene, complete cds
1555	14087	26547	7.18	2.0E-29	AI963804.1	EST_HUMAN	Homo sapiens envelope protein RIG-6 (env) gene, complete cds
1555	14087	26548	7.18	2.0E-29	AI963804.1	EST_HUMAN	wr65d10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15546
1735	14262	26747	1.92	2.0E-29	X84900.1	NT	HERV-E ENVELOPE GLYCOPROTEIN ;
1735	14262	26748	1.92	2.0E-29	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
4296	16821	29205	2.56	2.0E-29	AL163288.2	NT	H.sapiens mRNA for laminin-5, alpha3b chain
6110	18679	31375	0.83	2.0E-29	AI082459.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C068
6494	18048	31787	1.48	2.0E-29	AI080418.1	EST_HUMAN	oe71604.x1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.12 L1 repetitive element ;
							wr2707.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2355860 3' similar to contains element MER8 repetitive element ;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8074	18048	31787	1.34	2.0E-28	AI808418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2366860 3' similar to contains element MER8 repetitive element;
8815	21050	33956	1.3	2.0E-29	BE867157.1	EST_HUMAN	601442208F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846648 5'
9697	22109	35036	2.59	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9897	22109	35037	2.59	2.0E-28	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10205	22806	35571	3.39	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10205	22806	35572	3.39	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10736	23174	36157	1.84	2.0E-29	BF025947.1	EST_HUMAN	601869834F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3962833 5'
11232	23801		2.15	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dnaJ (SPF31), mRNA
8479	20892	33788	0.44	1.0E-28	AV700745.1	EST_HUMAN	AV700745 GK Homo sapiens cDNA clone GKCALE08 3'
8481	20894	33790	0.48	1.0E-29	AW629172.1	EST_HUMAN	h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
9208	21840	34549	5.86	1.0E-29	AW983880.1	EST_HUMAN	O76040 ORF2: FUNCTION UNKNOWN. ;
6935	19474	32263	3.37	9.0E-30	AA761215.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
11688	23995		2.45	9.0E-30	11422745	NT	n220c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1
6847	19195		12.62	8.0E-30	F08688.1	EST_HUMAN	MER4 repetitive element;
8828	21263	34169	2.28	8.0E-30	AA938973.1	EST_HUMAN	Homo sapiens zinc/iron regulated transporter-like (ZIRT), mRNA
9124	21558	34460	4.27	8.0E-30	AI557072.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1758	14285	26788	1.09	6.0E-30	D25303.1	NT	EST97317 Thymus l Homo sapiens cDNA 5' end similar to EST containing O family repeat
3147	15700	28118	2.44	8.0E-30	BE008028.1	EST_HUMAN	PT2.1_13_B11.r tumor2 Homo sapiens cDNA 3'
12561	18005		4.88	6.0E-30	X51755.1	NT	Human mRNA for integrin alpha subunit, complete cds
4026	16559	28955	43.64	5.0E-30	AI398992.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
5488	24713		3.6	5.0E-30	U87931.1	NT	Human lambda-immunoglobulin constant region complex (germline)
10670	23110		2.67	5.0E-30	AL163278.2	NT	1q92g03.x1 NCI_CGAP_GCL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element
2056	14571	27085	1.28	4.0E-30	AW937471.1	EST_HUMAN	Human acetylase hydratase (ACO2) gene, exon 7
2056	14571	27086	1.28	4.0E-30	AW937471.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5474	17959	30314	1.08	4.0E-30	AB018251.1	NT	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
9282	21714	34624	1.55	4.0E-30	AW812488.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
1179	13721		2.94	3.0E-30	AI338551.1	EST_HUMAN	Homo sapiens mRNA for KIAA0718 protein, partial cds
3758	16297	28698	0.9	3.0E-30	AF128893.1	NT	CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA
7708	20153	33011	0.57	3.0E-30	T18862.1	EST_HUMAN	qq83-c05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element;
							Homo sapiens telomerase reverse transcriptase (TER1) gene, exons 1-6
							b12056t Testis 1 Homo sapiens cDNA clone b12056

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10327	22727	35694	1	3.0E-30	BE360127.1	EST_HUMAN	ht09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
10982	23411	39423	2.98	3.0E-30	P34056	SWISSPROT	MER29 repetitive element;
694	13266	28673	1.1	2.0E-30	AW857315.1	EST_HUMAN	TRANSCRIPTION FACTOR AP-2
1111	13655		2.38	2.0E-30	F08888.1	EST_HUMAN	CMO-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1508	14040	26505	6.18	2.0E-30	BE175877.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
2697	16160	27671	11.15	2.0E-30	BE765232.1	EST_HUMAN	RC6-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2873	15428	27847	12.24	2.0E-30	AF114158.1	NT	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
3791	16328	28730	2.2	2.0E-30	AW206581.1	EST_HUMAN	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
4830	17342	29724	1.82	2.0E-30	BE298945.1	EST_HUMAN	UI-H-B11-efo-c-12-Q-U1.e1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722598 3'
4830	17342	29725	1.82	2.0E-30	BE298945.1	EST_HUMAN	601118860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
7139	19870	32468	0.67	2.0E-30	BF306337.1	EST_HUMAN	601118860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
8984	21417	34330	0.92	2.0E-30	AA019103.1	EST_HUMAN	601883208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138863 6'
8026	21459	34368	4.98	2.0E-30	C18839.1	EST_HUMAN	z558c10.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:363186 5'
							C18839 Human placenta cDNA (TF-ujwara) Homo sapiens cDNA clone GEN-570C01 5'
8094	21628	34432	2.52	2.0E-30	BE670617.1	EST_HUMAN	7637c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN
							P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8094	21628	34433	2.52	2.0E-30	BE670617.1	EST_HUMAN	7637c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN
10031	22433	35379	3.61	2.0E-30	AW971688.1	EST_HUMAN	P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
							EST1383657 IMAGE resequences, MAGL Homo sapiens cDNA
10101	22502	35465	5.35	2.0E-30	AW470791.1	EST_HUMAN	hs33406.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
300	12898	25316	13.68	1.0E-30	C18839.1	EST_HUMAN	THR repetitive element ;
							C18839 Human placenta cDNA (TF-ujwara) Homo sapiens cDNA clone GEN-570C01 5'
556	13128	25538	2.95	1.0E-30	AW468897.1	EST_HUMAN	hd30504.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains
736	13297	25721	3.36	1.0E-30	AL163203.2	NT	MER1.3 MER1 MER1 repetitive element ;
2118	14631	27154	4.33	1.0E-30	AA694377.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
2358	14863	27983	12.04	1.0E-30	BF347728.1	EST_HUMAN	ac77508.st Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
2859	15514	27834	1.24	1.0E-30	6803091	NT	602022560F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157991 5'
3015	15570	27982	0.84	1.0E-30	AA315045.1	EST_HUMAN	Homo sapiens methionine aminopeptidase; eIF-2-associated p67 (MNPEP), mRNA
8272	20889	33581	2.27	1.0E-30	BF183230.1	EST_HUMAN	EST186868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
12348	24813		11.18	1.0E-30	H65593.1	EST_HUMAN	601809932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
3766	16305	28705	0.98	9.0E-31	T73025.1	EST_HUMAN	CHR220332 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
							yc65606.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:865570 5'

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descrip
3768	18305	28706	0.98	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8870	21304	34214	0.98	9.0E-31	R18214.1	EST_HUMAN	y98b08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12853 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8870	21304	34215	0.98	9.0E-31	R18214.1	EST_HUMAN	y98b08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12853 RAS-RELATED PROTEIN RAB-2 (HUMAN);
6086	21518		1.84	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized Infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
12586	24664	30848	1.42	9.0E-31	6755441	NT	Mus musculus syndecan 4 (Sdc4), mRNA
1103	13848	26089	2.83	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2313	14820		8.1	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4991	17601	28876	1.1	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
4991	17501	28877	1.1	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
731	13292		1.4	7.0E-31	AA372637.1	EST_HUMAN	ESTB4555 Odon adenocarcinoma IV Homo sapiens cDNA 5' end
2607	15102	27619	5.08	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2607	15102	27620	5.08	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8933	21387	34278	0.97	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8933	21387	34279	0.97	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9524	21838		1.16	7.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12173	24294	30939	2.95	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3678	16218		3.38	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8739	21173		4.53	6.0E-31	AF05088.1	NT	Homo sapiens MHC class 1 region
11750	24032	31017	2.42	6.0E-31	AW372868.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
11898	24733		2.17	6.0E-31	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
198	12801	25217	2.74	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon B
198	12801	25218	2.74	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon B
8959	21392		0.9	5.0E-31	BF066540.1	EST_HUMAN	7k06r04.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443478 3' similar to TR:Q13537 Q13537
613	13181		4.97	4.0E-31	AJ271735.1	NT	SIMILAR TO POGO ELEMENT, contains L1 L1 L1 repetitive element;
1793	14318		1.43	4.0E-31	AL163280.2	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2747	16237		2.4	4.0E-31	6730038	NT	Homo sapiens chromosome 21 segment HS21C080
11928	24143		1.6	4.0E-31	AJ230125.1	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
12198	24317		1.44	4.0E-31	11430273	NT	Homo sapiens GGT1 gene, exon 1
12331	24400		1.48	4.0E-31	AB008691.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
						NT	Homo sapiens gene for activin receptor type IIB, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2519	15018	27534	3.81	3.0E-31	6005871	NT	Homo sapiens SEC83, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC83L), mRNA
7606	20248	33108	9.26	3.0E-31	4828853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUF88) mRNA
7697	20431	33288	1.45	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8359	20774	33671	0.45	3.0E-31	AW883062.1	EST_HUMAN	CM3-NN0006-300300-132-e07 NN0006 Homo sapiens cDNA
8359	20774	33672	0.45	3.0E-31	AW883062.1	EST_HUMAN	CM3-NN0006-300300-132-e07 NN0006 Homo sapiens cDNA
8746	21180		2.01	3.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
8752	22155	35086	6.25	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10932	23364		3.01	3.0E-31	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
1872	14394	26887	1.17	2.0E-31	AW838174.1	EST_HUMAN	QV2-LT0051-260300-111-f03 LT0051 Homo sapiens cDNA
2235	14744	27265	1.47	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513.1 1761 (synonym: hamy2) Homo sapiens cDNA clone IMAGE:838413 3' similar to contains
2341	14846	27363	3.28	2.0E-31	AA458824.1	EST_HUMAN	aa88f11.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:2733833 3'
5526	18116	30473	0.8	2.0E-31	AW444493.1	EST_HUMAN	THR12 TH-R repetitive element
5984	18560	31245	3.82	2.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148258 3' similar to contains MER29.B3
8982	21824		2.02	2.0E-31	AA877764.1	EST_HUMAN	nr0804.s1 NCI_CGAP_Oc10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537
9480	21911	34834	3.54	2.0E-31	7661635	NT	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9973	22375	35324	1.1	2.0E-31	AV710948.1	EST_HUMAN	Homo sapiens B9 protein (B9), mRNA
9973	22375	35325	1.1	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUAALB07 5'
10095	22496	35456	2.5	2.0E-31	BE408911.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUAALB07 5'
10095	22496	35457	2.5	2.0E-31	BE408911.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
11858	24105		2.43	2.0E-31	AF148512.1	NT	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12003	24977		2.66	2.0E-31	AI114527.1	EST_HUMAN	Homo sapiens hexokinase II gene, promoter region
16	12636	25024	9.38	1.0E-31	U93163.1	NT	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
1663	14184	26665	2	1.0E-31	O95371	SWISSPROT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
1663	14184	26668	2	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1663	14184	26667	2	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4681	17197	29573	1.03	1.0E-31	AL134376.1	EST_HUMAN	OLFACTORY RECEPTOR 2C1
4681	17197	29574	1.03	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
5544	18134	30491	4.27	1.0E-31	AW391079.1	EST_HUMAN	DKFZp547B235.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6446	16002	31733	1.97	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ceb1 repeat region
7746	20180	33051	1.01	1.0E-31	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
8446	20859	33780	0.59	1.0E-31	BE972818.1	EST_HUMAN	801652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3835283 5'
10695	23134	36116	2.82	1.0E-31	AJ086434.1	EST_HUMAN	q21h03.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16585
2817	15373		0.96	9.0E-32	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
7002	19538	32322	2.18	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAA:G01 5'
7846	20286	33148	0.54	9.0E-32	L31770.1	NT	Bos taurus vacuolar H ⁺ -ATPase subunit mRNA, complete cds
8114	20540		0.98	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2001	14517	27028	2.77	8.0E-32	AJ058770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
5742	18324	30760	0.87	8.0E-32	AW897214.1	EST_HUMAN	RC2-BN0048-200300-016-e04 BN0048 Homo sapiens cDNA
11832	24084		3.36	7.0E-32	X17283.1	NT	Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orthon and neighbouring non-amplified region
2687	15179	27690	2.13	8.0E-32	AK478104.1	EST_HUMAN	hm34e10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2158994 3' similar to contains MER29.13
7839	20279		1.3	8.0E-32	BE888076.1	EST_HUMAN	MER28 repetitive element;
12265	24956		1.36	8.0E-32	AA864653.1	EST_HUMAN	601611530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
1059	13605	26045	25.72	5.0E-32	AF116627.1	NT	oh37c03.s1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1458972 3' similar to contains L1.13 L1
955	13507		2.15	4.0E-32	AL163246.2	NT	Homo sapiens PRO1181 mRNA, complete cds
8130	20553	33428	3.4	4.0E-32	11432574	NT	Homo sapiens chromosome 21 segment HS21C046
8130	20553	33429	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
473	13047	25468	3.69	3.0E-32	Y17293.1	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
1483	14015	26481	6.59	3.0E-32	AV731500.1	EST_HUMAN	Homo sapiens FLI-1 gene, partial
2862	15417	27839	0.8	3.0E-32	5174574	NT	AV731500 HTF Homo sapiens cDNA clone HTFAK:07 5'
2862	15417	27840	0.8	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homodog), translocated to, 4
9615	22030	34960	10.65	3.0E-32	AV758634.1	EST_HUMAN	(MLL:T4) mRNA
9615	22030	34961	10.65	3.0E-32	AV758634.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homodog), translocated to, 4
10704	23143	36125	1.94	3.0E-32	AA77621.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFB:HH12 5'
11861	24107		5.24	3.0E-32	BE278086.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFB:HH12 5'
							z165a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.13 THR repetitive element;
							601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12259	15417	27839	3.77	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology); translocated to, 4 (MLLT4) mRNA
12259	15417	27840	3.77	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology); translocated to, 4 (MLLT4) mRNA
12425	24461		2.51	3.0E-32	BE278088.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
4944	17455	29832	2.72	2.0E-32	BE286613.1	EST_HUMAN	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528159 5'
6574	19125	31857	0.82	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6825	19366	32142	7.28	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6825	19366	32143	7.28	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8835	21269	34177	2.51	2.0E-32	AA114294.1	EST_HUMAN	z166c08.r1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:563150 5'
8835	21269	34178	2.51	2.0E-32	AA114294.1	EST_HUMAN	z166c08.r1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:563150 5'
12551	24538	30839	1.67	2.0E-32	AV738449.1	EST_HUMAN	AV738449 CB Homo sapiens cDNA clone CBFB/IA08 5'
12551	24538	30840	1.67	2.0E-32	AV738449.1	EST_HUMAN	AV738449 CB Homo sapiens cDNA clone CBFB/IA08 5'
2617	15112		3.82	1.0E-32	D84430.1	NT	Homo sapiens mRNA for phenylalanyl tRNA synthetase, complete cds
7486	19890	32487	6.95	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
9066	21498	34407	3.78	1.0E-32	AA720574.1	EST_HUMAN	hw21902.s1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
3456	16000						THR repetitive element
6759	19302						hw07c05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TRC088539 O88539 WW DOMAIN BINDING PROTEIN 11.
9205	21637	34346	5.11	9.0E-33	BE327112.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10581	23028		3.62	9.0E-33	AF223391.1	NT	602021164F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4156870 5'
63	12683	25089	1.6	9.0E-33	BF347228.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
63	12683	25090	3.51	9.0E-33	AL163280.2	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2070	14585	27103	3.2	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2584	15080		3.2	7.0E-33	5031736	NT	to12b09.x1 NCL_CGAP_Lu22 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element
3201	15753		1.98	7.0E-33	AI590115.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE06 5'
9306	21738		6.23	7.0E-33	AV730058.1	EST_HUMAN	EST383396 MAGL Homo sapiens cDNA
11014	23441	36459	18.52	7.0E-33	AW971307.1	EST_HUMAN	Human ILRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
11838	24080	30890	0.99	7.0E-33	X54890.1	NT	EST383657 MAGL Homo sapiens cDNA
			2.91	7.0E-33	AW971568.1	EST_HUMAN	no16r07.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.11 L1 repetitive element
			4.71	7.0E-33	AA601416.1	EST_HUMAN	

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3736	18276		1.04	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6373	18931	31687	1.02	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H08
6373	18931	31688	1.02	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H08
9056	21488	34400	3.47	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
9137	21568	34478	2.63	6.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
10041	22443	35390	1.32	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
10041	22443	35391	1.32	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1760	14287		1.41	6.0E-33	BF373615.1	EST_HUMAN	QV1-F10169-100700-271-e02 F10169 Homo sapiens cDNA
1861	14383	26873	1.02	6.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1861	14383	26874	1.02	6.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2172	14883		1.39	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4070	16801	28991	0.78	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
7034	19569	32359	0.54	6.0E-33	AA189080.1	EST_HUMAN	z45b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element
10211	22812	35577	0.91	5.0E-33	AW284679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2762461 3'
10211	22812	35578	0.91	5.0E-33	AW284679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2762461 3'
1155	13698		2.83	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2044	14560	27072	1.41	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2320	14827		3.12	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;
2456	14958	27471	9.28	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4519	17037	29415	2.06	4.0E-33	AW283349.1	EST_HUMAN	U-H-B12-af1-c-03-q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5659	18245	30643	25.01	4.0E-33	AA053053.1	EST_HUMAN	z171a08.l1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gpX12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6729	19275	32036	0.8	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6729	19275	32037	0.8	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1116	13660		7.66	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
1117	13660		11.47	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
2348	15335		7.09	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLC8CF09 3'
10331	22731	35697	1.02	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.s1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
17	12637		0.7	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
108	12637		2.05	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
4447	16967		4.95	2.0E-33	BE159039.1	EST_HUMAN	MRO-HT0405-160300-202-408 HT0405 Homo sapiens cDNA
5082	17562	29959	5.36	2.0E-33	AA626683.1	EST_HUMAN	ab57g11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to
5228	17730	30098	2.17	2.0E-33	11421332	NT	gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5228	17730	30099	2.17	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6762	19305	32070	1.09	2.0E-33	AI277492.1	EST_HUMAN	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
8409	21841		2.08	2.0E-33	A052256.1	EST_HUMAN	q21d03.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
12611	24581		1.2	2.0E-33	AJ132352.1	NT	gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
8	12628		1.31	1.0E-33	AF003528.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
5855	18434	31107	0.51	1.0E-33	AF199420.1	NT	Homo sapiens X-linked arylidrolite ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7887	20326	33192	1.14	1.0E-33	M13975.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
10050	25000		1.43	1.0E-33	U60822.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
10818	23254	36239	1.66	1.0E-33	AV744220.1	EST_HUMAN	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11088	23511	36544	2.41	1.0E-33	AW988818.1	EST_HUMAN	AV744220 CB Homo sapiens cDNA clone CBOAAA11 5'
11401	23762	36822	1.99	1.0E-33	U60822.1	NT	QV3-BN0047-230200-102-503 BN0047 Homo sapiens cDNA
12144	24275		2.29	1.0E-33	AI927191.1	EST_HUMAN	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12336	12628		4.48	1.0E-33	AF003528.1	NT	w088c06.x1 NCI CGAP_KD11 Homo sapiens cDNA clone IMAGE:2482410 3'
12369	24419	30895	1.6	1.0E-33	AV727809.1	EST_HUMAN	Homo sapiens X-linked arylidrolite ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12575	24556		2.7	8.0E-34	AJ271735.1	NT	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
2078	14592	27111	4.11	8.0E-34	8922751	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4535	17053	29430	1.48	8.0E-34	BE082570.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
8364	20779	33679	0.69	8.0E-34	BE069882.1	EST_HUMAN	QV2-BT0288-071299-019-g07 BT0288 Homo sapiens cDNA
1474	14006	28472	1.74	7.0E-34	T70845.1	EST_HUMAN	MR4-BT0399-200100-001-H03 BT0399 Homo sapiens cDNA
11809	24133		1.71	7.0E-34	H12868.1	EST_HUMAN	y418c05.t1 Soares_fetal_liver_spleen_1NFSL Homo sapiens cDNA clone IMAGE:108320 5'
488	13081	25480	1.62	6.0E-34	U10991.1	NT	y14c10.t1 Soares_placenta_NbZHP Homo sapiens cDNA clone IMAGE:148722 5'
488	13081	25481	1.62	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
11711	24010	31007	1.81	6.0E-34	U03686.1	NT	Human G2 protein mRNA, partial cds
							Mus musculus DAB/2J hair-specific (hac-1) gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1850	14372		1.63	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51728), mRNA
5183	17687	30047	4.49	5.0E-34	U30883.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
5323	17823		1.04	5.0E-34	N98282.1	EST_HUMAN	zsa27g11.1 r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283828 5'
9263	21695	34607	1.23	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10447	22898	35875	4.24	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
1941	14460	26984	1.27	4.0E-34	AB04667.1	EST_HUMAN	1894c06.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2249194 3'
2672	15165	27875	2.95	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA
6148	18719	31418	0.43	4.0E-34	AA661773.1	EST_HUMAN	ak35c01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407836 3'
8368	21800	34708	1.33	4.0E-34	BF209778.1	EST_HUMAN	601874950F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4102213 5'
6552	19104	31848	0.46	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
10831	23363		2.3	3.0E-34	BF035327.1	EST_HUMAN	601458331F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
5169	17673	30037	3.23	2.0E-34	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
9308	21740	34647	0.83	2.0E-34	AB678101.1	EST_HUMAN	w435g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element:
9308	21740	34648	0.83	2.0E-34	AB678101.1	EST_HUMAN	w435g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element:
1532	14064	26525	4.62	1.0E-34	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3673	16213	28618	1.35	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4085	16816	29004	0.86	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4085	16816	29005	0.86	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4516	17034		6.99	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-010-h08 BT0506 Homo sapiens cDNA
5010	17520	28894	3.14	1.0E-34	BF509718.1	EST_HUMAN	UHH-BI4-epb-h-04-0-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086839 3'
5010	17520	28895	3.14	1.0E-34	BF509718.1	EST_HUMAN	UHH-BI4-epb-h-04-0-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086839 3'
6451	19007	31739	2.19	1.0E-34	BE874052.1	EST_HUMAN	601494430F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3866999 5'
6451	19007	31740	2.19	1.0E-34	BE874052.1	EST_HUMAN	601494430F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3866999 5'
932	22236	35171	11.52	1.0E-34	AL036635.1	EST_HUMAN	DKFZp664A1563_r1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp664A1563 5'
10956	23385	33395	3.22	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
10956	23385	33396	3.22	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
10970	23399	36409	1.71	1.0E-34	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12103	24908		1.77	1.0E-34	AA807097.1	EST_HUMAN	oc31c1f1.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb.X68203
12361	24452		5.01	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS21C010

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3645	16185	28592	1.31	9.0E-35	AW663302.1	EST_HUMAN	h177006.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2968787 5'
233	12834		14.12	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
1730	14257	26742	2.36	8.0E-35	BF589937.1	EST_HUMAN	hna33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1730	14257	26743	2.36	8.0E-35	BF589937.1	EST_HUMAN	hna33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4924	17435	29810	3.12	8.0E-35	BF183195.1	EST_HUMAN	hna33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
11829	24081		3.42	8.0E-35	BF589282.1	EST_HUMAN	hna33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
6832	19373	32151	1.76	7.0E-35	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
1444	13978	28435	1.27	6.0E-35	AA757115.1	EST_HUMAN	h153h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
1913	14432	26931	1.89	6.0E-35	6006976	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
4084	16595	28986	0.93	6.0E-35	AW287191.1	EST_HUMAN	UHH-BWO-ajd-4-08-Q-J1.s1 NCI_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2731433 3'
5461	17856	30306	3.69	6.0E-35	AB02849.1	EST_HUMAN	QV-BT019-210189-135 BT018 Homo sapiens cDNA
8580	20995	33892	4.37	6.0E-35	6006921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9971	22373	35321	3.25	6.0E-35	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
1707	14235	26719	18.13	5.0E-35	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2742	15232	27745	2.85	5.0E-35	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
2867	15522	27943	1.69	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
							Homo sapiens cdk2 kinase (CLK2), propin1, cote1, glucocorticoidase (GBA), and metadn genes, complete cds; metadn pseudogene and glucocorticoidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
4435	16955	29344	1.9	5.0E-35	AF023268.1	NT	cds
8766	21169		3.88	5.0E-35	BE890992.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8785	21219	34124	2.48	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN_Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
8785	21219	34125	2.48	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN_Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
10852	23382		2.06	5.0E-35	AA001788.1	EST_HUMAN	zh84f12.f1 Soares_fetal_liver脾 INFIL5_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1463	13986	28461	11.54	4.0E-35	BE257807.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1784	14319	26812	7.65	4.0E-35	H91193.1	EST_HUMAN	yu98a07.r1 Soares_fetal_liver脾 INFIL5 Homo sapiens cDNA clone IMAGE:241238 5' similar to contains PTR5 repetitive element ;
4863	17375		0.65	4.0E-35	AF003528.1	NT	Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5249	17750		0.94	4.0E-35	BE409102.1	EST_HUMAN	601300705F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7654	20100		1.41	4.0E-35	BE350127.1	EST_HUMAN	h199g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28 b3 MER28 repetitive element;
9011	21444	34350	7.21	4.0E-35	AL046598.1	EST_HUMAN	DKFZp434L148.t1 434 (synonym: h19c3) Homo sapiens cDNA clone DKFZp434L148 5'
1566	14128	26594	17.6	3.0E-35	BE268182.1	EST_HUMAN	601125260F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3345063 5'
2226	14738		6.95	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5594	18182	30548	24.63	3.0E-36	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2;
5594	18182	30547	24.63	3.0E-36	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2;
9688	22098		1.53	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
112	15276	28140	1.14	2.0E-35	N88865.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
1219	13759	26204	1.19	2.0E-35	T11909.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971 Homo sapiens mRNA for Gab2, complete cds
2123	14636	27161	3.09	2.0E-35	AB018413.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3276	16826	28242	7.83	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3276	16825	28243	7.83	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3544	16086		0.88	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3922	16457	28864	1.22	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3922	16457	28865	1.22	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4713	17228		3.01	2.0E-35	HA9239.1	EST_HUMAN	y419a12r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
5847	18427	31097	2.11	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-198-b04 BT0701 Homo sapiens cDNA
7543	19983	32832	0.74	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7543	19983	32833	0.74	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
10578	23025	36009	13.88	2.0E-35	X59417.1	NT	H.sapiens PROS-27 mRNA
11577	15825	28242	1.39	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11577	15825	28243	1.39	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11765	24043	31020	1.57	2.0E-35	BE904978.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3888699 5'
11765	24043	31021	1.57	2.0E-35	BE904978.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3888699 5'
12338	24405		7.77	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
12469	15276	25140	2.51	2.0E-35	N88865.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
48	12669	26084	6.89	1.0E-35	AA631949.1	EST_HUMAN	fmf1c10 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	12669	26085	6.89	1.0E-35	AA631949.1	EST_HUMAN	fmf1c10 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
773	13333	25765	201.61	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-412 ST0162 Homo sapiens cDNA
773	13333	25768	201.61	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-412 ST0162 Homo sapiens cDNA
932	13486		1.58	1.0E-35	T87847.1	EST_HUMAN	yd93a01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 6' similar to
2453	14954	27468	9.31	1.0E-35	7705894	NT	SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
2725	15216	27730	2.12	1.0E-35	BE350127.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC51233), mRNA
2725	15216	27731	2.12	1.0E-35	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146266 3' similar to contains MER29.b3
3103	15656	28088	1.08	1.0E-35	6008030	NT	MER29 repetitive element ;
3122	15675	28088	1.53	1.0E-35	AV650422.1	EST_HUMAN	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
3122	15675	28089	1.53	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEFO8 3'
4450	16970	29356	6	1.0E-35	7658905	NT	AV650422 GLC Homo sapiens cDNA clone GLCCEFO8 3'
4450	16970	29357	5	1.0E-35	7658905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
6000	17610	29884	1.74	1.0E-35	AL163247.2	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5451	17946	30297	1.69	1.0E-35	8923266	NT	Homo sapiens chromosome 21 segment HS21C047
5772	18353	30813	1.63	1.0E-35	11826236	NT	Homo sapiens hypothetical protein FLJ20285 (FLJ20285), mRNA
7414	18083	30376	0.72	1.0E-35	AW808665.1	EST_HUMAN	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7414	18083	30377	0.72	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-407 ST0111 Homo sapiens cDNA
7984	20419	33286	0.68	1.0E-35	AB033105.1	NT	MR1-ST0111-111199-011-407 ST0111 Homo sapiens cDNA
8172	20594	33478	1.05	1.0E-35	11418002	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
9725	24654	35077	1.89	1.0E-35	AU168695.1	EST_HUMAN	Homo sapiens KIAA0845 gene product (KIAA0845), mRNA
9725	24654	35078	1.89	1.0E-35	AU168695.1	EST_HUMAN	AU168695 PLACES3 Homo sapiens cDNA clone PLACES3000382 3'
11468	23826	36892	2.31	1.0E-35	AB028980.1	NT	AU168695 PLACES3 Homo sapiens cDNA clone PLACES3000382 3'
11468	23826	36893	2.31	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
11608	24864		2.05	1.0E-35	11418274	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
11745	14954	27468	1.43	1.0E-35	7705894	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
11831	24083		1.9	1.0E-35	11418110	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
12215	24330		2.36	1.0E-35	BE792832.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
6311	18872	31598	0.64	8.0E-36	X78479.1	NT	601584933F NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938695 5'
3079	15633		6.21	7.0E-36	4557498	NT	B.bovis BBS6 mRNA for scinderin
8185	20807	33494	5.59	7.0E-36	U06872.1	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
							Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8185	20607	33495	5.59	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
11995	24184	30947	3.43	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1
1946	14465	28969	2.73	6.0E-36	7706822	NT	Homo sapiens nlrp2 (NINJ2), mRNA
2318	14825		5.96	6.0E-36	AB035346.1	NT	Homo sapiens TOL8 gene, exon 12
5584	18172	30536	5.06	6.0E-36	A1435169.1	EST_HUMAN	h83b06.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128195 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7548	19998	32839	3.29	6.0E-36	AW780143.1	EST_HUMAN	h80802.x1 NCL CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036827 3' similar to SW:IMA2_HUMAN
9105	21537	34446	2.39	6.0E-36	AF208161.1	NT	P52292 IMPORTIN ALPHA-2 SUBUNIT ; Homo sapiens syncytin precursor, mRNA, complete cds
11301	23666	36713	2.23	6.0E-36	A1380499.1	EST_HUMAN	h85c09.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MERR.b2
12452	24778	30684	1.5	6.0E-36	BE737164.1	EST_HUMAN	MERR repetitive element ;
142	12748	25167	35.64	5.0E-36	AJ271735.1	NT	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
2708	16168	27713	28.24	5.0E-36	BE388436.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3608	16146	28553	2.02	6.0E-36	AL163209.2	NT	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
4840	17352	29738	1.97	5.0E-36	5729729	NT	Homo sapiens chromosome 21 segment HS21C009
4840	17352	29737	1.97	6.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
8351	20768	33682	0.45	6.0E-36	11079227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
11575	12748	25167	3.57	6.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11887	24123	31004	3.37	6.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1257	13795	26241	1.84	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1471	14003	26470	1.11	4.0E-36	P10268	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1651	14182	26652	1.19	4.0E-36	BE382574.1	EST_HUMAN	601288574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3629386 5'
2128	14841		1.63	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3327	15874	28296	0.73	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3327	15874	28297	0.73	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5303	17803	30168	0.8	4.0E-36	AA905381.1	EST_HUMAN	605611.a1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1606809 3' similar to
5990	18566		0.97	4.0E-36	R64023.1	EST_HUMAN	SW:D3HL_RAT P28268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
6301	18919	31654	2.86	4.0E-36	11497041	NT	y19105.11 Soares placenta NB2-HP Homo sapiens cDNA clone IMAGE:139713 5'
8184	20608	33483	2.08	4.0E-36	M33320.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
9039	21471	34381	1.3	4.0E-36	D87675.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
9039	21471	34382	1.3	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds

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10770	23208	36190	3.16	4.0E-36	AA000370.1	EST_HUMAN	z169c10.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743260 5'
11903	24128		1.91	4.0E-36	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
11947	24738		5.43	4.0E-36	AV753829.1	EST_HUMAN	AV753829 TP Homo sapiens cDNA clone TPGABH01 5'
12597	24573		16.3	4.0E-36	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
716	13277	28699	3.33	3.0E-36	AF099810.1	NT	Homo sapiens neuradin III-alpha gene, partial cds
2193	14704	27223	1.28	3.0E-36	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4639	17057	29440	8.62	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
5422	17917	30288	0.71	3.0E-36	4605150	NT	Homo sapiens Mals1 (mouse) homolog (MEIS1), mRNA
3128	15881	28097	6.19	2.0E-36	BE259287.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
5048	17658	28926	6.19	2.0E-36	AW880376.1	EST_HUMAN	QV0-QT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5748	18328	30765	3.02	2.0E-36	AF287747.1	NT	Mus musculus p47-phox gene, complete cds
6135	18704	31400	3.93	2.0E-36	T08756.1	EST_HUMAN	EST066948 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBJ28 5' end
6929	19488	32246	14.13	2.0E-36	T69629.1	EST_HUMAN	yc44807.1 Stratagene liver (#837224) Homo sapiens cDNA clone IMAGE:83508 5'
9811	22026	34954	1.01	2.0E-36	BF512794.1	EST_HUMAN	U1-HBW1-apu-e-11-0-J1.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
908	13462	26910	2.81	1.0E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2057	14572	27087	1.92	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-H07 HT0217 Homo sapiens cDNA
2057	14572	27088	1.82	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-H07 HT0217 Homo sapiens cDNA
2107	14621	27142	3.52	1.0E-36	BF673791.1	EST_HUMAN	602136483F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272888 5'
2399	14903		1.48	1.0E-36	AW276898.1	EST_HUMAN	xp57a06.x1 NCL_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2744434 3' similar to WP:C13F10.7
3317	15886		1.22	1.0E-36	AF156962.1	NT	CE08148 ; Homo sapiens human endogenous retrovirus W proC8-19 protease (pro) gene, partial cds
6004	18578	31265	0.82	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G022 5'
6191	18757	31460	1.17	1.0E-36	4827084	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6497	19051		10.85	1.0E-36	AI887714.1	EST_HUMAN	w637c12.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element
6728	19272	32031	1.8	1.0E-36	R25012.1	EST_HUMAN	y336g10.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6728	19272	32032	1.8	1.0E-36	R25012.1	EST_HUMAN	y336g10.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
7051	19585	32380	0.84	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A229_r1 761 (synonym: hamv2) Homo sapiens cDNA clone DKFZp761A229 5'
7911	20350	33217	0.54	1.0E-36	11426108	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7911	20350	33218	0.54	1.0E-36	11426108	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
8602	21037	33940	3.43	1.0E-36	AA148034.1	EST_HUMAN	zs51a12.1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8602	21037	33941	3.43	1.0E-36	AA148034.1	EST_HUMAN	zs51a12.1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8671	21108	34008	1.11	1.0E-36	AA420467.1	EST_HUMAN	nc60608.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8671	21108	34009	1.11	1.0E-36	AA420467.1	EST_HUMAN	nc60608.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
9381	21793	34702	2.89	1.0E-36	AW103658.1	EST_HUMAN	xs82b07.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2614367 3'
10126	22527	35494	2.48	1.0E-36	BF364169.1	EST_HUMAN	QV3-NN1023-010600-189-h01 NN1023 Homo sapiens cDNA
11135	23587	36628	5.38	1.0E-36	AW504143.1	EST_HUMAN	UHF-BND-ale-c-03-q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 6'
11189	23549	36590	1.83	1.0E-36	AI905536.1	EST_HUMAN	RC-BT091-210189-110 BT091 Homo sapiens cDNA
11189	23549	36591	1.83	1.0E-36	AI905536.1	EST_HUMAN	RC-BT091-210189-110 BT091 Homo sapiens cDNA
11763	24041		5.28	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12249	24361		8.49	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
12533	24527		4.09	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7855	20295	33158	2.14	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2604245 3'
7855	20295	33159	2.14	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2604245 3'
12038	24209		1.59	9.0E-37	W22818.1	EST_HUMAN	73D4 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
5498	18089		1.78	8.0E-37	BE698077.1	EST_HUMAN	CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA
							h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146266 3' similar to contains MER29.b3
6113	18682	31377	3.35	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element;
							h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146266 3' similar to contains MER29.b3
6113	18682	31378	3.35	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element;
6165	18733	31437	8.66	8.0E-37	AW840840.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
							H sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
8550	20885	33884	7.11	8.0E-37	X87344.1	NT	
1317	13852		3.16	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
							wk25b11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
10538	22885	35965	10.61	7.0E-37	AI817700.1	EST_HUMAN	PTR5 repetitive element;
12393	24433		3.57	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6401	18958	31592	3.41	6.0E-37	AA307123.1	EST_HUMAN	EST178035 Cdon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6401	18958	31693	3.41	6.0E-37	AA307123.1	EST_HUMAN	EST178035 Cdon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9181	21613	34523	1.16	5.0E-37	AV750211.1	EST_HUMAN	AV750211 NPC Homo sapiens cDNA clone NPCB8GH09 5'
10598	23137		3.29	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
11758	24038		10.05	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2324	14831	27345	6.27	4.0E-37	AA702764.1	EST_HUMAN	z60b04.s1 Soares_fetal_liver_epilean_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6612	19162	31912	0.52	4.0E-37	AW794502.1	EST_HUMAN	RC8-UN0014-210200-021-H05 UM0014 Homo sapiens cDNA
1954	14472	26977	1.97	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
1954	14472	26978	1.97	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2420	14923		9.11	3.0E-37	AW981150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
2918	15473		3.78	3.0E-37	AW981150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
6152	18720	31424	0.63	3.0E-37	AL138274.1	EST_HUMAN	DKFZp47G087_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547G087 5'
7945	20382	33249	0.44	3.0E-37	T03080.1	EST_HUMAN	FB23B1 Fetal brain, Striatogene Homo sapiens cDNA clone FB23B1 3'end similar to Human somatic cytochrome c (HCS) gene
8070	20499	33378	0.82	3.0E-37	AI749952.1	EST_HUMAN	af34c05.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2373898 3' similar to TR:Q13537
388	13012	25435	1.27	2.0E-37	D89780.1	NT	Q13537 SIMILAR TO POGO ELEMENT. :.
398	13012	25436	1.27	2.0E-37	D89780.1	NT	Homo sapiens mRNA for AML1, complete cds
1107	13651	26093	2.88	2.0E-37	AU131202.1	EST_HUMAN	Homo sapiens mRNA for AML1, complete cds
1107	13651	26094	2.88	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'
3902	16437	28843	8.13	2.0E-37	4503210	NT	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002169 5'
5644	18231		0.74	2.0E-37	BF035327.1	EST_HUMAN	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
6897	19437	32213	0.98	2.0E-37	11980617	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
7025	19561	32348	4.18	2.0E-37	AA346720.1	EST_HUMAN	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
8658	21094	34000	2.96	2.0E-37	BF204032.1	EST_HUMAN	EST52931 Fetal heart II Homo sapiens cDNA 5' end
11311	23875	36726	7.13	2.0E-37	AF176013.1	NT	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111408 5'
12581	24560		5.38	2.0E-37	11417972	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
2012	14628	27043	3.96	1.0E-37	AL163281.2	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
5022	17532	29904	2.48	1.0E-37	BF371719.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
6307	18868		1.1	1.0E-37	7305360	NT	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
8789	21223	34128	0.96	1.0E-37	BE548032.1	EST_HUMAN	Mus musculus otogelin (Otog), mRNA
9182	21594	34502	3.16	1.0E-37	AA171408.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3488308 5'
10485	22835	35913	2.48	1.0E-37	M22878.1	NT	zpt1b02.r1 Striatogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1 L2 L1 repetitive element:
12092	24242		3.62	1.0E-37	BE771814.1	EST_HUMAN	Human somatic cytochrome c (HCT) processed pseudogene, complete cds
6058	18630	31322	1.82	9.0E-38	10048482	NT	GM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA
1254	13762	26238	3.31	8.0E-38	11436955	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
2405	14909	27429	3.61	8.0E-38	BF348221.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0371), mRNA
2089	14603	27120	2.12	7.0E-38	AW972825.1	EST_HUMAN	602018401F1 NCI_CGAP_Bim7 Homo sapiens cDNA clone IMAGE:4153992 5'
3061	15615	28024	2.97	7.0E-38	AW884259.1	EST_HUMAN	EST384920 IMAGE resequences, MAGL Homo sapiens cDNA
4240	16765	29150	0.71	7.0E-38	H19092.1	EST_HUMAN	QV3-OT0064-060400-144-409 OT0084 Homo sapiens cDNA
3002	15557	27971	2.06	6.0E-38	BF033033.1	EST_HUMAN	Yn5107.r1 Soares adult brain N2b5f1B55Y Homo sapiens cDNA clone IMAGE:171973 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5856	18435	31108	1.26	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5858	18435	31109	1.26	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7793	20235	33085	0.51	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7861	20300	33165	0.51	6.0E-38	AJ010969.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
7861	20300	33166	0.51	6.0E-38	AJ010969.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
11609	23841		2.95	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12130	24265	30633	12.2	6.0E-38	AB020259.1	NT	Homo sapiens DNA for Human P2M, complete cds
12559	24698	30778	1.36	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
747	13307	25732	1.66	5.0E-38	AW971819.1	EST_HUMAN	EST383908 MAGE resequences, MAGL Homo sapiens cDNA
2351	14856	27376	7.29	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
3875	16243	28648	0.71	5.0E-38	7549804	NT	Homo sapiens deiodinase, Iodothyronine, type II (DIO2), transcript variant 2, mRNA
7469	18869	32783	1.57	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
123	12733	26148	9.98	4.0E-38	Z25468.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
123	12733	25149	9.98	4.0E-38	Z25468.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1187	13729	26171	0.94	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2022	14538		3.71	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3693	16233		1.45	3.0E-38	7549807	NT	Homo sapiens HIRA Interacting protein 4 (dnaj-like) (HIRIP4), mRNA
3861	16397	28801	2.2	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3861	16397	28802	2.2	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4657	17173		0.59	3.0E-38	BE279301.1	EST_HUMAN	601187633F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
7134	24824	32461	8.04	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7693	20138	32694	0.69	3.0E-38	AW302461.1	EST_HUMAN	xc04d01.xt NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2827009 3'
8097	20524		0.55	3.0E-38	AA378327.1	EST_HUMAN	EST91188 Synovial sarcoma Homo sapiens cDNA 5' end
8110	20536	33414	7.48	3.0E-38	BF373684.1	EST_HUMAN	CM3-F10181-140700-241-407 F10181 Homo sapiens cDNA
9103	21635	34444	2.15	3.0E-38	H85494.1	EST_HUMAN	yw86504.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:249775 5'
9103	21636	34446	2.15	3.0E-38	H85494.1	EST_HUMAN	yw86504.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:249775 5'
10011	22413		1.53	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12389	13729	26171	1.19	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
62	12673	25072	1.45	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1412	13946	26402	2.02	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1652	14183	28853	1.59	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12, RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1652	14183	28854	1.59	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12, RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3514	16057		1.15	2.0E-38	AF070870.1	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4619	17135	29519	4.2	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5993	18587	31252	0.53	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
5993	18587	31253	0.53	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
8285	20682	33578	1.94	2.0E-38	AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8991	21424		4.78	2.0E-38	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9318	21748	34656	1.03	2.0E-38	AF089755.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9491	21922		1.25	2.0E-38	BE222256.1	EST_HUMAN	hu08g02.x1 NCL CGAP_L24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:002710 O02710
10339	22739	35708	1.8	2.0E-38	D63479.2	NT	GAG POLYPROTEIN.
11248	23612	36657	4.57	2.0E-38	BE712790.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11385	23747	36805	3	2.0E-38	AF190501.1	NT	QV2-HT0638-080800-293-a05 HT0638 Homo sapiens cDNA
11385	23747	36806	3	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11686	23980		6.77	2.0E-38	AV726988.1	EST_HUMAN	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11688	23981		2.44	2.0E-38	AB012723.1	NT	AV726988 HTG Homo sapiens cDNA clone HTCAHX07 5'
11972	24167		1.81	2.0E-38	M55630.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
11984	24177	30981	3.09	2.0E-38	H55641.1	EST_HUMAN	Human topoisomerase I pseudogene 2
12053	24219		1.85	2.0E-38	S74906.1	NT	CHR220680 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
12570	24552		2.63	2.0E-38	11418248	NT	E1 beta-pyruvate dehydrogenase beta [promoter] [human, placenta, Genomic, 1280 nt]
1120	13684		2.27	1.0E-38	AA401570.1	EST_HUMAN	Homo sapiens sulfoxidase-related protein (SUL-TX3), mRNA
1942	14481	26985	5.71	1.0E-38	4885288	NT	z062b02.r1 Scarses_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
1956	14474	26980	0.98	1.0E-38	7681869	NT	MER19 repetitive element
2400	14904	27423	1.43	1.0E-38	AF270831.1	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
4172	16689	29089	0.99	1.0E-38	AB037863.1	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4341	16883	29248	0.7	1.0E-38	4505016	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4346	16888	29251	2.76	1.0E-38	AL163203.2	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4346	16888	29252	2.76	1.0E-38	AL163203.2	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4637	17153	29333	1.08	1.0E-38	8922543	NT	Homo sapiens chromosome 21 segment HS21C003
6331	18889	31920	5.31	1.0E-38	7305360	NT	Homo sapiens chromosome 21 segment HS21C003
6331	18889	31921	5.31	1.0E-38	7305360	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
6331	18889	31921	5.31	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA

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7884	20323	33188	2.88	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9827	22042	34974	6.72	1.0E-38	BE350127.1	EST_HUMAN	h08g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
11828	24686		2.07	1.0E-38	AL163284.2	NT	MER29 repetitive element;
56	12877	25078	5.01	8.0E-39	4602312	NT	Homo sapiens chromosome 21 segment HS21C084
1426	13959	28415	1.15	8.0E-39	4758229	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1805	14328		1.64	8.0E-39	AI823404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
2018	14534	27047	5.02	7.0E-39	AL163227.2	NT	wh33110.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384481 3' similar to TR:P87880 P87890
10591	23038	36019	2.72	6.0E-39	BF331828.1	EST_HUMAN	POL PROTEIN;
10849	23380	36390	1.85	6.0E-39	BF371201.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
12474	24491		2.26	8.0E-39	BE870394.1	EST_HUMAN	QV1-BT0631-040800-357-R02 BT0631 Homo sapiens cDNA
1034	13583	26024	2.59	5.0E-39	AF003528.1	NT	RC2-FN0133-270600-012-b11 FN0133 Homo sapiens cDNA
2940	15495	27916	8.2	5.0E-39	AI750154.1	EST_HUMAN	7s34c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:161.6
12148	24279		1.72	5.0E-39	11420289	NT	CE00828;
587	13138	25648	21.87	4.0E-39	AB015810.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3582	10104	28518	0.95	4.0E-39	AL163210.2	NT	al36504.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
4508	17024		0.84	4.0E-39	AL163209.2	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT, contains LTR7.1 LTR7 repetitive element;
6114	18683	31379	0.74	4.0E-39	11422113	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
6114	18683	31380	0.74	4.0E-39	11422113	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
8689	21124	34024	0.93	4.0E-39	AA682949.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
12165	24290		3.77	4.0E-39	11418177	NT	Homo sapiens chromosome 21 segment HS21C009
12285	24379		3.2	4.0E-39	BE838462.1	EST_HUMAN	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
49	12870	25066	16.78	3.0E-39	AA631949.1	EST_HUMAN	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
49	12870	25067	16.78	3.0E-39	AA631949.1	EST_HUMAN	ae92g04.s1 Stratiene echizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
49	12870	25068	16.78	3.0E-39	AA631949.1	EST_HUMAN	OFR.b1 OFR repetitive element;
11657	23874	36550	9.5	3.0E-39	AI084557.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
							QV0-FN0063-260600-278-c08 FN0063 Homo sapiens cDNA
							fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
							fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
							fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
							ox63a10.s1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
							P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11657	23974	36551	9.5	3.0E-39	A084557.1	EST_HUMAN	cx63a10.s1 Scores_Nih-MP_u_31 Homo sapiens cDNA clone IMAGE:1660988 3' similar to SW:GTR5_RAT
11705	24007		6.52	3.0E-39	H37803.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
920	13474		8.23	2.0E-39	BE409203.1	EST_HUMAN	yp51c08.s1 Scores_ralina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'
935	13489		17.87	2.0E-39	AI625119.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
1057	13803		4.25	2.0E-39	AF000573.1	NT	prom1a-7.D01.r bitumal Homo sapiens cDNA 5'
1652	14084		13.82	2.0E-39	AW372318.1	EST_HUMAN	Homo sapiens homocitrate 1,2-dioxygenase gene, complete cds
1918	14437	26939	2.09	2.0E-39	AA720574.1	EST_HUMAN	PM0-BT0340-211299-003-402 BT0340 Homo sapiens cDNA
2560	16059	27574	3.15	2.0E-39	AL163248.2	NT	rw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
4427	16948	28338	1.63	2.0E-39	BF370207.1	EST_HUMAN	THR repetitive element ;
5751	18333	30786	5.87	2.0E-39	AA508890.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
7842	20282	33144	2.4	2.0E-39	AA080887.1	EST_HUMAN	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA
8041	20473	33347	0.82	2.0E-39	AL163202.2	NT	ng86f03.s1 NCI_CGAP_P6 Homo sapiens cDNA clone IMAGE:941693
8041	20473	33348	0.82	2.0E-39	AL163202.2	NT	zn06f02.r1 Stratagene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:646651 5'
8468	20881	33779	0.61	2.0E-39	AI538173.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
11182	23598	36841	2.88	2.0E-39	D88984.1	NT	U7509.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2137865 3' similar to TR:Q13537 Q13537
11335	23699	36752	2.2	2.0E-39	AA633972.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
11336	23699	36753	2.2	2.0E-39	AA633972.1	EST_HUMAN	Human mRNA for KIAA0209 gene, partial cds
12587	24548		5.07	2.0E-39	11425484	NT	ac73h11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868283 3'
1541	14072	26532	2.23	1.0E-39	AJ006345.1	NT	ac73h11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868283 3'
1541	14072	26533	2.23	1.0E-39	AJ006345.1	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
1553	14085	26544	4.12	1.0E-39	7657020	NT	Homo sapiens KVLQT1 gene
4704	17220	28602	8.15	1.0E-39	AW951995.1	EST_HUMAN	Homo sapiens KVLQT1 gene
4704	17220	28603	8.15	1.0E-39	AW951995.1	EST_HUMAN	Homo sapiens KVLQT1 gene
4752	17266	28647	11.34	1.0E-39	7657020	NT	Homo sapiens KVLQT1 gene
5614	18201	30598	0.97	1.0E-39	11417342	NT	Homo sapiens KVLQT1 gene
5614	18201	30599	0.97	1.0E-39	11417342	NT	Homo sapiens KVLQT1 gene
5697	18475	31155	1.18	1.0E-39	T80876.1	EST_HUMAN	Homo sapiens KVLQT1 gene
5933	18511	31196	4.98	1.0E-39	AJ278170.1	NT	Homo sapiens KVLQT1 gene

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5933	18511	31197	4.98	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X-1 (NIX1) (Nix1 gene)
7219	19831		1.74	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7837	20277	33140	2.22	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
9048	21478	34391	1.1	1.0E-39	O48530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNAse K6)
10703	23142	36124	1.62	1.0E-39	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
12086	24237		1.61	1.0E-39	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
572	13143	25551	1.72	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1268	13804	26252	10.97	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1288	13804	26253	10.97	9.0E-40	4755146	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1478	14010	26478	7.8	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Soreby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3787	16324	28725	0.71	9.0E-40	4603784	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3987	17884	28824	4.97	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
5460	17855	30305	5.02	9.0E-40	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3001	15556	27970	0.89	8.0E-40	AA078166.1	EST_HUMAN	7H15A04 Chromosome 7 Hela cDNA library Homo sapiens cDNA clone 7H15A04
3936	19471		2.7	8.0E-40	BE398541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619186 6'
8282	20679	33571	2.6	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
8282	20679	33572	2.6	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
2681	15173	27883	5.49	8.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
2681	15173	27884	5.49	8.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
6237	18801		2.32	6.0E-40	BE504768.1	EST_HUMAN	h240g01.x1 NCI_OGAP_GC8 Homo sapiens cDNA clone IMAGE:3210480 3'
6460	18018		0.92	6.0E-40	7861989	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7345	19757	32562	3.11	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7345	19757	32563	3.11	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10016	22418	35367	7.14	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
10016	22418	35368	7.14	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2531	15030	27540	8.26	6.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1847	14369	26864	1.71	4.0E-40	AI686005.1	EST_HUMAN	tt91b01.x1 NCI_OGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR-O73505 O73505 POL PROTEIN. ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2028	14545		3.75	4.0E-40	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4411	16932	28323	9.69	4.0E-40	7682117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8628	21063	33971	3.32	4.0E-40	AA742808.1	EST_HUMAN	n34e10.11 NCL CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
9382	21814	34729	6.08	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
9382	21814	34730	6.08	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10502	22851	35632	5.72	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4150	16878	28066	1.01	3.0E-40	AI825949.1	EST_HUMAN	wh1207.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2360549 3'
6808	19349	32123	0.5	3.0E-40	4508736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7003	18539	32323	7.98	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8917	21381	34267	4.03	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9320	21752	34850	1.31	3.0E-40	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9434	21915	34838	1.73	3.0E-40	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10486	22907	35886	2.32	3.0E-40	D66894.1	NT	Human mRNA for KIAA0209 gene, partial cds
11035	23482	36483	8.16	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
339	12831		4.71	2.0E-40	AI223038.1	EST_HUMAN	qg52h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
817	13375		6.6	2.0E-40	AW303888.1	EST_HUMAN	xc24e10.x1 NCL CGAP_UK4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW-RS5_MOUSE
1802	14325		1.71	2.0E-40	AV731601.1	EST_HUMAN	P97461.40S RIBOSOMAL PROTEIN S6 ;
1885	14408	26901	2.23	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1885	14408	26802	2.23	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2076	14590	27110	1	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
2638	16133		1.5	2.0E-40	BE275832.1	EST_HUMAN	601121587F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3087	16641	28049	6.17	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4969	17480	29858	1.77	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4969	17480	29859	1.77	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
906	13460		1.73	1.0E-40	AA225989.1	EST_HUMAN	nc09a08.s1 NCL CGAP_P71 Homo sapiens cDNA clone IMAGE:1007808
2652	15051	27967	2.15	1.0E-40	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863803 5'
2633	15128		1.99	1.0E-40	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z168 Q8Z168
2693	16184	27095	1.9	1.0E-40	BF541030.1	EST_HUMAN	SYNTAXIN 17 ;
							602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4087336 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2693	16184	27696	1.9	1.0E-40	BF641030.1	EST_HUMAN	602098604FT NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4067736 5'
3281	15812		2.13	1.0E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4851	17167	29547	3.45	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6577	19128	31872	0.81	1.0E-40	W92708.1	EST_HUMAN	zh78f11.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6577	19128	31873	0.81	1.0E-40	W92708.1	EST_HUMAN	zh78f11.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7524	19975	32809	2.02	1.0E-40	AA573201.1	EST_HUMAN	n42804.s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7524	19975	32810	2.02	1.0E-40	AA573201.1	EST_HUMAN	n42804.s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7881	20126	32879	0.53	1.0E-40	P28808	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
10898	23135	38117	18.78	1.0E-40	AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
12108	24820		6.16	1.0E-40	BF334112.1	EST_HUMAN	MR2-CT0222-21099-002-s10 CT0222 Homo sapiens cDNA
12219	24764		2.37	1.0E-40	AW197698.1	EST_HUMAN	xn87a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701424 3' similar to
3810	16347	28748	0.65	9.0E-41	W01588.1	EST_HUMAN	SWESTN_MOUSE P23953 LIVER CARBOXYESTERASE PRECURSOR;
8577	21012	33912	1.51	8.0E-41	AL163203.2	NT	za38a02.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294602 5'
851	15295	29851	1.38	7.0E-41	A834364.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
851	15295	29852	1.38	7.0E-41	A834364.1	EST_HUMAN	wp04h04.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5414	17910	30261	4.48	7.0E-41	11431114	NT	wp04h04.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5515	18105	30349	1.06	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6312	18873	31589	3	7.0E-41	11418208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6684	19232	31982	0.77	7.0E-41	11493010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7411	18080	30373	0.82	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11183	23599	35842	3.31	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
12579	24817		10.77	7.0E-41	11417072	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
294	12890	26311	0.94	6.0E-41	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2032	14648	27062	2.36	6.0E-41	7857042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4499	17017	29389	1.52	6.0E-41	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682977 5'
5137	17641	30004	0.95	6.0E-41	4504084	NT	Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), nuclear gene encoding mitochondrial protein, mRNA
8610	21045	33950	1.18	6.0E-41	BF513783.1	EST_HUMAN	UI-H-BW1-amp-B-03-O-UJ.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
6889	19439		2.64	6.0E-41	BE087042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
406	12982		1.83	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g08 HT0367 Homo sapiens cDNA
1125	13689	26108	2.82	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1441	13973	26430	7.06	4.0E-41	A1027117.1	EST_HUMAN	qw45e08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE. ;contains LTR6.b1 LTR5 repetitive element ;
1441	13973	26431	7.06	4.0E-41	A1027117.1	EST_HUMAN	qw45e08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE. ;contains LTR6.b1 LTR5 repetitive element ;
1454	13986	26448	1.59	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1643	14174	26643	5.51	4.0E-41	A1600406.1	EST_HUMAN	tm96c04.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2166958 3' similar to contains ORF.b1 OFR repetitive element ;
2642	15388	27813	3.81	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2842	15398	27814	3.81	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4163	16680	28076	2.36	4.0E-41	X92686.1	NT	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
6859	19389		1.78	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
6830	22233	35169	5.94	4.0E-41	BF304683.1	EST_HUMAN	60188096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11408	23707		7.37	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAAC007 5'
12309	24700		1.37	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
12507	24511	30856	2.14	4.0E-41	BE897118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910069 5'
12550	24815		1.24	4.0E-41	AJ132362.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
971	13524	25987	1.83	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4356	16880	26263	2.88	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5258	17759		1.09	3.0E-41	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5752	18334	30787	10.3	3.0E-41	X87889.1	NT	H. sapiens mRNA for putative p64 CLCP protein
6715	19281	32018	0.84	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7711	20156	33015	0.71	3.0E-41	AA335198.1	EST_HUMAN	EST64683 Jurkat T-cells VI Homo sapiens cDNA 5' end
8354	20769	33665	0.82	3.0E-41	R64765.1	EST_HUMAN	y75d08.t1 Soares breast 2NHb1st Homo sapiens cDNA clone IMAGE:164575 5'
11616	23947		1.65	3.0E-41	AA609768.1	EST_HUMAN	af17710.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'
1801	14113	26580	18.84	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1907	14426	26923	1.46	2.0E-41	AA331940.1	EST_HUMAN	EST355819 Embryo, 8 week I Homo sapiens cDNA 5' end
2124	14637	27162	1.83	2.0E-41	D66962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2170	14681	27206	3.36	2.0E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2766	14113	26580	8.3	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3297	15846	28264	0.64	2.0E-41	AA449549.1	EST_HUMAN	z08b04.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:765839 5'
4655	17181	28560	1.03	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4665	17181	29561	1.03	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
5802	19382	31042	0.59	2.0E-41	AA584575.1	EST_HUMAN	nc12c07.e1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb:X52851_mai
6988	19525	32308	0.85	2.0E-41	4504778	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
8027	20459	33334	0.44	2.0E-41	11439575	NT	Homo sapiens Integrin, beta 8 (ITGB8) mRNA
8209	20629	33518	7.5	2.0E-41	AF038404.1	NT	Homo sapiens tylophatan hydroxylase (tylophatan 5-monooxygenase) (TPH), mRNA
8472	20885	33783	0.54	2.0E-41	11422047	NT	Homo sapiens homolog of Nedd6 (hNedd6) mRNA, complete cds
8684	21119	34021	1.57	2.0E-41	M86844.1	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCEL), mRNA
8684	21119	34022	1.57	2.0E-41	M86844.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8701	21136	34040	1.46	2.0E-41	AA328265.1	EST_HUMAN	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
9324	21756	34664	1.51	2.0E-41	P52742	SWISSPROT	EST31723 Embryo, 12 week 1 Homo sapiens cDNA 5' and
3163	15716	28137	1.18	1.0E-41	BE869735.1	EST_HUMAN	ZINC FINGER PROTEIN 135
4603	17119	29508	10.81	1.0E-41	6878468	NT	ZINC FINGER PROTEIN 135
7246	18020	30435	0.58	1.0E-41	H99079.1	EST_HUMAN	801445947F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
9833	22048	34979	1.62	1.0E-41	AI217868.1	EST_HUMAN	801445947F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
11757	24037		2.43	1.0E-41	11526291	EST_HUMAN	801445947F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
9013	21448		1.14	9.0E-42	BE179191.1	EST_HUMAN	Mus musculus tubulin alpha 6 (Tuba6), mRNA
9457	21888	34808	3.13	9.0E-42	11560151	NT	yx18b03.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262081 3'
9457	21888	34809	3.13	9.0E-42	11560151	NT	q75c10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1756858 3'
480	13054	25471	6.47	8.0E-42	AF003530.1	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
2030	14546	27060	2.1	8.0E-42	AB026898.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
11802	24824		31.76	8.0E-42	AA493898.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
956	13508		2.64	7.0E-42	AL163286.2	NT	h07c02.e1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304
9507	23170	34893	1.43	7.0E-42	AI204358.1	EST_HUMAN	387BP EXPRESSED SEQUENCE TAG MRNA;
10947	23378	36387	2.88	7.0E-42	AA569592.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
10947	23378	36388	2.88	7.0E-42	AA569592.1	EST_HUMAN	q158g12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
11258	23622		1.64	7.0E-42	AA840580.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
1827	14349	26846	3.67	6.0E-42	AF012872.1	NT	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
1827	14349	26847	3.67	6.0E-42	AF012872.1	NT	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
2184	14695		1.82	6.0E-42	AW238656.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1206635
							Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
							Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
							rp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.1 L1 repetitive element;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5726	18308	30739	1.69	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
5891	18308	30739	1.73	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
140	12746		6.4	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
455	13030	25452	1.63	5.0E-42	BE217913.1	EST_HUMAN	h31e11.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3176052 3'
604	13078		3.8	5.0E-42		NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
505	13078		2.29	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7058	19560	32384	0.98	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
7058	19560	32385	0.98	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
7180	18900	32728	2.52	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7847	20093	32945	1.52	5.0E-42	AF071699.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
8413	20827	33725	0.55	5.0E-42	4826977	NT	Homo sapiens reelin (RELN) mRNA
8520	20931	33828	0.42	5.0E-42	114377174	NT	Homo sapiens hypothetical protein FLJ20647 (FLJ20647), mRNA
8198	21630	34539	3.53	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10779	23217	36200	2.54	5.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
11602	23860	36936	1.77	5.0E-42	X98411.1	NT	H.sapiens mRNA for myosin-IE
11502	23860	36937	1.77	5.0E-42	X98411.1	NT	H.sapiens mRNA for myosin-IE
774	13334	25767	27.25	4.0E-42	AF055068.1	NT	Homo sapiens MHC class 1 region
774	13334	25768	27.25	4.0E-42	AF055068.1	NT	Homo sapiens MHC class 1 region
1092	13637	26076	1.44	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4210	16735	28126	1.37	4.0E-42	X59417.1	NT	H.sapiens PROS-27 mRNA
4265	16790	29174	5.88	4.0E-42	4506498	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4622	17138	29520	15.26	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5344	17843	30201	1.25	4.0E-42	7661635	NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
5107	17615	29977	4.78	3.0E-42	T09068.1	EST_HUMAN	EST06961 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBO66 5' end
1611	14043	26510	3.61	2.0E-42	BF376834.1	EST_HUMAN	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2290	14797	27315	3.31	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKCCBB08 5'
2312	14816		2.7	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2326	14833	27347	12.47	2.0E-42	AW260059.1	EST_HUMAN	2819283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819283 3'
6035	18609	31286	12.02	2.0E-42	AW955368.1	EST_HUMAN	EST367438 IMAGE resequences, MAGC Homo sapiens cDNA
6036	18609	31297	12.02	2.0E-42	AW955368.1	EST_HUMAN	EST367438 IMAGE resequences, MAGC Homo sapiens cDNA
6837	19378	32154	0.53	2.0E-42	M29145.1	NT	Human hepatocyte growth factor (hHGF) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7133	19668	32460	1.14	2.0E-42	AI052586.1	EST_HUMAN	cx63405.x1 Scarsa_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1653417 3'
9925	22327	35274	1.1	2.0E-42	BE538919.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
764	13313	25742	1.73	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1067	13613	26055	3.8	1.0E-42	AW296809.1	EST_HUMAN	U1-H-B11-afh-a-04-Q.U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1128	13672	26111	1	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1128	13672	26112	1	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1275	15305	26284	15.88	1.0E-42	AF067168.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1275	15305	26265	15.88	1.0E-42	AF067168.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1697	14226	26707	1.02	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2455	14957	27470	7.05	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2817	15472	27895	10.02	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3705	16246	28650	2.51	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3787	16334	28736	0.82	1.0E-42	5031810	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
3938	16473	28882	1.27	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4262	16787	29172	3.63	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4633	17149	29529	0.63	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA
4798	17312	29691	2.31	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4798	17312	29692	2.31	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4831	17343	29726	6.61	1.0E-42	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4930	17441	29818	2.21	1.0E-42	AB033114.1	NT	Homo sapiens mRNA for KIAA1288 protein, partial cds
5048	17558	29927	0.63	1.0E-42	Z46120.1	EST_HUMAN	HSCOFF071 normalized infant brain cDNA Homo sapiens cDNA clone c-0ff07
10104	22505	35469	4.77	8.0E-43	4757069	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
671	13236	25648	17.64	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
671	13236	25649	17.64	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
720	13281	25703	5.37	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
720	13281	25704	5.37	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
720	13281	25705	5.37	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
6989	18545	31230	5.2	8.0E-43	H13952.1	EST_HUMAN	J08611.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3940	16180	26588	10.08	7.0E-43	AW246442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
8180	21822		2.96	7.0E-43	AJ938748.1	EST_HUMAN	wp89b01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O16475 O15475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element ;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1376	13910		6.4	6.0E-43	AA491890.1	EST_HUMAN	ne72d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:998803 similar to gb:L05085 60S
2514	15015		3	6.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN); AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
6639	19187	31638	2.73	6.0E-43	9955973	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
7316	19728	32532	2.36	6.0E-43	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910891 3' similar to contains MER1.k3 MER1 MER1 repetitive element ;
9832	22334	36282	2.25	6.0E-43	AA195154.1	EST_HUMAN	z35e08.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:685410 5' similar to TR:G529841
147	12752		2.41	5.0E-43	AL163213.2	NT	G529841 DB1, COMPLETE CDS, contains element PTR7 repetitive element ;
520	13093	25506	3.55	6.0E-43	AA382780.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2802	16359	27777	1.53	6.0E-43	AV732578.1	EST_HUMAN	EST86033 Testis I Homo sapiens cDNA 5' end
6633	19722	32524	1	6.0E-43	AI613508.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC08 5'
7310	19722	32524	0.75	6.0E-43	AI613508.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260452 3'
9595	22075	35000	3.85	6.0E-43	AA465288.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260452 3'
10302	22702	35687	2.36	6.0E-43	AI73244.1	EST_HUMAN	aa33d08.r1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:815055 5'
10328	22728	35685	1.3	5.0E-43	AL049110.1	EST_HUMAN	cc52e10.x6 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P00591 P00591 PV14 GENE. ;
10346	22983	35975	7.28	5.0E-43	AW8663007.1	EST_HUMAN	DKFZp434D0119.J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0119
10751	23189	36175	8.13	5.0E-43	W29011.1	EST_HUMAN	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
11209	22861	36835	4.19	5.0E-43	X15804.1	NT	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA Human mRNA for alpha-actinin
897	15260	25892	4.15	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6609	18100	30343	1.14	4.0E-43	AI056338.1	EST_HUMAN	cy47h03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1669013 3'
6702	19249	32000	0.7	4.0E-43	6996009	NT	Homo sapiens glycyl-RNA synthetase (GARS), mRNA
7570	20020		1.78	4.0E-43	11416793	NT	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
8761	21195	34097	5.72	4.0E-43	AI244341.1	EST_HUMAN	q76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element ;
8761	21195	34098	5.72	4.0E-43	AI244341.1	EST_HUMAN	q76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element ;
10250	22651	35614	1.46	4.0E-43	6005967	NT	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
11073	23498	36526	1.68	4.0E-43	T77380.1	EST_HUMAN	y472h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113827 5'
11732	24022		3.94	4.0E-43	R20950.1	EST_HUMAN	yq08b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element ;

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Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1244	13782		3.46	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1693	14222	26702	1.71	3.0E-43	X97869.1	NT	H. sapiens gene encoding La autoantigen
3561	16103	28517	1.4	3.0E-43	S69002.1	NT	AML1-EV1-1-AML1-EV1-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4307	16832	29221	0.94	3.0E-43	AA548164.1	EST_HUMAN	hK55d06.s1 NCL_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
5606	18194	30558	0.6	3.0E-43	M56259.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 6
5606	18194	30559	0.6	3.0E-43	M56259.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 6
6184	18751	31451	1.44	3.0E-43	D34613.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6689	19237	31988	1.61	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6689	19237	31987	1.61	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
7105	19638	32433	4.47	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8748	21182		5.44	3.0E-43	AA458824.1	EST_HUMAN	ea88f1.1 s1 Stragene fetal retina 637202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element ;
9230	21682	34571	1.19	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
188	12780		10.85	2.0E-43	A1180794.1	EST_HUMAN	qd61c08.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1733988 3' similar to contains PTR7.13
6821	19362	32138	1.25	2.0E-43	BE222778.1	EST_HUMAN	PTR7 PTR7 repetitive element ;
6821	19362	32139	1.25	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCL_CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element ;
7730	20174	33033	1.27	2.0E-43	AW207390.1	EST_HUMAN	hu53a08.x1 NCL_CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element ;
8858	21292		6.02	2.0E-43	U43701.1	NT	UL-H-B1-af1-a-09-Q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
10973	23402		3.84	2.0E-43	T03007.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
1654	14185	26658	5.64	1.0E-43	AF154838.1	NT	FB1G5 Fetal brain, Stragene Homo sapiens cDNA clone FB1G5 3'end similar to LINE-1
1654	14185	26657	5.54	1.0E-43	AF154838.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1703	14231	26716	1.94	1.0E-43	AL163284.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2677	15170	27678	3.48	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5666	18251	30652	0.73	1.0E-43	4885644	NT	60202315F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4167668 5'
6967	19504	32282	6.87	1.0E-43	4507168	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6967	19504	32283	6.87	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
7382	18052	30360	1.17	1.0E-43	R19751.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4) mRNA
8586	21021	33922	1.71	1.0E-43	AF176265.1	NT	y840e01.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to SP-BD38 MOUSE P28656 BRAIN PROTEIN DN38 ;
							Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8682	21117		3.89	1.0E-43	AF188490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
9241	21673	34983	33.19	1.0E-43	AW983976.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
10744	23182	36167	3.7	1.0E-43	AI984961.1	EST_HUMAN	wr87h01.x1 NCI_CGAP_K1a11 Homo sapiens cDNA clone IMAGE:2494706 3'
11123	23576	36817	4.65	1.0E-43	11424378	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
11670	23983		3.59	1.0E-43	AL137984.1	EST_HUMAN	DKFZp761D1015_1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1015 5'
11976	24170	30979	3.1	1.0E-43	AI875416.1	EST_HUMAN	wb98b04.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2313778 3'
12213	24328	30920	3.38	9.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
913	13487	25915	7.32	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
913	13487	25916	7.32	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
9028	21460	34369	2.5	8.0E-44	X94394.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10941	23373	36383	3.12	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
11418	23779	36840	2.17	8.0E-44	L29139.1	NT	Homo sapiens myosin mRNA, partial cds
11928	24144	30973	3.44	8.0E-44	11527389	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
11970	24525	30860	2.38	8.0E-44	11418088	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12357	24723	30872	2.47	8.0E-44	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12628	24626	30860	1.81	8.0E-44	11418088	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
878	13243		1.61	7.0E-44	R06035.1	EST_HUMAN	yes9e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124920 5'
2142	14655	27179	1.12	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2919	15474	27896	2.3	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2919	15474	27897	2.3	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3688	16404	28808	3.31	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4258	16783	29168	1.04	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4258	16783	29167	1.04	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
8768	21200	34101	4.42	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
6412	18669	31705	0.72	6.0E-44	Z20946.1	EST_HUMAN	HSAAADEVUP, Human foetal Brain Whole tissue Homo sapiens cDNA
317	12912		2.87	6.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZ1FL1 gene
346	12936		2.21	6.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZ1FL1 gene
8553	20988	33986	3.92	6.0E-44	AI568523.1	EST_HUMAN	ln40d02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
3392	19338	28350	2.48	4.0E-44	AL163303.2	NT	OFR OFR repetitive element
5116	17623		1.06	4.0E-44	AI435225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7970	20408	33276	0.64	4.0E-44	BE883178.1	EST_HUMAN	ft11d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
11004	23432	36450	27.79	4.0E-44	U90878.1	NT	601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
2437	14939	27456	1.03	3.0E-44	BE880626.1	EST_HUMAN	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3058	15813	28022	6.16	3.0E-44	AA168851.1	EST_HUMAN	zp18b06.t1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
8356	20771	33668	0.67	3.0E-44	BE884820.1	EST_HUMAN	601510547F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
9706	22129	36056	0.83	3.0E-44	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1075	13621	26060	4.8	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1075	13621	26061	4.8	2.0E-44	4826688	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1238	13776	26223	2.68	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1238	13776	26224	2.68	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1344	13879	26334	5.23	2.0E-44	AF133588.1	NT	Homo sapiens RAB39 (RAB39) mRNA, complete cds
1401	13935	26391	1.37	2.0E-44	BE465325.1	EST_HUMAN	hw14g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW:OXYB_HUMAN
2063	14578	27098	3.42	2.0E-44	AF070651.1	NT	P22059 OXYSTEROL-BINDING PROTEIN ;
2450	14951		9.16	2.0E-44	4507592	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2539	15037		2.68	2.0E-44	5901933	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
3446	15990	28409	1.32	2.0E-44	D87875.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
4607	17123	28508	2.68	2.0E-44	AW884379.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
6403	18980	31695	1.61	2.0E-44	11449601	NT	P1M4-SN0016-120500-003-e04 SN0016 Homo sapiens cDNA
7042	19577	32368	0.44	2.0E-44	AF182034.1	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
7258	18030	30413	2.39	2.0E-44	AF038968.1	NT	Homo sapiens polyomavirus kidney disease-like 2 protein (PKDL2) mRNA, complete cds
7895	20334	33201	3.7	2.0E-44	11419226	NT	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, alternatively spliced product, complete cds
7895	20334	33202	3.7	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
9081	21513	34422	2.45	2.0E-44	BE389058.1	EST_HUMAN	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
11571	23916		1.82	2.0E-44	BE244902.1	EST_HUMAN	601286914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813886 5'
12460	24480	30877	2.77	2.0E-44	8567387	NT	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2785
12548	24538		1.71	2.0E-44	11528293	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
54	12676	25076	6.64	1.0E-44	7657334	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
54	12676	25076	6.64	1.0E-44	7657334	NT	Homo sapiens Missheper/NIK-related kinase (MINK), mRNA
597	13168	25570	2.09	1.0E-44	AW853132.1	EST_HUMAN	Homo sapiens Missheper/NIK-related kinase (MINK), mRNA
1228	13767		1.46	1.0E-44	AW994803.1	EST_HUMAN	RC1-CT0249-030300-026-h12 CT0249 Homo sapiens cDNA
1591	14123		4.89	1.0E-44	AL163303.2	NT	RC1-BN0039-110300-012-501 BN0039 Homo sapiens cDNA
2130	14643	27168	5.09	1.0E-44	AA434554.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103 zw53402.t1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.k3 THR repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2130	14843	27167	5.09	1.0E-44	AA434554.1	EST_HUMAN	zw63d02.r1 Soares_tetal_fetus_Nh2HF8_0w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.3 THR repetitive element;
2718	15208	27724	2.83	1.0E-44	AF198778.1	NT	Homo sapiens transcription factor IGIM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3724	16284		5.28	1.0E-44	AA455869.1	EST_HUMAN	aa01c08.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811884 3'
5270	17771	30138	0.64	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5270	17771	30139	0.84	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8825	21259	34164	1.02	1.0E-44	AW987073.1	EST_HUMAN	EST378147 MAGE resequences, MAGJ Homo sapiens cDNA
8825	21259	34165	1.02	1.0E-44	AW987073.1	EST_HUMAN	EST378147 MAGE resequences, MAGJ Homo sapiens cDNA
9100	21532	34441	0.97	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10793	23231		3.28	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
11286	23651	36639	3.74	1.0E-44	10092664	NT	Homo sapiens Sushi domain (SCR repeat) containing (BK65A6.2), mRNA
11339	23703	36756	2.95	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150399-011-C08 CT0198 Homo sapiens cDNA
11339	23703	36757	2.95	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150399-011-C08 CT0198 Homo sapiens cDNA
7013	19549	32335	1.42	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2429	14932	27447	4.38	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
6212	17715	30080	8.49	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8708	21143	34047	1.09	8.0E-45	AA377885.1	EST_HUMAN	EST90893 Synovial sarcoma Homo sapiens cDNA 5' and
3992	16526		5.77	6.0E-45	AW157570.1	EST_HUMAN	au63h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
12319	24936		1.75	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
915	13489		2.45	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1945	14484	26988	4.59	6.0E-45	BF33627.1	EST_HUMAN	GM4-CN0044-180200-615-f01 CN0044 Homo sapiens cDNA
3168	15721	28143	2.42	5.0E-45	A1523766.1	EST_HUMAN	tg94f07.x1 NCJ_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2118453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1;
5774	18355	30814	9.5	5.0E-45	AA397781.1	EST_HUMAN	z72d03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element;
6323	18883	31612	1.27	6.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6323	18883	31613	1.27	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6371	18929	31684	0.99	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for Inducible nitric oxide synthase, complete cds
6371	18929	31685	0.99	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for Inducible nitric oxide synthase, complete cds
6503	19057	31789	0.76	5.0E-45	11490288	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6503	19057	31800	0.76	5.0E-45	11490288	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8833	21267	34173	0.84	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9370	21802	34711	1.71	5.0E-45	4760223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
11423	23784	36845	3.33	5.0E-45	8923698	NT	Homo sapiens golgi-like protein (GLP), mRNA
1171	13713	26153	8.81	4.0E-45	X95926.1	NT	H. sapiens ART4 gene
2166	14697	27217	1.54	4.0E-45	BE265622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
9312	21744		0.92	4.0E-45	AA228220.1	EST_HUMAN	nc26e07.s1 NC1_CGAP_P1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element;
11586	24874	30572	1.53	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
12205	24322		1.35	4.0E-45	BF676077.1	EST_HUMAN	602084052F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248253 5'
3302	15850		1.34	3.0E-45	T71480.1	EST_HUMAN	Yd35f07.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
4103	15850		2.23	3.0E-45	T71480.1	EST_HUMAN	Yd35f07.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
6557	19109	31853	1.31	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
6557	19109	31854	1.31	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
8964	21397		1.59	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
9207	21639	34548	4	3.0E-45	4759451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10244	22645	35609	10.82	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10244	22645	35610	10.82	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12443	24868		2.91	3.0E-45	X98211.1	NT	H. sapiens DNA for endogenous retroviral like element
2409	14913		1.57	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
2991	15546	27968	0.99	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6872	19412	32187	4.48	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysochospholipase) gene, promoter and exon 1
8137	20660	33438	1.15	2.0E-45	BE782184.1	EST_HUMAN	601467793F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'
8942	21375	34288	0.89	2.0E-45	AW834834.1	EST_HUMAN	RC0-L10001-150200-032-d11 L10001 Homo sapiens cDNA
10585	24656	36015	16.81	2.0E-45	BE934350.1	EST_HUMAN	MRO-HT0923-190800-201-e02 HT0923 Homo sapiens cDNA
10951	23381	36391	4.63	2.0E-45	AA458770.1	EST_HUMAN	ea87f12.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
12491	24500		2.16	2.0E-45	11418157	NT	TR:G1144568 G1144568 R-SLY1.;
128	13000		1.28	1.0E-45	BE389855.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
426	13000		2.04	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
490	13063	25483	1.44	1.0E-45	4506412	NT	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
1205	13746	28191	2.05	1.0E-45	7657280	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
3064	15618	28028	8.97	1.0E-45	U32169.1	NT	Homo sapiens Langerhans cell specific o-type lectin (LANGERIN), mRNA
3468	16012	28434	1.19	1.0E-45	8659558	NT	Human pro- $\alpha 2$ chain of collagen type XI (COL11A2) gene, complete cds
						NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3593	16105	28519	0.93	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
4512	17030	29409	5.92	1.0E-45	BE396833.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3618803 5'
5057	17587	29935	1.06	1.0E-45	11645796	NT	Homo sapiens ribon protein (NIBAN), mRNA
9075	21507	34416	0.84	1.0E-45	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9423	21855	34771	4.63	1.0E-45	BE887843.1	EST_HUMAN	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
9709	22132	35058	1.09	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0289 gene, partial cds
11798	24061	31028	6.73	1.0E-45	11418089	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
11887	24180		8.05	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
11993	24183		6.2	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12451	24475	30876	3.37	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
8799	21233	34141	2.45	9.0E-46	8910283	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
9093	21525		6.55	9.0E-46	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
10382	22782	35730	7.7	9.0E-46	AW246984.1	EST_HUMAN	2822449.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2342	14847	27384	6.04	8.0E-46	AI433261.1	EST_HUMAN	1032108.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
2342	14847	27385	6.04	8.0E-46	AI433261.1	EST_HUMAN	1032108.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
8672	21107		3.92	8.0E-46	BE167244.1	EST_HUMAN	RC5-HT0508-280200-012-C12 HT0508 Homo sapiens cDNA
4618	17134		7.85	7.0E-46	BE396185.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4884	17376		1.24	7.0E-46	BE084386.1	EST_HUMAN	RC4-BT0310-110300-016-f10 BT0310 Homo sapiens cDNA
6348	18908	31639	3.97	7.0E-46	8922708	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
6843	19384	32159	1.41	7.0E-46	BF105845.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
12132	24266		1.67	7.0E-46	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2712	15202	27718	3.59	6.0E-46	AI884381.1	EST_HUMAN	WM31f08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
2712	15202	27719	3.59	6.0E-46	AI884381.1	EST_HUMAN	MER19 repetitive element;
6442	18998	31730	11.85	6.0E-46	AI635448.1	EST_HUMAN	WM31f08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
7684	20110	32961	0.7	8.0E-46	AW513244.1	EST_HUMAN	165810.x1 NCI_CGAP_K18 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363
7857	20287	33162	0.62	6.0E-46	BF509740.1	EST_HUMAN	SA GENE.;
210	12813		6.48	5.0E-46	AL163210.2	NT	xc42604.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2706054 3' similar to gb:L08069 DNAJ
3510	16053	28474	1.38	5.0E-46	BE577194.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
							UI-H-B14-epg-b-06-Q-U1.x1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087298 3'
							Homo sapiens chromosome 21 segment HS21C010
							7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3510	16053	28476	1.38	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408.3'
7114	19847	32443	1.84	5.0E-46	BF690442.1	EST_HUMAN	nas38107.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258767.3' similar to TR:O75202
7352	19809	32621	4.25	5.0E-46	BF347228.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
7534	19984	32819	0.69	5.0E-46	AW582253.1	EST_HUMAN	602021164F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670.5'
7862	20301	33167	0.87	5.0E-46	BE549744.1	EST_HUMAN	QV4-ST0212-120100-076-109 ST0212 Homo sapiens cDNA
660	13225		2.31	4.0E-46	AA601143.1	EST_HUMAN	7b38b05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481.3'
1701	14229	26711	2.6	4.0E-46	AW770544.1	EST_HUMAN	nc54609.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520.3' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1701	14229	26712	2.5	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836.3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
2696	15187	27699	10.89	4.0E-46	M18048.1	NT	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008838.3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
4445	16965	29351	0.95	4.0E-46	AB014522.1	NT	Human endogenous retrovirus RTVL-H2
4445	16965	29352	0.95	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0822 protein, partial cds
5693	18278	30700	2.52	4.0E-46	M36862.1	NT	Homo sapiens mRNA for KIAA0822 protein, partial cds
5693	18278	30701	2.52	4.0E-46	M36862.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12264	24360	30903	1.77	4.0E-46	AB002059.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
2068	14583	27101	5.26	3.0E-46	6453620	NT	Homo sapiens DNA for Human P2XM, complete cds
2182	14693	27216	1.47	3.0E-46	7657203	NT	Homo sapiens solute carrier family 35 (CMP-sialic acid transporter), member 1 (SLC35A1), mRNA
4828	17340	29721	1.7	3.0E-46	Z73660.1	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
4828	17340	29722	1.7	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
9174	21606	34516	9.23	3.0E-46	AB81462.1	EST_HUMAN	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
11321	23685	36734	2.63	3.0E-46	D31765.1	NT	wf49c04.x1 NCL_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2406160.3' similar to contains THR.b2 THR repetitive element;
860	13416	26861	10.12	2.0E-46	AA468646.1	EST_HUMAN	Human mRNA for KIAA0061 gene, partial cds
1582	14114		1.17	2.0E-46	AA678246.1	EST_HUMAN	ne08a09.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408.3' similar to contains THR.b2 THR repetitive element;
1648	14179	26848	2.94	2.0E-46	U78027.1	NT	z127a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431896.3'
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6070	17580	29947	1.03	2.0E-46	AA398286.1	EST_HUMAN	z569d02.1 Scores_testie_NHT Homo sapiens cDNA clone IMAGE:728650 5' similar to SW:RSP1_MOUSE
7985	20420	33287	8.5	2.0E-46	9910569	NT	Q01730 RSP-1 PROTEIN ;
8885	21120		1.89	2.0E-46	BF5869151.1	EST_HUMAN	Mus musculus sperm tail associated protein (Stap), mRNA
11715	24828		1.4	2.0E-46	BF028854.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849287 5'
11880	24716		1.18	2.0E-46	H483991.1	EST_HUMAN	601765225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3897326 5'
12018	24195		1.21	2.0E-46	AA001786.1	EST_HUMAN	y324001.1 Scores_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:206977 5'
12342	24709	30780	4.33	2.0E-46	AW277214.1	EST_HUMAN	z184f12.1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1266	13802	26251	7.44	1.0E-46	4502694	NT	xq78h03.x1 NCL_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
2178	14690	27214	2.65	1.0E-46	AW978516.1	EST_HUMAN	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2298	14805	27323	2.04	1.0E-46	H97330.1	EST_HUMAN	EST3908255 MAGC resequences, MAGP Homo sapiens cDNA
3208	15780	28178	3.41	1.0E-46	AA631912.1	EST_HUMAN	EST485095 WATM1 Homo sapiens cDNA clone 485095
4933	17444		3.13	1.0E-46	AB023197.1	NT	np78b02.s1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens
5970	18546	31231	5.02	1.0E-46	BF194707.1	EST_HUMAN	MT-11 mRNA. (HUMAN);
6278	24605	31557	5.96	1.0E-46	8923762	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
6278	24605	31558	5.96	1.0E-46	8923762	NT	7c62b01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'
6989	19506	32286	0.77	1.0E-46	BF198247.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272185), mRNA
8377	20791	33690	0.43	1.0E-46	Z12341.1	NT	Homo sapiens centaurin-alpha 2 protein (HSA272185), mRNA
10644	18546	31231	4.7	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272185), mRNA
10922	23364	36363	1.94	1.0E-46	AJ245621.1	NT	Homo sapiens centaurin-alpha 2 protein (HSA272185), mRNA
11747	24030	31016	1.73	1.0E-46	BF531102.1	EST_HUMAN	7c62b01.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element
11747	24030	31018	1.73	1.0E-46	BF531102.1	EST_HUMAN	MER22 repetitive element ;
12571	24653		2.04	1.0E-46	AV715377.1	EST_HUMAN	H.sapiens germline lg H-chain V-region (DP-41)
768	13346		3.49	9.0E-47	AJ271735.1	NT	7c62b01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'
5011	17521	28886	3.07	9.0E-47	AW770928.1	EST_HUMAN	Homo sapiens CTL2 gene
6710	19257	32011	0.82	9.0E-47	11425439	NT	602072284F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
12281	24816	30586	1.59	9.0E-47	11417896	NT	602072264F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
1784	14309	26789	102.74	8.0E-47	Y18536.1	NT	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
1784	14309	26800	102.74	8.0E-47	Y18536.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2259	14767	27287	8.16	8.0E-47	8923898	NT	HYPOTHETICAL 12.4 KD PROTEIN ;
							Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
							Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
							Homo sapiens HLA-C gene, exon 5, individual 19323
							Homo sapiens HLA-C gene, exon 5, individual 19323
							Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2669	16162	27673	1.74	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2682	15537	27654	1.78	8.0E-47	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3621	16161	28571	0.63	8.0E-47	AB041928.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
3621	16161	28572	0.63	8.0E-47	AB041928.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
12371	24705		1.41	7.0E-47	AV683284.1	EST_HUMAN	AV683284 GSK Homo sapiens cDNA clone GKCASH11 5'
2459	14961	27472	2.21	6.0E-47	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
9533	21948	34871	6.91	6.0E-47	A1695189.1	EST_HUMAN	tz98h02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2266659 3'
9930	19469	32247	6.13	5.0E-47	11423972	NT	Homo sapiens CDC37 (Cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
10577	23024		5.58	5.0E-47	M76590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
1432	13984	26421	2.6	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
7225	19937	32854	0.95	4.0E-47	BE93896.1	EST_HUMAN	MR4-TN0108-280800-201-d04 TN0108 Homo sapiens cDNA
8988	21421	34332	2.61	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8988	21421	34333	2.61	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
11383	23745		4.58	4.0E-47	AW515509.1	EST_HUMAN	xx68b07.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT8_MOUSE
561	13133	26544	2.79	3.0E-47	BE907634.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
561	13133	26545	2.79	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
841	13398	26837	6.44	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
869	13522	26966	11.76	3.0E-47	AL163284.2	NT	y64b04.s1 Soares_multiple_sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:277327 3'
1664	14482	26991	1.15	3.0E-47	AB007898.1	NT	Homo sapiens chromosome 21 segment HS21C084
3268	15817	26234	0.81	3.0E-47	4504116	NT	Homo sapiens KIAA0439 mRNA, partial cds
3680	16515		5.81	3.0E-47	U93181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
6318	18877	31602	4.84	3.0E-47	AW408800.1	EST_HUMAN	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
6318	18877	31603	4.84	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6917	19456		1.71	3.0E-47	A1222413.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7956	20266	33160	0.74	3.0E-47	A1819755.1	EST_HUMAN	q04e07.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
7956	20266	33161	0.74	3.0E-47	A1819755.1	EST_HUMAN	wj11h08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
152	12757	25175	1.65	2.0E-47	4505318	NT	wj11h08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
992	13644	25996	2.07	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
992	13544	25997	2.07	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1610	14141	26610	1.41	2.0E-47	7662109	NT	Homo sapiens chromosome 21 segment HS21C009
1677	14207	26683	3.38	2.0E-47	AA524514.1	EST_HUMAN	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
2140	14653	27175	5.7	2.0E-47	AF060568.1	NT	hg43h12.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:937607 3'
							Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4369	16891	29272	2.16	2.0E-47	4504866	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4408	16928	29316	1.66	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4408	16928	29317	1.66	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4544	17061	29444	2.37	2.0E-47	5174848	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
6066	18638	31332	0.98	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
6277	18840	31555	1.55	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3887487 5'
6277	18840	31556	1.55	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3887487 5'
8238	24846		1.24	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
9148	21680	34486	1.69	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9697	22099	35027	1.08	2.0E-47	11526136	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
11225	22877	35853	2.38	2.0E-47	M76125.1	NT	Human tyrosine kinase receptor (axl) mRNA, complete cds
11783	24863	30568	2.45	2.0E-47	R42423.1	EST_HUMAN	yf92508.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:29868 3' similar to contains ORF repetitive element;
1437	13969	28424	3.93	1.0E-47	A1333429.1	EST_HUMAN	qp98h03.x1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:1831189 3'
2660	15183	27665	2.54	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
3831	16368	28766	0.68	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3831	16368	28767	0.68	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5205	17708	30072	2.58	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
7473	19877	32473	6.21	1.0E-47	AI880886.1	EST_HUMAN	at19e06.x1 Barsstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22895
9265	21697		3.46	1.0E-47	AW864648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10275	22676	35638	2.1	1.0E-47	L30115.1	NT	h184a11.x1 Soares NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to gb:M28328
1626	14157	26626	2.93	9.0E-48	AF223391.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
3542	16084	28503	1.09	9.0E-48	BF359947.1	EST_HUMAN	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
5949	18525	31208	0.89	9.0E-48	BE888196.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5949	18525	31209	0.89	9.0E-48	BE888196.1	EST_HUMAN	spliced
6409	18966	31702	0.68	9.0E-48	AI833168.1	EST_HUMAN	CN2-MT0100-310700-290-05 MT0100 Homo sapiens cDNA
8543	18095	31838	0.77	9.0E-48	AU123240.1	EST_HUMAN	CM2-MT0100-310700-290-05 MT0100 Homo sapiens cDNA
10897	23329	36330	3.28	9.0E-48	BE36813.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
1283	13819		1.66	8.0E-48	4501900	NT	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
1284	13819		1.36	8.0E-48	4601600	NT	at75h09.x1 Barsstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:060844
							O60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN.;
							AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
							601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
							Homo sapiens aminocyclase 1 (ACY1), mRNA
							Homo sapiens aminocyclase 1 (ACY1), mRNA

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3096	15650	28061	2.89	8.0E-48	AW768477.1	EST_HUMAN	hk61b03.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
3096	15650	28062	2.89	8.0E-48	AW768477.1	EST_HUMAN	hk61b03.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
3944	16476	28889	0.6	8.0E-48	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
508	13082		2.23	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
509	13082		22.7	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1626	14058	26521	0.94	7.0E-48	6912719	NT	Homo sapiens taurine-like kinase 1 (TLK1), mRNA
1645	14176	26945	3.41	7.0E-48	5730038	NT	Homo sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
6908	19447	32225	28.19	7.0E-48	11416831	NT	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
3592	16134	28547	0.71	6.0E-48	AI761111.1	EST_HUMAN	wf69h03.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
6364	18922	31857	0.92	6.0E-48	AB006955.1	NT	Homo sapiens mRNA for AIE-75, complete cds
7170	19883	32708	1.04	6.0E-48	11420395	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
7957	24640	33259	0.82	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
7957	24640	33260	0.82	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9425	21857	34774	1.85	6.0E-48	AF026816.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
9724	22147	35078	2.02	6.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
9826	22229	35166	3.28	6.0E-48	AA189080.1	EST_HUMAN	zq45b06.s1 Stratagene tNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element
3274	17882	28241	1.43	5.0E-48	4828691	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
5032	17542	29914	1.44	5.0E-48	7662479	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
11353	23717	36777	2.51	6.0E-48	AW890299.1	EST_HUMAN	MRO-N70039-010500-002-f08 N70039 Homo sapiens cDNA
2728	16218	27733	1.03	4.0E-48	R45715.1	EST_HUMAN	Hat140-f Adult heart, Clontech Homo sapiens cDNA clone at140-f
10738	23178	36160	5.98	4.0E-48	AI620420.1	EST_HUMAN	Iu47a02.x1 NCL CGAP_Fr28 Homo sapiens cDNA clone IMAGE:2264154 3'
1417	13951	28406	1.14	3.0E-48	AV690964.1	EST_HUMAN	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'
1921	14440	26942	18.71	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1921	14440	26943	18.71	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3398	15942	28354	0.95	3.0E-48	AF172453.1	NT	Homo sapiens opid growth factor receptor mRNA, complete cds
3629	16169	28579	1.15	3.0E-48	AW664531.1	EST_HUMAN	h14b12.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B.;
4283	18788		0.68	3.0E-48	AA009541.1	EST_HUMAN	z04g03.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428844 5'
6185	18752	31452	2.03	3.0E-48	BE084571.1	EST_HUMAN	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
7442	19945	32779	0.99	3.0E-48	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8925	21359		3.51	3.0E-48	AA650930.1	EST_HUMAN	nv03105.s1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1
10856	23098	36077	4.43	3.0E-48	BF514170.1	EST_HUMAN	PTR5 repetitive element;
47	12688	25063	1.24	2.0E-48	AA631940.1	EST_HUMAN	U1-H-BW1-ent-e-10-0-U1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
1251	13789		0.61	2.0E-48	H24278.1	EST_HUMAN	fmfc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-28
4568	17085	29472	1.2	2.0E-48	BE246065.1	EST_HUMAN	ym55e10.11 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52182 5' similar to
6088	18667	31360	0.79	2.0E-48	AA613171.1	EST_HUMAN	SP-M6B_MOUSE P36803 MEMBRANE GLYCOPROTEIN ;
6088	18687	31361	0.79	2.0E-48	AA613171.1	EST_HUMAN	TCBAP ID3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo
8025	20457	33330	4.37	2.0E-48	AB040834.1	NT	sapiens cDNA clone TCBAP3842
8025	20457	33331	4.37	2.0E-48	AB040834.1	NT	no18g01.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
8042	20474	33349	3.7	2.0E-48	11496238	NT	no18g01.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
8894	21328	34239	1.07	2.0E-48	AV743451.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
11743	17997	30325	3.09	2.0E-48	AA465007.1	EST_HUMAN	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light
12095	24776	30883	1.4	2.0E-48	BE737154.1	EST_HUMAN	polyptide gene enhancer in B-cells 3 (p65) (RELA), mRNA
58	12678	25080	2.3	1.0E-48	7706634	NT	AV743451 CB Homo sapiens cDNA clone CBCCGG10 5'
898	13451	26899	7.31	1.0E-48	4502166	NT	z80c03.r1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:810052 5'
1102	13647	26087	1.3	1.0E-48	7657430	NT	601305084F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
1102	13647	26088	1.3	1.0E-48	7657430	NT	Homo sapiens disphatin resistance-associated overexpressed protein (LOC51747), mRNA
1328	13864	26314	4.78	1.0E-48	5032032	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1873	14395	26888	7.29	1.0E-48	AL163302.2	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
3464	16008	28428	1.04	1.0E-48	AL163248.2	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
5305	17805	30171	1.41	1.0E-48	M10976.1	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
6613	19163	31813	1.07	1.0E-48	A1889077.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
6813	19163	31914	1.07	1.0E-48	A1889077.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
6849	19390		1.09	1.0E-48	Y18000.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6950	19487	32286	0.64	1.0E-48	AB028594.1	NT	td17c01.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588
6950	19487	32287	0.64	1.0E-48	AB028594.1	NT	SIMILARITY TO U73941 ;
7709	20154	33012	2.68	1.0E-48	4755137	NT	td17c01.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588
							SIMILARITY TO U73941 ;
							Homo sapiens NF2 gene
							Homo sapiens mRNA for KIAA1071 protein, partial cds
							Homo sapiens mRNA for KIAA1071 protein, partial cds
							Homo sapiens huntingtin (Huntington disease) (HD) mRNA

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9486	21917	34841	1.07	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9525	21940	34863	8.22	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9753	22156	35087	3.85	1.0E-48	BF304983.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10284	22685	35647	4.33	1.0E-48	11428808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10284	22685	35648	4.33	1.0E-48	11428808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
11703	24803		1.96	1.0E-48	W28785.1	EST_HUMAN	15d8 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
1948	14467	26971	0.91	8.0E-49	AB028497.1	NT	Mus musculus MyoPDZ mRNA for myosin containing PDZ domain, complete cds
6359	18917	31661	3.68	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6359	18917	31652	3.58	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
7235	19847	32665	0.49	8.0E-49	AA642035.1	EST_HUMAN	hs18h03.r1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1184021 5'
8848	21282	34194	1.43	8.0E-49	U23850.1	NT	Human Inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
10025	22427	35376	1.02	8.0E-49	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
10636	23077	36061	1.9	8.0E-49	AI623722.1	EST_HUMAN	ts38d12.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element/contains element PTR5 repetitive element;
144	12985	25408	1.42	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
144	12985	25407	1.42	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
409	12985	25406	1.39	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
409	12985	25407	1.39	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
410	12985	25406	2.36	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
410	12985	25407	2.36	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1253	13761	26237	3.74	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5717	18289	30729	1.82	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2366663 3' similar to TR:O54923
5728	18310	30741	1.49	7.0E-48	AL120637.1	EST_HUMAN	Q54923 RSEC15.;
6089	18299	30729	0.71	7.0E-49	AI807191.1	EST_HUMAN	DKFZp762C033_s1 762 (synonym: hme12) Homo sapiens cDNA clone DKFZp762C033 3'
							wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2366663 3' similar to TR:O54923
203	12806	25223	20.64	6.0E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:U17208 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
1388	13923	26378	1.25	6.0E-49	BF038269.1	EST_HUMAN	601457738F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3861272 5'
1388	13923	26380	1.25	6.0E-49	BF038269.1	EST_HUMAN	601457738F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3861272 5'
4132	16660	29047	0.67	6.0E-48	AL162081.1	EST_HUMAN	DKFZp761A138_s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138 3'
6118	18687	31385	0.53	6.0E-49	AW511225.1	EST_HUMAN	hd44e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812378 3' similar to TR:O85638
							O85638 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.;

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6782	19325	32092	0.77	6.0E-49	AU140742.1	EST_HUMAN	AU140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'
7896	20335	33203	0.59	6.0E-49	AW511225.1	EST_HUMAN	hd44e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:065638
11049	23475	36500	2.63	6.0E-49	AW452218.1	EST_HUMAN	O95638 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
11400	23761	36820	3.17	6.0E-49	AA366558.1	EST_HUMAN	UH-H-B13-alo-a-05-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:3068048 3'
11400	23761	36821	3.17	6.0E-49	AA366558.1	EST_HUMAN	EST17525 Pancreas tumor III Homo sapiens cDNA 5' end
12091	24685		4.14	6.0E-49	AA707567.1	EST_HUMAN	EST17525 Pancreas tumor III Homo sapiens cDNA 5' end
732	13283	25716	8.23	5.0E-49	AL163210.2	NT	228c08.s1 Soares_feld_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
732	13283	25717	8.23	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens chromosome 21 segment HS21C010
1774	14287	26783	4.27	5.0E-49	AA172121.1	EST_HUMAN	zp29c07.r1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to
2707	15197	27712	5.82	5.0E-49	U17714.1	NT	TR:G233228 G233228 RTVL-H PROTEIN ; contains LTR7.13 LTR7 LTR7 repetitive element ;
3235	15787	28204	8.48	5.0E-49		NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
543	13116	25523	37.01	4.0E-49	AW189533.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S27 (metalloproteinin 1) (H. sapiens) (LOC633362), mRNA
7695	20140	32996	0.65	4.0E-49	Z26634.2	NT	x08b01.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2875593 3' similar to WP:B0350.2B
7695	20140	32997	0.65	4.0E-49	Z26634.2	NT	CE08703 ;
7726	20170	33030	0.73	4.0E-49		NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7726	20170	33031	0.73	4.0E-49		NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7989	20424	33290	0.57	4.0E-49	AB002354.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
8412	20826	33724	0.78	4.0E-49	7662209	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8
8440	20854	33755	0.43	4.0E-49	AF182034.1	NT	(GalNAc-T8) (GALNT8), mRNA
11941	24926		4.31	4.0E-49	AA210788.1	EST_HUMAN	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8
12035	24206		2.97	4.0E-49	AF240786.1	NT	(GalNAc-T8) (GALNT8), mRNA
577	13148	25565	0.98	3.0E-49	X68988.1	NT	Homo sapiens mRNA for KIAA0356 protein, partial cds
5080	17580	28958	2.33	3.0E-49	U46999.1	NT	Homo sapiens KIAA0823 gene product (KIAA0823), mRNA
7901	20340	33208	11.67	3.0E-49	H39479.1	EST_HUMAN	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
11071	23498	36524	1.85	3.0E-49	AA337561.1	EST_HUMAN	zr80f05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:982977 5'
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
							H. sapiens mRNA for acetyl-CoA carboxylase
							Human type IV collagen (COL4A6) gene, exon 40
							EST25e12 WATM1 Homo sapiens cDNA clone 25e12
							EST142672 Endometrial tumor Homo sapiens cDNA 5' end

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11552	23909	36984	2.06	3.0E-49	AI167357.1	EST_HUMAN	α286402.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1682403 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN); contains Alu repetitive element; contains element MER22 repetitive element;
680	13245		2.21	2.0E-49	BE165980.1	EST_HUMAN	
3181	15734	28193	1.47	2.0E-49	N28446.1	EST_HUMAN	MR3-H10487-150200-113-g01 HT0487 Homo sapiens cDNA
3558	16100	28515	0.67	2.0E-49	AF028564.1	NT	yc23d08.1 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:282671 5'
							Homo sapiens RNA binding protein II (RBMII) gene, complete cds
4854	17368	29748	1.31	2.0E-49	AI167357.1	EST_HUMAN	α286402.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1682403 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN); contains Alu repetitive element; contains element MER22 repetitive element;
4867	17379	29766	0.64	2.0E-49	BF51846.1	EST_HUMAN	UI-H-B14-aps-d-02-0-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:308838 3'
7116	19849	32446	1.03	2.0E-49	AV717938.1	EST_HUMAN	AV717938 DOB Homo sapiens cDNA clone DGBALB01 5'
8703	21138		1.89	2.0E-49	M86033.1	EST_HUMAN	EST02558 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFB0Y60
12046	24765		1.76	2.0E-49	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
922	13476		9.9	1.0E-49	BF035327.1	EST_HUMAN	601458631F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1576	14107	28570	6.41	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1778	14303	26791	2.13	1.0E-49	BE255216.1	EST_HUMAN	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
5616	18202	30600	3.31	1.0E-49	BF131007.1	EST_HUMAN	601820083F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4052082 5'
6385	18942	31879	0.94	1.0E-49	H18291.1	EST_HUMAN	yn48h04.1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP:GBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT;
6391	18948	31884	1.08	1.0E-49	AW984640.1	EST_HUMAN	EST7376713 MAGC resequences, MAGH Homo sapiens cDNA
7865	20111	32962	0.56	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBGVD11 5'
7885	20111	32963	0.56	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBGVD11 5'
7871	20117	32971	2.94	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7671	20117	32972	2.84	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7762	20206	33068	2.56	1.0E-49	N25884.1	EST_HUMAN	yn78g12.s1 Soares_placenta_8to9weeks_2NbhP8to9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7762	20206	33069	2.56	1.0E-49	N25884.1	EST_HUMAN	yn78g12.s1 Soares_placenta_8to9weeks_2NbhP8to9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
9337	21769	34672	1.38	1.0E-49	BE409340.1	EST_HUMAN	601300892F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
10134	22835	36503	1.41	1.0E-49	AL043129.2	EST_HUMAN	DKFZp434D2423_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D2423 5'
10842	23276	36266	2.21	1.0E-49	AB020335.1	NT	Homo sapiens Pancreas-specific TSA305 mRNA, complete cds
11078	23503	36533	4.3	1.0E-49	11427366	NT	Homo sapiens Prefoldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11567	23913		1.51	1.0E-49	BE159343.1	EST_HUMAN	MRO-HT0407-010200-006-02 HT0407 Homo sapiens cDNA
11935	24147		3.22	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12609	24578	30808	1.35	1.0E-49	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
5094	17604		1.48	9.0E-50	AF101476.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
6742	24987		0.88	9.0E-50	BE295758.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531588 5'
174	12778	25192	2.59	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21 C002
739	13300	25724	2.2	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
739	13300	25725	2.2	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1751	14278	26762	3.25	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2382	14886	27408	4.7	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51874), mRNA
2382	14886	27407	4.7	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51874), mRNA
2848	15141	27852	4.1	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
638	13202	25610	0.81	7.0E-50	BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
7169	19882	32706	0.84	7.0E-50	BF091922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7169	19882	32707	0.84	7.0E-50	BF091922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7768	20211	33074	0.7	7.0E-50	AA627822.1	EST_HUMAN	n459s12.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X65391 60S
10537	22984	35984	37.35	7.0E-50	A1872137.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN);
4365	16987		0.7	6.0E-50	BE794381.1	EST_HUMAN	wm55g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
8788	21222		4.81	6.0E-50	BE044076.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
10597	23042	36028	11.14	6.0E-50	AA312079.1	EST_HUMAN	h038h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
10597	23042	36027	11.14	6.0E-50	AA312079.1	EST_HUMAN	MER29 repetitive element;
9403	21835		4.98	5.0E-50	AA557683.1	EST_HUMAN	EST182775 Jurkat T-cells V1 Homo sapiens cDNA 5' end
940	13493		2.07	4.0E-50	AA601143.1	EST_HUMAN	EST182775 Jurkat T-cells V1 Homo sapiens cDNA 5' end
3428	15970	28393	1.07	4.0E-50	AL163248.2	NT	n45h10.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043983 similar to contains PTR5.13 PTR5
6994	19241	31992	0.61	4.0E-50	11440883	NT	repetitive element;
7683	20128	32881	1.1	4.0E-50	BE097536.1	EST_HUMAN	no54609.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X63741_ma1
11148	23527	36566	2.5	4.0E-50	AB038490.1	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1989	14410		6.47	3.0E-50	M18048.1	NT	Homo sapiens chromosome 21 segment HS21 C048
3262	15813	28230	1.3	3.0E-50	AA746142.1	EST_HUMAN	Homo sapiens cyatiny-fRNA synthetase (CARS), mRNA
3752	16281	28694	1.02	3.0E-50	AW755264.1	EST_HUMAN	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA
7046	19560	32373	0.48	3.0E-50	11419317	NT	Homo sapiens gene for fukutin, complete cds
							Human endogenous retrovirus RTVL-H2
							ob03108.s1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1322627 3'
							Cardiomyopathy associated gene 6
							CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
							Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7046	19580	32374	0.48	3.0E-50	11419317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
7146	19859	32678	1.5	3.0E-50	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC83232), mRNA
8175	20597	33481	5.42	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
8175	20597	33482	5.42	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
9905	22307	35250	1.21	3.0E-50	AB048818.1	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
9913	22316	35261	1.03	3.0E-50	11419514	NT	Homo sapiens t-complex 10 (a murine top homolog) (TCP10), mRNA
10388	22768	35755	1	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0289 gene, partial cds
11216	22868	35942	12.88	3.0E-50	AJ246621.1	NT	Homo sapiens CTL2 gene
800	13358		5.56	2.0E-50	AF055086.1	NT	Homo sapiens MHC class 1 region
1109	13650	26092	5.69	2.0E-50	4557762	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
1472	14004	28471	10.6	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
4277	16802	29185	0.59	2.0E-50	D88424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
4938	17449	29824	0.98	2.0E-50	AW869159.1	EST_HUMAN	MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA
4938	17449	29825	0.98	2.0E-50	AW869159.1	EST_HUMAN	MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA
5390	17887	30244	2.17	2.0E-50	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
5390	17887	30245	2.17	2.0E-50	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
7271	19776	32584	0.54	2.0E-50	AU124065.1	EST_HUMAN	AU124065 NT2RM2 Homo sapiens cDNA clone NT2RM2001609 5'
8882	21286	34205	1.35	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8862	21296	34206	1.35	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8969	21402	34316	4.92	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8969	21402	34318	4.92	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
9957	22359	35308	1.54	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9957	22359	35309	1.54	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
248	12849	25264	2.09	1.0E-50	BE007080.1	EST_HUMAN	PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA
248	12849	25265	2.08	1.0E-50	BE007080.1	EST_HUMAN	PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA
479	13053	25470	2.18	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2298	14766		11.31	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8246	20683		0.54	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
10173	22674	35541	1.46	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6284	18846	31555	0.88	9.0E-51	AW511225.1	EST_HUMAN	hd44e02.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR-O95636 O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6542	19094	31835	0.74	9.0E-51	AA744837.1	EST_HUMAN	hy67h03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283381 3'
9569	21892	34921	1.02	9.0E-51	AA043738.1	EST_HUMAN	zk51c09.r1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486352 5'
11229	22881	35858	1.84	9.0E-51	H89078.1	EST_HUMAN	yw24g08.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
11228	22881	35859	1.64	9.0E-51	H89078.1	EST_HUMAN	yw24g08.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
11478	23838	38904	2	9.0E-51	AA885514.1	EST_HUMAN	am10h02.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1468451 3' similar to SW:CAVP_CANFA P10463 CALYPHOSINE ;
4606	17122	29507	8.28	8.0E-51	AA010842.1	EST_HUMAN	np98e09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gbX12871_mal HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
5312	17812	30177	1.74	8.0E-51	AF092132.1	NT	Homo sapiens PAK2 mRNA, complete cds
7614	20063	32915	0.64	8.0E-51	AF064264.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
8183	20808	33492	1.74	8.0E-51	11439687	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
3244	15795	28213	1.33	7.0E-51	AW889219.1	EST_HUMAN	QV4-NT0028-200400-180-405 NT0028 Homo sapiens cDNA
3339	15886	28307	0.89	7.0E-51	AW274720.1	EST_HUMAN	xt934a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
4183	18710	29100	1.46	7.0E-51	AL079628.1	EST_HUMAN	Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
4183	18710	29101	1.46	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4373	18895	29278	2.7	7.0E-51	AW295603.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
5260	17761	30130	0.96	7.0E-51	AW188285.1	EST_HUMAN	UIH-BWO-4p-b-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
1824	14443	26946	4.58	6.0E-51	7657266	NT	x94cd09.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2664881 3'
3449	15993	28412	17.3	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4328	16850	29235	0.77	6.0E-51	9910553	NT	Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4328	16850	29236	0.77	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6293	18555	31578	1.34	6.0E-51	X01788.1	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6304	18865	31590	6.13	6.0E-51	AF070083.1	NT	Human hemoglobin related (Hpr) gene exon 3
6304	18865	31591	6.13	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
7142	19555	32876	1.07	6.0E-51	4508736	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
7287	19802	32613	0.73	6.0E-51	11416751	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7380	18050	30388	2.34	6.0E-51	11429685	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56990), mRNA
9822	22225	35181	1.87	6.0E-51	7661535	NT	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
11023	23460	36499	1.73	6.0E-51	11526289	NT	Homo sapiens B9 protein (B9), mRNA
11285	23650	36897	2.44	6.0E-51	5453949	NT	Homo sapiens Interleukin 17 receptor (IL-17R), mRNA
11285	23650	36897	2.44	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B58), alpha isoform (PPP2R5A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11285	23650	36698	2.44	6.0E-51	6453948	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R6A) mRNA
814	13372	26609	11.57	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
826	13383	26623	2.04	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1017	15299	26012	1.01	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
2515	15016	27628	6.26	5.0E-51	AJ007668.1	NT	Homo sapiens mRNA for nucleoporin 155
3958	16493	28902	1.27	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3958	16493	28903	1.27	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5189	17702	30067	1.56	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11050	23476	36501	6.3	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
139	12745	25165	6.47	3.0E-51	A1587348.1	EST_HUMAN	tr81c09.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26328
1207	13748	26183	10.7	3.0E-51	A1587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4349	16871	29255	1.89	3.0E-51	AL159142.1	NT	tr81c09.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26328
						NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
						NT	Novel human gene mapping to chromosome 22
8096	20523	33403	1.83	3.0E-51	R15914.1	EST_HUMAN	ye47c08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cd04
9243	21676		4.89	3.0E-51	M26063.1	NT	RETROVIRUS-RELATED POLYPROTEIN (HUMAN); contains LTR5 repetitive element;
12282	24373		1.9	3.0E-51	AF003528.1	NT	Human hnRNP C2 protein mRNA
381	12968	25388	2.13	2.0E-51	4507798	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
708	13270	25686	0.6	2.0E-51	BE391063.1	EST_HUMAN	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
708	13270	25687	0.6	2.0E-51	BE391063.1	EST_HUMAN	G01285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1686	14215	26696	5.1	2.0E-51	AA233352.1	EST_HUMAN	G01285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
3731	16271	28675	2.99	2.0E-51	A492415.1	EST_HUMAN	z30a05.r1 Stratagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:664850 5' similar to TR:G233228 G233228 RTVL-H PROTEIN; contains LTR7.13 LTR7 repetitive element;
4530	17048	29430	0.85	2.0E-51	AW137826.1	EST_HUMAN	tr27603.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
5695	18280	30703	0.49	2.0E-51	A1732851.1	EST_HUMAN	U1H-B11-adj-d-02-0-JLs1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718651 3'
5695	18280	30704	0.49	2.0E-51	A1732851.1	EST_HUMAN	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
6319	18879	31606	3.85	2.0E-51	BE1782015.1	EST_HUMAN	G01470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7773	20216		0.73	2.0E-51	AF218927.1	NT	Homo sapiens diacylglycerol kinase α (DGK) gene, exon 23
7942	20379	33248	1.58	2.0E-51	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIA00868), mRNA
9133	21565	34470	1.46	2.0E-51	BE901894.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9133	21665	34471	1.46	2.0E-51	BE901894.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9365	21797	34705	0.89	2.0E-51	11037084	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9701	22124	35050	1.76	2.0E-51	AB17078.1	EST_HUMAN	ts74s07 x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
9787	22170	35102	5.93	2.0E-51	BE165980.1	EST_HUMAN	Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
10326	22726	35693	1.53	2.0E-51	AV682474.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10357	22757	35724	1.22	2.0E-51	AA378559.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
11091	18280	30703	4.96	2.0E-51	A1732851.1	EST_HUMAN	EST01298 Synovial sarcoma Homo sapiens cDNA 5' end
11091	18280	30704	4.96	2.0E-51	A1732851.1	EST_HUMAN	cb34409.x5 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
12275	24388	30906	2.13	2.0E-51	11419159	NT	P35436 GLUTAMATE [NM2A] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
118	12730	25143	13.4	1.0E-51	4503528	NT	cb34409.x5 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
1522	14054		23.24	1.0E-51	AV742248.1	EST_HUMAN	P35436 GLUTAMATE [NM2A] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
4434	18954	29342	1.02	1.0E-51	4759071	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24)) homolog; translocated to, 4 (MLLT4), mRNA
4434	18954	29343	1.02	1.0E-51	4759071	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
5845	18232	30832	3.78	1.0E-51	T18882.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBC12 5'
8180	20602	33489	1.05	1.0E-51	A1572532.1	EST_HUMAN	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
12030	24202		5.39	9.0E-52	AA777621.1	EST_HUMAN	b120561 Testis 1 Homo sapiens cDNA clone b12056
156	12761	25178	8.8	8.0E-52	AA720574.1	EST_HUMAN	ts39g02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'
1525	14057	26520	2.09	8.0E-52	X84900.1	NT	z195s07 s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.13 THR repetitive element ;
1656	14187	26659	1.95	8.0E-52	11868028	NT	nm21g02.s1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element ;
1656	14187	26660	1.95	8.0E-52	11868028	NT	H. sapiens mRNA for laminin-5, alpha3b chain
4008	14187	26659	7.61	8.0E-52	11868028	NT	Homo sapiens hypothetical protein FLJ13558 similar to N-myo downstream regulated 3 (FLJ13558), mRNA
							Homo sapiens hypothetical protein FLJ13555 similar to N-myo downstream regulated 3 (FLJ13555), mRNA
							Homo sapiens hypothetical protein FLJ13556 similar to N-myo downstream regulated 3 (FLJ13556), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4008	14187	26860	7.61	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
8023	20455	33326	0.61	8.0E-52	11416595	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
8023	20455	33327	0.61	8.0E-52	11416588	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
9350	21782	34690	1.7	7.0E-52	W68471.1	EST_HUMAN	z559a06.t1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:328578 5' similar to contains Alu repetitive element
1218	13768		0.67	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271289-049-d07 BT0537 Homo sapiens cDNA
1892	14221	28701	4.25	6.0E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
6002	18576	31262	1.17	6.0E-52	AI208794.1	EST_HUMAN	q944f04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
10984	23413	36426	2.2	6.0E-52	BE048172.1	EST_HUMAN	tz46f04.y1 NCL CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGM_MOUSE Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ;
4470	16990	29374	2.29	5.0E-52	Z78898.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA18H7
1682	14193	26864	1.07	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1767	14293	26777	1.07	4.0E-52	4758943	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
3939	16474	28883	0.61	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4780	17304	29884	1.26	4.0E-52	AI766814.1	EST_HUMAN	w89b02.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400459 3'
5420	17915	30266	3.21	4.0E-52	5453365	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
5538	18128	30484	1.35	4.0E-52	4508132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5538	18128	30485	1.35	4.0E-52	4508132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
8660	21095	34001	1.95	4.0E-52	BE822032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915836 5'
9023	21456	34368	5.88	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
11857	24104		5.33	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12396	24434		6.92	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4108	16638		14.46	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10676 (FLJ10676), mRNA
676	13150	25556	2.32	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
579	13150	25557	2.32	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1747	14274	26759	1.08	2.0E-52	AB007889.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
2406	14910	27430	1.08	2.0E-52	BE207576.1	EST_HUMAN	bb65b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:Xi16493 M.musculus mRNA for Zfp-1 zinc finger protein (MOUSE);
2692	15183		10.23	2.0E-52	BF077892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5073	17583	29949	3.4	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5115	17622	29894	1.09	2.0E-52	AI141802.1	EST_HUMAN	q656e05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5115	17622	29985	1.09	2.0E-52	A1141802.1	EST_HUMAN	qab5e05.s1 Soares NIH/MPV_S1 Homo sapiens cDNA clone IMAGE:1680784 3'
5974	18560	31235	4.15	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231299-053-E12 CT0214 Homo sapiens cDNA
6700	19247	31988	1.93	2.0E-52	11141868	NT	Homo sapiens Interleukin 21 receptor (IL21R), mRNA
7086	19620	32415	1.02	2.0E-52	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7363	19810	32622	0.76	2.0E-52	A1782148.1	EST_HUMAN	cs45d12.y6 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1608311 5'
8426	20840	33738	0.6	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8428	20840	33739	0.6	2.0E-52	5032159	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
9106	21538		8.63	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
9299	21731	34638	0.9	2.0E-52	AA778795.1	EST_HUMAN	z46g05.a1 Soares_fetal_liver_spleen_1NFUS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
9878	22026		1.06	2.0E-52	4758789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (16kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10127	22528	35495	4.8	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10127	22528	35496	4.8	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10980	23409	36420	2.63	2.0E-52	A1831462.1	EST_HUMAN	wf48c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
10980	23409	36421	2.63	2.0E-52	A1831462.1	EST_HUMAN	wf48c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
10991	23420	36437	2.24	2.0E-52	AV715377	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
11110	23563		1.86	2.0E-52	W70260.1	EST_HUMAN	z449g12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344038 5'
11365	23727		2.84	2.0E-52	11417890	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
11654	24872	30449	11.33	2.0E-52	AW236297.1	EST_HUMAN	xn72a07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element;
12078	24231		5.6	2.0E-52	AI808985.1	EST_HUMAN	wf87d05.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2360849 3' similar to TR:Q16859 Q16859 CARBOXYL ESTERASE;
551	13123	25533	1.48	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1404	13938	26394	13.21	1.0E-52	4504026	NT	Homo sapiens glutamate-aminonitrile ligase (glutamine synthase) (GLUL) mRNA
2442	14944		12.29	1.0E-52	4502238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
3020	16576	27986	1.57	1.0E-52	S61070.1	NT	pol-reverse transcriptase homodog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 680 nt]
5586	18174	30538	4.98	1.0E-52	M29426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6730	19276	32038	2.38	1.0E-52	U38694.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
7915	20353	33220	2.52	1.0E-52	X07282.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8473	20886	33784	0.63	1.0E-52	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p-44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8977	21410		1.08	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9487	21898	34820	0.9	1.0E-52	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10416	22816		0.87	1.0E-52	AW020370.1	EST_HUMAN	d108g05.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10548	22895	35978	3.38	1.0E-52	U48288.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
10616	23059		7.02	1.0E-52	11426321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
3793	16330	28731	0.78	9.0E-53	4506084	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4414	16935	29326	1.03	9.0E-53	AF001448.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
6142	17846	30011	18.56	9.0E-53	7861713	NT	Homo sapiens predicted osteoblast protein (GS3788), mRNA
11504	23862	36839	1.84	7.0E-53	AW787342.1	EST_HUMAN	CM2-UM0038-280200-108-07 UM0038 Homo sapiens cDNA
11807	24131		3.11	7.0E-53	BF238465.1	EST_HUMAN	601604771F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4132783 5'
12387	24835		7.14	7.0E-53	A1421782.1	EST_HUMAN	t44f07.x1 NCI CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2089077 3' similar to contains THR.L1
4115	16845	29030	8.46	5.0E-53	4768543	NT	THR repetitive element;
11955	24167		1.83	5.0E-53	AW813563.1	EST_HUMAN	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
51	12872	26070	1.9	4.0E-53	AL163285.2	NT	RC3-ST0197-151089-011-g10 S70197 Homo sapiens cDNA
51	12872	25071	1.9	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
9859	22272		1	4.0E-53	F13080.1	EST_HUMAN	HSC3ID041 normalized infant brain cDNA Homo sapiens cDNA clone c-3ld04
10988	23417	36432	3.14	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
10988	23417	36433	3.14	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2597	15093	27609	5.65	3.0E-53	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4628	17144	29525	0.62	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-240300-055-D03 UM0081 Homo sapiens cDNA
4992	17502	29878	2.83	3.0E-53	BE069344.1	EST_HUMAN	QV3-BT0381-270100-073-d08 BT0381 Homo sapiens cDNA
6881	18268	30667	0.96	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 8 mRNA, complete cds
5893	18472	31152	0.95	3.0E-53	11526297	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6508	19082	31803	0.93	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
7537	19887	32823	0.83	3.0E-53	Y10388.3	NT	H.sapiens grat gene
7537	19887	32824	0.83	3.0E-53	Y10388.3	NT	H.sapiens grat gene
8854	21288	34199	11.96	3.0E-53	S72043.1	NT	GLF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
9383	21816		9.88	3.0E-53	5901953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
11787	24050		1.4	3.0E-53	11428423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
475	13049		5.85	2.0E-53	AA368550.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' and
1950	14469	26973	1.77	2.0E-53	7705394	NT	Homo sapiens hyaluronate acid receptor (HAR), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2222	14732	27252	4.35	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2443	14945		18.29	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP8E), mRNA
2679	15172	27680	1.28	2.0E-53	4767916	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2679	15172	27681	1.28	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3177	15730	28149	0.95	2.0E-53	7705687	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
4072	16803	28953	2.29	2.0E-53	M81873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5882	18267	30668	2.82	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA
5882	18267	30669	2.82	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA
8541	20976	33876	0.99	2.0E-53	AW97598.1	EST_HUMAN	EST387707 MAGE resequences, MAGN Homo sapiens cDNA
8625	22040		8.55	2.0E-53	AW246076.1	EST_HUMAN	2822865.5prime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822865 5'
1475	14007	28473	1.22	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3387	15933	28347	1.5	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4158	16885	28072	0.77	1.0E-53	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
5054	17594	28632	0.84	1.0E-53	BE296386.1	EST_HUMAN	601176726F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531919 5'
5410	17808	30259	1.35	1.0E-53	AW957429.1	EST_HUMAN	EST368019 MAGE resequences, MAGE Homo sapiens cDNA
7082	19596	32391	1.44	1.0E-53	BF364201.1	EST_HUMAN	CM4-NN1028-150800-543-e02 NN1028 Homo sapiens cDNA
7697	20142	32999	0.89	1.0E-53	BE012071.1	EST_HUMAN	RC6-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
8588	21023	33924	0.84	1.0E-53	AA249072.1	EST_HUMAN	II9571.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9400	21832	34748	4.42	1.0E-53	X79636.1	NT	H. sapiens mRNA for hnRNPcore protein A1
11519	23877	36959	4.09	1.0E-53	X98411.1	NT	H. sapiens mRNA for myosin-IE
11519	23877	36960	4.09	1.0E-53	X98411.1	NT	H. sapiens mRNA for myosin-IE
11648	23970	36548	1.25	1.0E-53	AW245422.1	EST_HUMAN	2822843.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822943 3'
3212	15794	28184	0.59	9.0E-54	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5555	24587	30505	8.19	9.0E-54	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
213	12816	25232	1.61	8.0E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1810	14333	28627	1.43	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
6233	18798	31507	25.54	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
399	13015	26438	1.37	7.0E-54	AA812537.1	EST_HUMAN	ai79c12.61 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1808	14328	26822	1.85	7.0E-54	Y16045.1	NT	Homo sapiens mRNA for monocyte chemoattractant protein-2
2110	14623	27145	11.34	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_8tcoWeeks_2NbHP8tcoW Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element:
10135	22536	35504	2.38	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
10886	23318	36315	3.08	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
10886	23318	36316	3.08	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
10859	23388	36308	2.74	7.0E-54	9508384	NT	Homo sapiens hypothetical protein (FLJ20488), mRNA
11061	23487		2.42	7.0E-54	AH160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.t1 ORF repetitive element:
24	12844	25033	2.67	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MIOB, exon 4, 5 and partial cds
400	13016	25439	0.69	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
400	13016	25440	0.69	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3245	15796	28214	0.82	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4018	16551	28948	1.33	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4494	17012	29386	0.95	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAG10 5'
4901	17412	29784	1.12	6.0E-54	4505808	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4934	17445		1.32	6.0E-54	Y09848.1	NT	H. sapiens shc pseudogene, p68 isoform
5100	17445		2.35	6.0E-54	Y09848.1	NT	H. sapiens shc pseudogene, p68 isoform
187	12789		118.52	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
880	13533	25976	17.02	4.0E-54	AA306764.1	EST_HUMAN	EST177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1781	14308	26785	2.27	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1781	14308	26786	2.27	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3160	15713		1.79	4.0E-54	A1935088.1	EST_HUMAN	wd26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328268 3' similar to TR:002711
7768	20209		0.6	4.0E-54	BE544893.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN;
96	12713	25126	9.4	3.0E-54	AA313487.1	EST_HUMAN	601075004F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3481017 5'
2485	14986	27489	3.36	3.0E-54	AL110383.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2555	15054		1.58	3.0E-54	A1908757.1	EST_HUMAN	DKFZp434E0731_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E0731 5'
6195	18781	31484	1.97	3.0E-54	4502434	NT	IL-BT189-190399-007 BT189 Homo sapiens cDNA
7867	20306	33171	1.47	3.0E-54	AA844061.1	EST_HUMAN	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7867	20306	33172	1.47	3.0E-54	AA844061.1	EST_HUMAN	a192c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
8388	20783	33683	0.48	3.0E-54	A1742822.1	EST_HUMAN	a192c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
							wg44b11.x1 Soares_NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2307893 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10801	23238		4.01	3.0E-54	11434808	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA
10868	23301	38295	4.93	3.0E-54	BF345600.1	EST_HUMAN	602019408F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4155121 5'
11128	23678	38920	4.31	3.0E-54	AA393382.1	EST_HUMAN	z17012.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
11759	24039	31019	4.43	3.0E-54	AW064569.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.;
11806	24930		2.37	3.0E-54	AW748965.1	EST_HUMAN	EST366829 MAGE resequences, MAGC Homo sapiens cDNA
661	13228	25638	12.79	2.0E-54	5031900	NT	RC1-BT0313-131189-011-b09 BT0313 Homo sapiens cDNA
1397	13931	26388	1.57	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1570	14102	26584	1	2.0E-54	AA655008.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2448	14949	27485	3.88	2.0E-54	AW163175.1	EST_HUMAN	repetitive element.;
2526	15025	27641	2.71	2.0E-54	AL163210.2	NT	aus2g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to
2848	15404	27824	1.44	2.0E-54	AW057524.1	EST_HUMAN	SW-CUL1_HUMAN Q13616 CULLIN HOMOLOG 1.;
3283	15832	28250	0.7	2.0E-54	AJ278314.1	NT	Homo sapiens chromosome 21 segment HS21C010
3533	16076		5.01	2.0E-54	AA632925.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_BW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2582927 3' similar to
3855	16391	28791	0.85	2.0E-54	4506378	NT	TR-Q82084 Q82084 PHOSPHOLIPASE C NEIGHBORING.;
3855	16391	28792	0.85	2.0E-54	4506378	NT	Homo sapiens mRNA for phospholipase C-beta-1b (PLCB1 gene)
4220	16745		2.17	2.0E-54	4502842	NT	n45g08.s1 NCI_CGAP_P18 Homo sapiens cDNA clone IMAGE:985469 similar to gb:X63777 60S
4471	16991		1.26	2.0E-54	AF208161.1	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
5311	17811	30178	11.38	2.0E-54	AL163201.2	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
5734	18316	30750	1.81	2.0E-54	4759069	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
5870	18449	31125	1.22	2.0E-54	BE047864.1	EST_HUMAN	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
6042	18615	31303	4.44	2.0E-54	11428657	NT	Homo sapiens syncytin precursor, mRNA, complete cds
6149	18717	31419	11.16	2.0E-54	AB046811.1	NT	Homo sapiens chromosome 21 segment HS21C001
6149	18717	31420	11.16	2.0E-54	AB046811.1	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
7023	19559	32346	0.92	2.0E-54	AF008915.1	NT	tz43ct11.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291348 5'
7201	19912	32741	0.72	2.0E-54	AB023212.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
7201	19912	32742	0.72	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7563	20013	32857	9.65	2.0E-54	11428544	NT	Homo sapiens EVI5 homolog mRNA, complete cds
9783	22186	35122	4.21	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
							Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
							Homo sapiens mRNA for brain natriuretic receptor, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10040	22442	36389	1.28	2.0E-54	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10131	22532	35500	0.84	2.0E-54	11416782	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10131	22532	35501	0.84	2.0E-54	11416782	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
11447	23807		2.03	2.0E-54	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
11455	23814	36875	1.87	2.0E-54	6715588	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12301	24382	30883	1.74	2.0E-54	8567387	NT	Homo sapiens perlecan (Drosophila) homolog 3 (PER3), mRNA
4498	17016		1.34	1.0E-54	BF315418.1	EST_HUMAN	001899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
12490	24499		4.59	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone IMAGE:127938 5' similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 end
10278	22679	35641	0.97	9.0E-55	BE081469.1	EST_HUMAN	QV2-BT0635-160400-143-h12 BT0635 Homo sapiens cDNA
1347	13882		0.87	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1350	13885		2.2	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
10988	23397		1.98	8.0E-55	AW409714.1	EST_HUMAN	fn02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2660807 5'
11818	24074		1.24	8.0E-55	BE327189.1	EST_HUMAN	hw08a08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182315 3' similar to TR:Q821J8
1108	13652	26095	2.39	7.0E-55	RO9346.1	EST_HUMAN	Q821J8 45 KDA SECRETORY PROTEIN ;
9481	21892	34813	1.6	7.0E-55	AA89581.1	EST_HUMAN	Y26604.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127938 5' similar to SP:C561_BOVIN P10897 CYTOCHROME ;
9488	21919	34843	1.58	7.0E-55	AU139809.1	EST_HUMAN	ac28a11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'
10985	23414	36427	5.15	7.0E-55	AI581056.1	EST_HUMAN	AU139809 PLACE1 Homo sapiens cDNA clone PLACE1011676 5'
10985	23414	36428	5.15	7.0E-55	AI581056.1	EST_HUMAN	tq29f09.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
12455	24853		4.79	7.0E-55	H23398.1	EST_HUMAN	tq29f09.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
11269	23634	36886	2.73	6.0E-55	AB040934.1	NT	ym67g07.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:52444 5'
4823	17335	28715	1.07	5.0E-55	AW206021.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
6891	19431	32208	1.82	5.0E-55	4502240	NT	UHL-B11-afy-g-09-0-JL.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'
6891	19431	32207	1.62	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
7033	24621	32356	0.59	5.0E-55	4505862	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
7033	24621	32357	0.59	5.0E-55	4505862	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
7468	19968	32802	1.16	5.0E-55	7382477	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
7753	20197	33059	0.77	5.0E-55	11434422	NT	Homo sapiens Rho GTPase activating protein 6 (RHGAP6), transcript variant 5, mRNA
9373	21805	34716	2.85	5.0E-55	4508302	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
9584	21987		1.49	5.0E-55	BE064386.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
10064	22465	35420	1.55	5.0E-55	AB014511.1	NT	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
10064	22465	35421	1.55	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10193	22594	35581	1.2	5.0E-55	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
11848	24097		2.63	5.0E-55	11417872	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRC1 domain (PES1), mRNA
67	16275	25079	4.53	4.0E-55	AW957094.1	EST_HUMAN	EST370064 MAGE resequences, MAGE Homo sapiens cDNA
691	13254	25671	53.07	4.0E-55	4828973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1469	14002	26467	1.03	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1469	14002	26468	1.03	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1542	14073		1.15	4.0E-55	BF061411.1	EST_HUMAN	7/52b10.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element:
1980	14478	26985	1.05	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
1980	14478	26986	1.05	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2010	14526	27039	5.29	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2010	14526	27040	5.29	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2205	14716	27238	3.69	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
2510	15011		1.08	4.0E-55	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5340	17839	30188	5.52	4.0E-55	BE698671.1	EST_HUMAN	RC2-UT0023-290700-011-f03 UT0023 Homo sapiens cDNA
8956	21319		7.56	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11780	24040		2.66	4.0E-55	BF303941.1	EST_HUMAN	6018865762 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
6953	19490	32270	0.8	3.0E-55	AA077156.1	EST_HUMAN	7B09A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B09A09
11694	24000		2.98	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
12502	24507		1.62	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C0384
392	12977	25399	1.52	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
568	13139		1.2	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete proviral segment
668	13233	25645	4.03	2.0E-55	4507206	NT	Homo sapiens syntaxin-binding protein 1 (STXB1) mRNA, and translated products
2912	15487	27890	0.69	2.0E-55		NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4827	17339	29720	2.57	2.0E-55	BE719986.1	EST_HUMAN	GM1-HT0876-150800-367-g03 HT0876 Homo sapiens cDNA
8009	24642	33310	1	2.0E-55	AW501988.1	EST_HUMAN	UJHF-BNO-aks-f-08-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
9447	21878		5.01	2.0E-55	AI002836.1	EST_HUMAN	am98h05.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1884185 3' similar to contains THR.b2 THR repetitive element:
10728	23166	36150	4.06	2.0E-55	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
99	12716	25129	2.31	1.0E-55	4505060	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
195	12798	25213	53.18	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefia2) mRNA, complete cds
591	13161	25564	0.75	1.0E-55	AI028718.1	EST_HUMAN	on65g09.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1844160 3'

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1177	13719	26160	5.23	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1901	14420	26918	2.48	1.0E-55	BE277881.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
1901	14420	26919	2.48	1.0E-55	BE277881.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
2220	14730		2.67	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2424	14927	27442	88.58	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2457	14968	27480	7.93	1.0E-55	AB007888.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
2467	14968	27481	7.93	1.0E-55	AB007888.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
2541	15039	27555	8.37	1.0E-55	L54057.1	NT	Homo sapiens GLP mRNA, partial cds
2748	15238	27751	1.12	1.0E-55	AB033045.1	NT	Homo sapiens mRNA for KIAA1219 protein, partial cds
3386	15932	28348	1.19	1.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4003	16537	28935	4.53	1.0E-55	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4313	16837	29227	1.26	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C070
4781	17295		1.05	1.0E-55	N77261.1	EST_HUMAN	y44g03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245620 5'
4884	17396	29768	2.1	1.0E-55	AB037163.1	NT	Homo sapiens DSCR6b mRNA, complete cds
4884	17396	29767	2.1	1.0E-55	AB037163.1	NT	Homo sapiens DSCR6b mRNA, complete cds
6375	17873	30234	2.09	1.0E-55	BE077198.1	EST_HUMAN	RC5-BT0606-150200-031-B11 BT0606 Homo sapiens cDNA
6769	18340	30798	0.44	1.0E-55	AF119856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6595	19146	31895	8.01	1.0E-55	11433048	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
6595	19146	31896	8.01	1.0E-55	11433048	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
8628	21061	33969	1.21	1.0E-55	11432894	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8628	21061	33970	1.21	1.0E-55	11432894	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8692	21127	34026	1.25	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8692	21127	34027	1.25	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
11187	22849	35822	2.85	1.0E-55	U60950.1	NT	Human infant brain unknown product mRNA, complete cds
7838	20278	33141	1.88	9.0E-58	BE378074.1	EST_HUMAN	601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3809552 5'
2689	15181	27692	11.23	7.0E-56	H19934.1	EST_HUMAN	y62g03.r1 Soares adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:179044 5' similar to contains THR repetitive element:
8171	20593	33476	2.2	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
8171	20593	33477	2.2	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
1690	14219	26689	1.31	5.0E-58	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
10296	22697		1.29	5.0E-56	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
11940	24917	30458	3.01	5.0E-58	H55099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
29	12649	26037	8.29	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
29	12649	25038	8.29	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds

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2083	14597		0.9	4.0E-56	BF207886.1	EST_HUMAN	601862059F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081551 5'
2658	16151	27662	3.47	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2658	16151	27663	3.47	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2770	13116	25525	3.93	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2789	15043	27559	2.6	4.0E-56	AI632488.1	EST_HUMAN	wb09f08.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA
2789	15043	27560	2.6	4.0E-56	AI632488.1	EST_HUMAN	P27119 ORNITHINE DECARBOXYLASE ;
6580	19131	31877	6.1	4.0E-56	AF217508.1	NT	P27119 ORNITHINE DECARBOXYLASE ;
6580	19131	31878	6.1	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10380	22780	35748	1.99	4.0E-56	AF043349.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10701	23140	36120	7.65	4.0E-56	AI498066.1	EST_HUMAN	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
10701	23140	36121	7.65	4.0E-56	AI498066.1	EST_HUMAN	tm65g12.x1 NCI CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2163046 3'
1373	13908	26364	1.33	3.0E-56	8924029	NT	tm65g12.x1 NCI CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2163046 3'
1752	14278	26763	1.07	3.0E-56	6912743	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
2062	14577	27085	1.73	3.0E-56	6912697	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
3086	15840	28047	1.82	3.0E-56	AA325826.1	EST_HUMAN	Homo sapiens oncogene TC21 (TC21), mRNA
3086	15840	28048	1.82	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3845	16382		2.14	3.0E-56	AF055060.1	NT	EST28889 Cerebellum II Homo sapiens cDNA 5' end
4410	16931	29322	0.96	3.0E-56	7657042	NT	Homo sapiens MHC class 1 region
4452	16972	29359	4.74	3.0E-56	AL163288.2	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4611	17127	29513	2.8	3.0E-56	5902085	NT	Homo sapiens chromosome 21 segment HS21C068
5953	18529	31211	2.48	3.0E-56	4769163	NT	Homo sapiens superkiller viral-like activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
5953	18529	31212	2.48	3.0E-56	4769163	NT	Homo sapiens superkiller viral-like activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
7278	19783	32593	6.45	3.0E-56	11421124	NT	Homo sapiens sparc/osteonectin, cwcw and kazal-like domains proteoglycan (SPOCK) mRNA
7787	20229	33089	0.41	3.0E-56	4504970	NT	Homo sapiens sparc/osteonectin, cwcw and kazal-like domains proteoglycan (SPOCK) mRNA
7787	20229	33090	0.41	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2) mRNA
9226	21658	34567	6.46	3.0E-56	11418704	NT	Homo sapiens LIM binding domain 2 (LDB2) mRNA
9902	22304	35247	1.07	3.0E-56	D63479.2	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10363	22763	35731	1.58	3.0E-56	11434956	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10525	22972	35952	2.25	3.0E-56	AB042556.1	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
						NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11078	23504	36534	10.8	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA
11079	23504	36535	10.6	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA
11408	23769	36827	4.44	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
11408	23769	36828	4.44	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
11804	24066	30983	1.34	3.0E-56	11434876	NT	Homo sapiens cavedin 3 (CAV3), mRNA
11804	24066	30984	1.34	3.0E-56	11434876	NT	Homo sapiens cavedin 3 (CAV3), mRNA
542	13114		2.78	2.0E-56	AA189818.1	EST_HUMAN	zq52a08.a1 Strategene neuroepithelium (#337231) Homo sapiens cDNA clone IMAGE:645208 3'
753	15282	25740	1.17	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
753	15282	25741	1.17	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2943	15498	27918	1.28	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3282	15831		0.97	2.0E-56	AB080681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3516	16059	28481	1.48	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ABCFCG10 5'
7528	18978	32814	2.19	2.0E-56	5730308	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1005	13556		4.77	1.0E-56	AF190930.1	NT	Maceca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3874	16214	28819	2.31	1.0E-56	AW588833.1	EST_HUMAN	hg23c11.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2946452 3'
3874	16214	28820	2.31	1.0E-56	AW588833.1	EST_HUMAN	hg23c11.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2946452 3'
7214	19826	32642	0.6	1.0E-56	AW609520.1	EST_HUMAN	MR3-ST0203-180100-208-h02 ST0203 Homo sapiens cDNA
10075	22478	35434	1.8	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220999-001-E02 CT0163 Homo sapiens cDNA
844	13208		1.54	9.0E-57	AW880885.1	EST_HUMAN	GV0-OJ0033-070300-162-h03 OT0033 Homo sapiens cDNA
4219	16744	29133	1	9.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4219	16744	29134	1	9.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
11274	23640	36892	2.91	9.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
13	12633	25020	0.88	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
311	12806	26326	2.88	8.0E-57	AW818405.1	EST_HUMAN	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA
907	13401	25909	8.87	8.0E-57	AW264959.1	EST_HUMAN	xr05d10.x1 NCL CGAP_Bn63 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb-U05875
1792	14317	28811	0.95	8.0E-57	AA406109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
3359	15905	28325	6.28	8.0E-57	4758279	NT	zq51b12.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
3359	15905	28326	6.28	8.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4980	17491	29888	1.07	8.0E-57	4557630	NT	Homo sapiens EphA4 (EPHA4) mRNA
5143	17047	30012	0.59	8.0E-57	BE299916.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIA4) mRNA
5490	24823	30590	2.54	8.0E-57	11418185	NT	600944440F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980864 5'
6737	19282	32043	0.53	8.0E-57	AB020705.1	NT	Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
6809	18350	32124	11.77	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6809	19350	32125	11.77	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0880 protein, partial cds
7834	20371	33237	0.7	8.0E-57	7682283	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8302	20717	33612	2.18	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
8302	20717	33613	2.18	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11233	12833	25020	2.8	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
11505	12863	36940	3.78	8.0E-57	11431260	NT	Homo sapiens Ras suppressor protein 1 (RSU1), mRNA
12047	24215		1.3	8.0E-57	7016528	NT	Homo sapiens monooxygenase transporter 3 (SLC16A8), mRNA
12200	24319	30916	2.46	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1250	13788	26235	0.84	7.0E-57	AJ003100.1	NT	Homo sapiens GYS2 gene, exon 14
2566	15094	27578	0.94	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2566	15094	27579	0.94	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3209	15761	28179	1.31	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3209	15761	28180	1.31	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3233	15785	28203	1.07	7.0E-57	5005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3885	16420	28824	2.07	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
3885	16420	28826	2.07	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
4460	16980		1	7.0E-57	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
12582	24881		3.74	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudocautosomal region; segment 1/2
3765	16294	28888	1.9	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
827	13384	26824	0.87	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1363	13897		18.2	3.0E-57	AA230279.1	EST_HUMAN	nc1307.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2652	15145	27656	10.45	3.0E-57	BE976622.1	EST_HUMAN	P46783 40S RIBOSOMAL PROTEIN S10. ;
2652	15145	27657	10.45	3.0E-57	BE976622.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2
3684	18234	28966	40.88	3.0E-57	AW853084.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2
4076	18607	28966	0.97	3.0E-57	P08547	SWISSPROT	CE20263 ;
6333	18891	31823	1.33	3.0E-57	11225608	NT	7f33b10.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2
8436	18992	31723	3.51	3.0E-57	BE766537.1	EST_HUMAN	RC3-C10254-110300-027-d10 CT0254 Homo sapiens cDNA
8734	21168	34073	3.91	3.0E-57	W21810.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							Homo sapiens angiotensin I converting enzyme (popliteal-dipeptidase A) 2 (ACE2), mRNA
							601889896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
							4216 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8754	21188	34089	1.98	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8754	21188	34090	1.98	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
9260	21692	34603	5.43	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
9513	21976	34801	0.85	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
9513	21976	34902	0.85	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
10889	23129	36109	5.38	3.0E-57	AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
11811	24938	30464	7.12	3.0E-57	W23871.1	EST_HUMAN	zb45d11.1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
12201	24828		2.03	3.0E-57	AW178575.1	EST_HUMAN	RCO-HT0112-080999-001-C08 HT0112 Homo sapiens cDNA
2289	14808	27324	1.75	2.0E-57	BE172528.1	EST_HUMAN	MR0-HT0559-010400-008-H10 HT0559 Homo sapiens cDNA
2684	15176	27687	6.72	2.0E-57	AA845419.1	EST_HUMAN	ak02b02.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
3416	15860		3.94	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3536	16079	28496	0.61	2.0E-57	R07702.1	EST_HUMAN	ye88h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3536	16079	28497	0.61	2.0E-57	R07702.1	EST_HUMAN	ye88h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3943	16478	28888	1.07	2.0E-57	BE073264.1	EST_HUMAN	MR0-BT0551-060300-103-b03 BT0551 Homo sapiens cDNA
4204	16729	29117	0.61	2.0E-57	AA018299.1	EST_HUMAN	zb40c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4204	16729	29118	0.61	2.0E-57	AA018299.1	EST_HUMAN	zb40c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4547	17084	29446	6.88	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5937	18515		1.58	2.0E-57	AA016131.1	EST_HUMAN	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element;
6338	18886		36.64	2.0E-57	BF115286.1	EST_HUMAN	7n80f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570866 3' similar to contains TAR1.H1 MER22 repetitive element;
6473	18028	31765	0.79	2.0E-57	11431281	NT	Homo sapiens small inducible cytokine subfamily A (Oys-Oys), member 22 (SCYA22), mRNA
9091	21523	34430	1.03	2.0E-57	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
9928	22330	35278	2.28	2.0E-57	AF057722.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
11040	23467	36489	2.45	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11040	23467	36490	2.45	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
2138	14651	27173	1.13	1.0E-57	AW503208.1	EST_HUMAN	UHF-BNO-akt-g-07-Q-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
8516	20928	33824	0.52	1.0E-57	H56076.1	EST_HUMAN	CHR220015 Chromosome 22 exon Homo sapiens cDNA clone C22_25 5'
9130	21562		2.12	1.0E-57	BE043031.1	EST_HUMAN	hc32a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039082 3' similar to TR:O00246 O00246 HYPOTHETICAL 8.3 KD PROTEIN;
11971	24168		5.7	1.0E-57	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2876499 3' similar to contains THR.b3 THR repetitive element;
5946	18523	31206	0.84	9.0E-68	AA297847.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12267	24302	30804	2.64	9.0E-58	BE395061.1	EST_HUMAN	601309485F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
606	13174		2.07	8.0E-58	BE868715.1	EST_HUMAN	601446948F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3850211 6'
673	13238	25651	4.32	8.0E-58	AI798376.1	EST_HUMAN	60134507.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
673	13238	25652	4.32	8.0E-58	AI798376.1	EST_HUMAN	60134507.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
1828	14350	26848	4.15	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1828	14350	26849	4.15	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2929	15484		2.66	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
7687	20132	32887	0.72	7.0E-58	BE561971.1	EST_HUMAN	601346704F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687577 5'
10835	23076		6.57	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B), mRNA
10708	23145	36128	3.75	7.0E-58	AW504109.1	EST_HUMAN	U1-HF-BND-ali-g-10-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
10708	23145	36129	3.75	7.0E-58	AW504109.1	EST_HUMAN	U1-HF-BND-ali-g-10-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2169	14872	27195	6.59	6.0E-58	BE395061.1	EST_HUMAN	601309485F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2270	14778	27301	4.48	8.0E-58	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3007263 5'
2854	15408	27829	1.29	6.0E-58	BE242150.1	EST_HUMAN	TCAAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP1219
2854	15409	27830	1.29	6.0E-58	BE242150.1	EST_HUMAN	TCAAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP1219
8484	19039	31779	0.95	6.0E-58	AF106911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma), mRNA, complete cds
10246	22647	35613	1.4	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12075	24228		1.52	6.0E-58	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
314	12809	25328	4.78	6.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
730	13261	25715	6.46	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-018-b05 NT0057 Homo sapiens cDNA
1225	13765	26210	3.37	5.0E-58	AW797948.1	EST_HUMAN	GM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1225	13765	26211	3.37	6.0E-58	AW797948.1	EST_HUMAN	GM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1226	13765	26210	2.34	5.0E-58	AW797948.1	EST_HUMAN	GM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1226	13765	26211	2.34	5.0E-58	AW797948.1	EST_HUMAN	GM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3291	15840	26256	5.31	6.0E-58	AA888183.1	EST_HUMAN	α88e07.s1 NCL_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1603908 3'
4274	16789	29182	0.97	5.0E-58	AI636745.1	EST_HUMAN	ts88e07.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2239468 3' similar to SW:PRO2_ACACA P19994 PROFILIN II ;
5896	18474		2.29	5.0E-58	11498282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6482	19046	31786	6.69	5.0E-58	H23072.1	EST_HUMAN	vm51h07.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:52071 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6731	19277	32039	0.94	5.0E-58	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6816	19357	32134	0.91	5.0E-58	11421330	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
7162	19875	32698	0.97	5.0E-58	AF051334.1	NT	Homo sapiens nibrin (NBS) mRNA, complete cds
7646	19875	32698	0.97	5.0E-58	AF051334.1	NT	Homo sapiens nibrin (NBS) mRNA, complete cds
7646	19895	32835	0.72	5.0E-58	4885400	NT	Homo sapiens holocytochrome c synthase (cytochrome c heme-base) (HCCS) mRNA
8609	21044	33949	7.46	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10828 (FLJ10828), mRNA
10132	22533	35502	1.59	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11777	24855		3.92	5.0E-58	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
12513	24514		1.88	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
398	12975	25396	2.24	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
819	13377	25814	1.6	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1497	14029	26482	1.29	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2494	14895	27609	17.13	4.0E-58	AF265655.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2594	15063	27676	1.19	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3293	15842	28260	1.65	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3739	16279	28682	1.22	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
8425	20839	33737	0.65	4.0E-58	BE468857.1	EST_HUMAN	hy18a02.x1 NCJ CGAP GC8 Homo sapiens cDNA clone IMAGE:3197842 3'
11102	23526	36565	16.91	4.0E-58	11424039	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
349	12939		1.68	3.0E-58	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
1421	13954	28410	2.89	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
2894	15539		0.75	3.0E-58	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
3136	16688	28104	3	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3135	15688	28105	3	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6583	19134	31880	0.59	3.0E-58	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194409 BT0702 Homo sapiens cDNA
6786	16326	32067	0.92	3.0E-58	F07056.1	EST_HUMAN	HSC1TG081 normalized infant brain cDNA Homo sapiens cDNA clone c-11g08
7004	19540	32324	1.46	3.0E-58	AV712977.1	EST_HUMAN	AV712977 DCA Homo sapiens cDNA clone DCAAZG04 5'
964	13517	25961	13.48	2.0E-58	AF068824.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
							ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391.6S
1322	13857		12.89	2.0E-58	BE208532.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81887 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
2492	14993	27496	2.1	2.0E-58	AU129905.1	EST_HUMAN	AU129905 NT2RP2 Homo sapiens cDNA clone NT2RP2009479 5'
5589	18177	30542	1.03	2.0E-58	AW074831.1	EST_HUMAN	xa08a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567704 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5613	24589	30566	2.91	2.0E-58	BE907188.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901811 6'
5613	24589	30597	2.91	2.0E-58	BE907188.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901811 5'
6363	18921	31656	1.35	2.0E-58	BF513488.1	EST_HUMAN	UI-H-BW1-ame-g-11-0-UI.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'
6434	18990	31721	1.61	2.0E-58	AI124874.1	EST_HUMAN	am57e02x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539074 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME, RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
6468	19023	31758	0.79	2.0E-58	R02567.1	EST_HUMAN	yq08108.t1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196379 5'
7336	19748	32551	0.82	2.0E-58	AI291407.1	EST_HUMAN	qm84c01.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1896424 3'
7598	20047	32898	2.78	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7598	20047	32897	2.78	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
10524	22971	35951	29.2	2.0E-58	BF307745.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
742	13303	25727	0.94	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
1094	13639	26078	1.37	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1359	13894	26349	1.4	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGC resequences, MAGD Homo sapiens cDNA
1359	13894	26350	1.4	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGC resequences, MAGD Homo sapiens cDNA
1428	13961	28417	1.1	1.0E-58	AJ238083.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
2580	15088	27600	1.94	1.0E-58	AF217514.1	NT	Homo sapiens uncharacterized bone marrow protein BM038 mRNA, complete cds
2760	15250	27765	1.53	1.0E-58	4759169	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA
3520	16063	28486	0.88	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3620	16063	28487	0.88	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3718	16258	28962	0.61	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA
4784	17298	29882	7.9	1.0E-58	M95963.1	NT	Human prothymine converting enzyme (NEC2) gene, exon 4
6069	17576	29945	5.84	1.0E-58	AI141063.1	EST_HUMAN	oz43h01.x1 Scores NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
6128	18697	31394	1.38	1.0E-58	BE061860.1	EST_HUMAN	RC1-BT0254-280100-015-e01 BT0254 Homo sapiens cDNA
7265	19770	32577	0.74	1.0E-58	11422031	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
9328	21760	34868	0.88	1.0E-58	AV751001.1	EST_HUMAN	AV761001 NPC Homo sapiens cDNA clone NPCACH09 5'
11020	23447	36466	3.36	1.0E-58	11431260	NT	Homo sapiens Ras suppressor protein 1 (RSU1), mRNA
11482	23840		2.78	1.0E-58	X53392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
11503	23861	36938	43.8	1.0E-58	D61405.1	NT	Human MSH3 gene, exon10
2136	14649	27171	32.82	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
7233	19845	32663	0.75	8.0E-59	AA382291.1	EST_HUMAN	EST95683 Testis 1 Homo sapiens cDNA 5' end.
7233	19845	32664	0.75	8.0E-59	AA382291.1	EST_HUMAN	EST95683 Testis 1 Homo sapiens cDNA 5' end
8763	21197	34099	2.39	8.0E-59	AI761963.1	EST_HUMAN	wh50d09.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8423	20837	33733	0.52	7.0E-59	BE149117.1	EST_HUMAN	RC4-HT0251-140100-013-h01 HT0251 Homo sapiens cDNA
8423	20837	33734	0.52	7.0E-59	BE149117.1	EST_HUMAN	RC4-HT0251-140100-013-h01 HT0251 Homo sapiens cDNA
182	15277		2.85	6.0E-59	BF035327.1	EST_HUMAN	G01468531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
8476	20859	33767	0.6	6.0E-59	AA962431.1	EST_HUMAN	om81a04.s1 NCL_CGAP_Ki03 Homo sapiens cDNA clone IMAGE:1553550 3' similar to TR:Q13732 Q13732
3088	15942	28050	8.88	5.0E-59	AI807484.1	EST_HUMAN	SA GENE PRODUCT PRECURSOR...
4702	17218	28600	6.82	5.0E-59	X83497.1	NT	wf48ct11.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
6982	18568	31243	0.48	5.0E-59	6005698	NT	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
7407	18076	30370	9.71	5.0E-59	AW162304.1	EST_HUMAN	Homo sapiens ataxin 2 related protein (A2LP), mRNA
9838	22241	35177	1.23	5.0E-59	AV762869.1	EST_HUMAN	eu86c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element;
10697	23127	36107	3.57	5.0E-59	11434808	NT	AV762869 MDS Homo sapiens cDNA clone MDSEIG12 5'
816	13374	25812	3.2	4.0E-59	D80006.1	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
5789	18380	31039	0.84	4.0E-59	11034810	NT	Human mRNA for KIAA0184 gene, partial cds
11924	24782		3.69	4.0E-59	AF057720.1	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
9	12629		5.12	3.0E-59	AW065524.1	EST_HUMAN	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
235	12836	25247	4.15	3.0E-59	7692247	NT	EST377582 MAGI resequences, MAGI Homo sapiens cDNA
1708	14236	28720	9.79	3.0E-59	4505860	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1708	14236	28721	9.79	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2048	14594	27077	5.63	3.0E-59	AB029035.1	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2048	14584	27078	5.63	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2998	15553	27965	0.64	3.0E-59	T18865.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
2998	15553	27968	0.64	3.0E-59	T18865.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3090	15644	28054	3.95	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3090	15644	28055	3.95	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3835	16372	28772	1.07	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4071	16802	28992	1.46	3.0E-59	AW451832.1	EST_HUMAN	UHH-B13-alk-f-01-Q-UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
4734	17249	29631	1.59	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4899	17410	29783	1.79	3.0E-59	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
6538	19090	31831	2.31	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7832	20272	33136	2.2	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
8585	21020	33920	1.26	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8585	21020	33921	1.28	3.0E-59	X12558.1	NT	Human mRNA for dkl proto-oncogene
10071	22472	35428	0.87	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
10071	22472	35429	0.87	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
12055	24221		5.81	3.0E-59	11417868	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
6173	18741	31442	0.58	2.0E-59	BF509893.1	EST_HUMAN	UH-B14-eyy-b-02-0-UI.s1 NCL CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086522 3'
6173	18741	31443	0.58	2.0E-59	BF509893.1	EST_HUMAN	UH-B14-eyy-b-02-0-UI.s1 NCL CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086522 3'
7197	19908		0.57	2.0E-59	AA470073.1	EST_HUMAN	z88d05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730377 3'
7502	19706	32505	0.72	2.0E-59	AF135187.1	NT	Homo sapiens Interferon-induced protein p78 (MX1) gene, complete cds
8369	20784		0.45	2.0E-59	BF373329.1	EST_HUMAN	MRO-FT0144-250700-002-a10 FT0144 Homo sapiens cDNA
9788	22191		5.5	2.0E-59	AA309774.1	EST_HUMAN	EST1800333 Jurkat T-cells V Homo sapiens cDNA 5' end
10391	22791		1.8	2.0E-59	BF365554.1	EST_HUMAN	RCO-NT0038-100700-032-a07 NT0038 Homo sapiens cDNA
10611	23084	36040	3.55	2.0E-59	AW410698.1	EST_HUMAN	fn07n04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'
10811	23084	36041	3.55	2.0E-59	AW410698.1	EST_HUMAN	fn07n04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'
11800	24064	31027	8.77	2.0E-59	AI631809.1	EST_HUMAN	wa36r12.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
12372	24808	30580	4.09	2.0E-59	L11645.1	NT	Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
167	12772		8.32	1.0E-59	BE289411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
2372	14877	27396	11.68	1.0E-59	AI139341.1	EST_HUMAN	601178757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
2372	14877	27397	11.68	1.0E-59	AI139341.1	EST_HUMAN	qc21c08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1710254 3'
2547	15046		1.91	1.0E-59	AA748468.1	EST_HUMAN	qc21c08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1710254 3'
5378	17876	30236	0.96	1.0E-59	8922563	NT	ca56h11.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1368029 3' similar to TR:Q13537
5378	17876	30237	0.96	1.0E-59	8922563	NT	Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
8078	20506	33386	1.21	1.0E-59	AJ130894.1	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
8263	20680	33573	1.1	1.0E-59	BE256814.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
8263	20680	33574	1.1	1.0E-59	BE256814.1	EST_HUMAN	Homo sapiens mRNA for transcription factor
9608	22088	35016	1.01	1.0E-59	11418630	NT	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
10633	20506	33385	8.52	1.0E-59	AJ130894.1	NT	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
785	13344	25778	0.99	8.0E-60	AW977845.1	EST_HUMAN	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
1500	14032	26485	2.12	8.0E-60	4759159	NT	Homo sapiens mRNA for transcription factor
2078	14593	27112	2.93	8.0E-60	5174656	NT	EST389849 MAGC resequences, MAGO Homo sapiens cDNA
2078	14593	27113	2.93	8.0E-60	5174656	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
6263	18845	31584	1.14	8.0E-60	AB029004.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
							Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
							Homo sapiens mRNA for KIAA1081 protein, partial cds

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6854	19394	32170	1.01	8.0E-60	S63182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog (human, plasma, mRNA, 2408 nt)
9238	20655	33548	0.96	8.0E-60	11420841	NT	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCYT1B), mRNA
8605	21040	33845	2.68	8.0E-60	X17033.1	NT	Human mRNA for Integrin alpha-2 subunit
9301	21733	34640	2.79	8.0E-60	11428949	NT	Homo sapiens S-antigen, retina and pineal gland (arrestin) (SAG), mRNA
9671	22018	34948	1.55	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9674	22018	34949	1.55	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10613	23056	36043	7.45	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10613	23056	36044	7.45	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
775	13335	25769	40.85	7.0E-60	AF055086.1	NT	Homo sapiens MHC class I region
776	13335	25769	197.18	7.0E-60	AF055086.1	NT	Homo sapiens MHC class I region
838	13395	25833	1.4	7.0E-60	4504634	NT	Homo sapiens intrateukin 10 receptor, beta (IL10RB), mRNA
2047	14563	27076	1.24	7.0E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2743	15233	27748	1.69	7.0E-60	AB0111163.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
4198	18721	29109	2.5	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
9624	22039	34973	4.83	7.0E-60	H68041.1	EST_HUMAN	y1204.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
11122	23574	36618	3.87	7.0E-60	H68041.1	EST_HUMAN	y1204.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
8957	21390		7.56	6.0E-60	H52456.1	EST_HUMAN	y47808.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201853 5' similar to contains ORF repetitive element;
86	12703	25116	1.43	5.0E-60	AB07917.1	EST_HUMAN	wf52c07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2369212 3'
86	12703	25117	1.43	5.0E-60	AB07917.1	EST_HUMAN	wf52c07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2369212 3'
2926	15481		1.46	4.0E-60	AA298037.1	EST_HUMAN	EST11488 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7822	20263	33124	0.79	4.0E-60	BF196088.1	EST_HUMAN	h81805.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE Q61085 GTP-RHO BINDING PROTEIN 1;
11066	23492	36517	1.78	4.0E-60	11433597	NT	Homo sapiens v-rat-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA
11069	23492	36518	1.78	4.0E-60	11433597	NT	Homo sapiens v-rat-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA
1831	14353	26852	3.13	3.0E-60	BE592811.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1831	14353	26853	3.13	3.0E-60	BE592811.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1839	14361		1.89	3.0E-60	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
4487	17008	29391	2.36	3.0E-60	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5634	18221	30821	0.54	3.0E-60	BF365143.1	EST_HUMAN	QV4NN149-250900-423-01 N1149 Homo sapiens cDNA
5609	18487	31169	2.3	3.0E-60	AW836188.1	EST_HUMAN	RC3-LT0023-200100-012-01 LT0023 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7368	18038	30420	1.11	3.0E-60	A1792814.1	EST_HUMAN	cl60h11.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1634053 5' similar to SW:UDP_MOUSE
8934	21368	34280	4.51	3.0E-60	5174844	NT	P62824 URIDINE PHOSPHORYLASE;
8934	21368	34281	4.51	3.0E-60	5174844	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8169	21601	34511	2.87	3.0E-60	5174844	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
10978	23407	36416	2.24	3.0E-60	11427120	NT	Homo sapiens CGI-162 protein (LOC57130), mRNA
10978	23407	36417	2.24	3.0E-60	11427120	NT	Homo sapiens CGI-162 protein (LOC57130), mRNA
12459	24948		1.74	3.0E-60	AA485286.1	EST_HUMAN	ab07h04.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.11 LTR10 repetitive element;
32	12652	25042	1.59	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1455	13987	28449	2.25	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1718	14248	26728	1.43	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
2387	14891	27410	2.38	2.0E-60	AW380450.1	EST_HUMAN	RC1-HT0268-031288-012-02 HT0268 Homo sapiens cDNA
2534	16032	27548	14.37	2.0E-60	7657229	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
2691	15154	27658	1.45	2.0E-60	AW978005.1	EST_HUMAN	EST390114 MAGE resequences, MAGE Homo sapiens cDNA
3569	16111	28528	0.89	2.0E-60	4757687	NT	Homo sapiens v-ref murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3928	18463	28871	1.61	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4141	16669		0.64	2.0E-60	BF513458.1	EST_HUMAN	UHL-BW1-ams-e-05-Q-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070852 3'
6628	19177	31931	0.84	2.0E-60	A1791952.1	EST_HUMAN	nr01f12.y5 NCI_CGAP_Oc9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element;
6941	19382	32157	1.63	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
7088	19622	32418	0.94	2.0E-60	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
7247	18021	30436	2.44	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7247	18021	30437	2.44	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7549	19999	32840	3.7	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7549	19999	32841	3.7	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7672	20118	32973	0.5	2.0E-60	A1308124.1	EST_HUMAN	ib23d08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055185 3' similar to SW:GALR_RAT
8163	20885		1.19	2.0E-60	BF512808.1	EST_HUMAN	Q62805 GALANIN RECEPTOR;
8630	21074	33982	1.15	2.0E-60	X85597.1	EST_HUMAN	UHL-BW1-emu-e-02-Q-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
9284	21686	34608	1.7	2.0E-60	L36033.1	NT	HS15BEST human adult testis Homo sapiens cDNA clone CAM_EST16
10017	22419	35369	2.47	2.0E-60		NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
							Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10017	22419	35370	2.47	2.0E-60	11891659	NT	Homo sapiens sema domain, transmembrane domain (TIM), and cytoplasmic domain, (semaphorin) &A (SEMA6A), mRNA
11223	22875	35850	1.58	2.0E-60	11434729	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5), mRNA
11509	23887	36943	1.71	2.0E-60	AW751191.1	EST_HUMAN	CM0-CT0013-280689-017-103 CT0013 Homo sapiens cDNA
11509	23887	36944	1.71	2.0E-60	AW751191.1	EST_HUMAN	CM0-CT0013-280689-017-103 CT0013 Homo sapiens cDNA
12093	24243		3	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NH2P2.1), mRNA
12241	24770		1.56	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12244	24347		2.53	2.0E-60	11418098	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC83504), mRNA
12262	24359		1.44	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
640	13112	25521	1.39	1.0E-60	BE178586.1	EST_HUMAN	PM3-HT0605-270200-001-e06 HT0605 Homo sapiens cDNA
5043	17553	28824	1.43	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
9180	21612		3.11	1.0E-60	AA244041.1	EST_HUMAN	nc04e12.1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.11 L1 repetitive element:
9201	21633	34541	1.4	1.0E-60	AV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
1126	13670	26109	2.59	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2609	16104	27622	1.25	8.0E-61	AW006478.1	EST_HUMAN	w005b10.x1 NCL_CGAP_C63 Homo sapiens cDNA clone IMAGE:2606555 3'
2609	15104	27623	1.25	8.0E-61	AW006478.1	EST_HUMAN	w005b10.x1 NCL_CGAP_C63 Homo sapiens cDNA clone IMAGE:2606555 3'
2905	15460		3.03	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
8558	20993	33891	0.93	8.0E-61	AA589969.1	EST_HUMAN	nm59g06.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
132	12739	25157	0.6	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
132	12739	25158	0.6	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
279	12876	26292	3.72	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3635480 5'
834	13391	26830	2.36	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3635480 5'
1353	13898	26342	15.08	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1653	14184	26655	2.61	6.0E-61	AA589033.1	EST_HUMAN	nm56h09.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
3271	15822	28239	12.6	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
6335	18893	31625	3.3	6.0E-61	S79249.1	NT	Ig-beta/B29=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 376 nt]
7809	20261	33112	1.63	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
8147	20570	33446	2.16	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-1 (GTF2i) mRNA, complete cds
11248	23614	36659	39.57	6.0E-61	AF090386.1	NT	Homo sapiens napsin A mRNA, complete cds
11248	23614	36660	39.57	6.0E-61	AF090386.1	NT	Homo sapiens napsin A mRNA, complete cds
11899	13391	26630	1.94	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3635480 5'
12553	24540	30941	1.57	6.0E-61	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
374	12892	26381	0.7	6.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA

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1678	14208	26684	2.07	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
2895	15550	27982	2.02	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
3154	15707	28128	4.15	5.0E-61	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3999	16528		2.1	5.0E-61	AJ229041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5105	12982	25381	0.83	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1749	14276	26760	1.1	4.0E-61	AU140307.1	EST_HUMAN	AU140307 PLACE2 Homo sapiens cDNA clone PLAGE2000302 5'
6099	18668	31362	0.88	4.0E-61	7661637	NT	Homo sapiens DKFZP566B023 protein (DKFZP566B023), mRNA
11774	24049		4.69	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'
516	13089	25502	1.84	2.0E-61	8922828	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1243	13781	26228	3.12	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1243	13781	26229	3.12	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1885	14198	26670	0.96	2.0E-61	NS0309.1	EST_HUMAN	w63d11.s1 Scars fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb:U25444 603 RIBOSOMAL PROTEIN L35A (HUMAN);
6765	19308	32073	0.83	2.0E-61	11428166	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP9N1A), mRNA
9351	21783	34691	1.27	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKC Homo sapiens cDNA clone GKCELG08 5'
9742	22069		0.91	2.0E-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
9955	22387	35338	1.71	2.0E-61	AW600266.1	EST_HUMAN	UHF-BND-akd-f12-o-UJ.r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3076774 5'
10213	22614	35581	2.9	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
10667	23107		3.74	2.0E-61	11419728	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
452	13027		0.92	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
795	13353	25789	1.26	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1430	13863	28419	1.01	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1830	14352	28951	2.83	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2102	14616	27135	1.08	1.0E-61	AW827281.1	EST_HUMAN	xt11b09.y1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:2893389 5' similar to contains element MSR1 repetitive element;
3353	15899	28320	0.92	1.0E-61	7662319	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3730	16270	28674	1.17	1.0E-61	BE174455.1	EST_HUMAN	QV2-HT0577-140300-077-g08 HT0577 Homo sapiens cDNA
4276	16801	29184	1.41	1.0E-61	M68840.1	NT	Human monomelic oxidase A (MAOA) mRNA, complete cds
4499	16989	28372	0.83	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4499	16989	28373	0.83	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4916	17427	29789	10.49	1.0E-61	AW288181.1	EST_HUMAN	UIH-BWD-ajl-b-08-o-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4916	17427	28800	10.49	1.0E-61	AW288181.1	EST_HUMAN	UIH-BWD-ajl-b-08-o-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5849	18239	30635	0.72	1.0E-61	M76423.1	NT	H.sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5959	18535	31219	0.85	1.0E-61	7662303	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6172	18740	31441	1.13	1.0E-61	11416891	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
7308	19720	32522	7.91	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds
7630	19981	32815	0.66	1.0E-61	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRP128), mRNA
7635	20082	32835	1.43	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7636	20082	32836	1.43	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8725	21160	34066	3.35	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8860	21294	34202	3.73	1.0E-61	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9537	21952		3.04	1.0E-61	AW999726.1	EST_HUMAN	MR0-BN0070-040400-010-H01 BN0070 Homo sapiens cDNA
9588	22011	34940	0.95	1.0E-61	11416280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
10057	22458	35409	5.84	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
10433	22855	35662	9.96	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
10714	23152	36135	1.81	1.0E-61	AB044550.1	NT	Homo sapiens POKcd.19 mRNA for ubiquitin-conjugating enzyme E2, complete cds
10852	23286	36276	3.25	1.0E-61	AB007830.1	NT	Homo sapiens mRNA for GSR2, complete cds
11664	24833		1.48	1.0E-61	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
11707	24819	30587	4.14	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11707	24819	30588	4.14	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12100	24249	30928	11.38	1.0E-61	M20809.1	NT	Human kappa-immunoglobulin germline pseudogene (Chrt) variable region (subgroup V kappa I)
12429	24464	30871	10.23	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10276	22877	35639	1.3	9.0E-62	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-f10 BT0310 Homo sapiens cDNA
4587	17103	29494	0.96	8.0E-62	AA830420.1	EST_HUMAN	cc68h11.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1364725 3' similar to SW:POL_MLVRK
1134	13678	26117	1.33	7.0E-62	AV714334.1	EST_HUMAN	P31785 POL POLYPROTEIN ;
3485	16028	28450	0.72	7.0E-62	P17480	SWISSPROT	AV714334 DCB Homo sapiens cDNA clone DCBAMA08 6'
6211	18777	31483	1.04	7.0E-62	11427865	NT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)
11108	23561	36602	9.48	7.0E-62	AI208981.1	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20261), mRNA
2963	15508		1.65	6.0E-62	U09410.1	NT	qg56a04.x1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O16103
3362	15908		4.72	6.0E-62	11418256	NT	O15103 HYPOTHETICAL 27.3 KD PROTEIN ;
8156	20578	33456	3.95	6.0E-62	AI762801.1	EST_HUMAN	Human zinc finger protein ZNF131 mRNA, partial cds
8156	20578	33457	3.95	6.0E-62	AI762801.1	EST_HUMAN	Homo sapiens CGI-58 protein (CGI-58), mRNA
							w044002.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
							w044002.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'

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8818	21252	34168	1.69	6.0E-62	11431139	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
9586	22009	34937	3.48	6.0E-62	AW814393.1	EST_HUMAN	MR3-ST0203-130100-025-409 ST0203 Homo sapiens cDNA
433	13007	25433	3.07	5.0E-62	A1950528.1	EST_HUMAN	w61e07.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
2305	14812	27328	2.33	5.0E-62	AJ271735.1	NT	Q08379 GOLGIN-95, contains element MIER22 repetitive element;
2305	14812	27330	2.33	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2512	15013	27524	0.91	5.0E-62	U39487.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2512	15013	27525	0.91	5.0E-62	U39487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3397	15943	28355	2.8	5.0E-62	4506758	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
4350	18872	28256	2.05	5.0E-62	AA431093.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4595	17111		1.02	5.0E-62	AW905887.1	EST_HUMAN	zw78e09.a1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
9705	22128	35054	7.7	5.0E-62	AW410687.1	EST_HUMAN	P47245 NARDILYSIN
11034	23461	36481	8.66	5.0E-62	11425574	NT	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
11034	23461	36482	8.66	5.0E-62	11425574	NT	fh07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2981616 5'
863	13419	25884	2	4.0E-62	AW161479.1	EST_HUMAN	Homo sapiens muscle specific gene (M9), mRNA
863	13419	25885	2	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
864	13419	25884	1.59	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
864	13419	25885	1.59	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
1491	14023		1.48	4.0E-62	AA311281.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2355	14860	27380	1.04	4.0E-62	A1827800.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2355	14860	27381	1.04	4.0E-62	A1827800.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
3377	19924		8.32	4.0E-62	4557887	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
5392	17889	30247	4.06	4.0E-62	4768323	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
6220	18786	31492	1.84	4.0E-62	4508978	NT	EST182043 Jurkat T-cells V Homo sapiens cDNA 5' end
6624	19173	31927	2.69	4.0E-62	11420654	NT	EST182043 Jurkat T-cells V Homo sapiens cDNA clone IMAGE:2350359 3' similar to
							wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
							gb:X57138_maf1 HISTONE H2B.2 (HUMAN);
							wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
							gb:X57138_maf1 HISTONE H2B.2 (HUMAN);
							Homo sapiens keratin 18 (KRT18) mRNA
							Homo sapiens enhancer of zeste (Drosophila) homolog 2 (EZH2) mRNA
							Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
							Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7616	20094	32916	1.88	4.0E-62	11421041	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
8165	20687	33466	2.35	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
8165	20687	33467	2.35	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
8755	21189	34091	1.1	4.0E-62	11428973	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
8250	21682	34593	7.27	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
10792	23230	36214	2.91	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA16D3
10792	23230	36215	2.91	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA16D3
11461	23819	36880	3.08	4.0E-62	AB029025.1	NT	Homo sapiens mRNA for KIAA1102 protein, partial cds
11461	23819	36881	3.08	4.0E-62	AB029025.1	NT	Homo sapiens mRNA for KIAA1102 protein, partial cds
11691	23987	36559	1.89	4.0E-62	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
11923	24774		1.86	4.0E-62	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12358	24450	30868	2.44	4.0E-62	11418322	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12412	24444	30865	7.06	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12412	24444	30866	7.06	4.0E-62	11417862	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12470	24488	30880	3.18	4.0E-62	11417862	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
77	12695	25107	0.82	3.0E-62	11430460	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3008	15561	27973	1.05	3.0E-62	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3006	15561	27974	1.05	3.0E-62	AB040809.1	NT	Human cyclophilin-related processed pseudogene
3695	18235	28643	8.76	3.0E-62	X62868.1	NT	wa33f04.x1 NCL CGAP_Ki611 Homo sapiens cDNA clone IMAGE:2288903 3' similar to contains THR.12
8029	21461	34370	2.39	3.0E-62	AI632733.1	EST_HUMAN	THR repetitive element
1264	13801	26250	2.67	2.0E-62	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8457	20870	33770	0.48	2.0E-62	AA307490.1	EST_HUMAN	EST178374 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9185	21627	34536	5.09	2.0E-62	BF328911.1	EST_HUMAN	RCO-BN0284-300600-031-e05 BN0284 Homo sapiens cDNA
9195	21627	34537	5.09	2.0E-62	BF328911.1	EST_HUMAN	RCO-BN0284-300600-031-e05 BN0284 Homo sapiens cDNA
10159	22560		3.65	2.0E-62	AF224659.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11419	23780		31.44	2.0E-62	BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
1069	13815	26057	1.34	1.0E-62	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1667	14089	26592	11.53	1.0E-62	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
1776	14301	26788	1.01	1.0E-62	AA625207.1	EST_HUMAN	af70e11.1 Soares_NthMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
4563	17080	29466	1.68	1.0E-62	8923201	NT	CE03453 : Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5298	17798	30163	1.37	1.0E-62	AA148822.1	EST_HUMAN	z106b08.t1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491511 5' similar to SW:C561_BOVIN P10897 CYTOCHROME B561.1
6814	19164	31915	0.72	1.0E-62	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cez2/Cadmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (ORTR), CDM protein (CDM), adrenoleukodystrophy protein >
7574	20024	32887	1.02	1.0E-62	AA490060.1	EST_HUMAN	ab05c02.s1 Stratigene fetal retina 637202 Homo sapiens cDNA clone IMAGE:839906 3'
7585	20034	32881	2.9	1.0E-62	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
7586	20034	32882	2.9	1.0E-62	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
9384	21816	34731	1.98	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9384	21816	34732	1.98	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9410	21842	34755	2.14	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9410	21842	34756	2.14	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9737	22084	34891	2.6	1.0E-62	AA465170.1	EST_HUMAN	aa33d08.s1 NCL_GGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
11124	23576	36618	2.81	1.0E-62	Z78698.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14D8
12217	24331	30875	2.84	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12445	24473	30875	3	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
362	12942	26366	2.63	9.0E-63	AW818405.1	EST_HUMAN	QV4-ST0234-181189-037-j05 ST0234 Homo sapiens cDNA
2240	14749		0.99	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-558C10 5'
4053	16585	28974	9.82	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4053	16585	28975	9.82	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5493	18003	37000	2.81	9.0E-63	11418186	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5724	18306	30737	1.42	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PKB kinase
7628	20074	32927	3.61	9.0E-63	11426985	NT	Homo sapiens nucleoporin 88kD (NUP88), mRNA
8433	20847	33748	0.41	9.0E-63	X08178.1	NT	Human adult muscle mRNA fragment of DMD gene (DMD= Duchenne muscular dystrophy)
8454	20867	33768	0.76	9.0E-63	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8871	21305	34216	1.97	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
10680	23120	36098	2.17	9.0E-63	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
10680	23120	36099	2.17	9.0E-63	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
10821	23257	36242	1.97	9.0E-63	BF203408.1	EST_HUMAN	601855628F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4098487 5'
2238	14747	27267	1.76	8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2287	14775	27298	2.92	8.0E-63	5031810	NT	Homo sapiens IL-2-inducible T-cell kinase (ITK), mRNA
3438	15982	28397	5.1	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3438	15982	28398	5.1	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4282	18807	29191	3.32	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
5412	17908	30260	0.96	8.0E-63	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
953	13505		1.79	7.0E-63	AB182137.1	EST_HUMAN	wn55g11.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:2439908 3'
5593	18181		28.55	8.0E-63	AA420803.1	EST_HUMAN	nc63102.1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S
3289	18838	28257	0.88	4.0E-63	AL163278.2	NT	RIBOSOMAL PROTEIN (HUMAN);
3818	16353	28762	1.15	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3816	16353	28763	1.15	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6787	19330	32098	1.8	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
6787	19330	32099	1.8	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
10910	23342	36349	4.45	4.0E-63	AW134709.1	EST_HUMAN	CM3-BT0595-190100-072-e09 BT0595 Homo sapiens cDNA
10910	23342	36350	4.45	4.0E-63	AW134709.1	EST_HUMAN	U1H-B11-abq-a-02-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
12522	24520		1.24	4.0E-63	AA629056.1	EST_HUMAN	U1H-B11-abq-a-02-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1886	14407	26903	3.4	3.0E-63	AB018260.1	NT	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.H L1
2739	16229	27741	1.01	3.0E-63	J00310.1	NT	repetitive element;
2780	13608	26259	13.84	3.0E-63	6005963	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
6820	19361	32137	37.83	3.0E-63	11546610	NT	Human Met-tRNA-Ile gene 1
9839	22242	35178	1.34	3.0E-63	BE876158.1	EST_HUMAN	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
9839	22242	35179	1.34	3.0E-63	BE876158.1	EST_HUMAN	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC68928), mRNA
197	12800	25216	1.58	2.0E-63	U07804.1	NT	601485556F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
204	12807	25224	1.84	2.0E-63	4885226	NT	601485556F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
515	13088		1.17	2.0E-63	4557624	NT	Human DNA topoisomerase I mRNA, partial cds
840	13406	26849	4.91	2.0E-63	7657042	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
1586	14118	26586	1.4	2.0E-63	AB030388.1	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1586	14118	26586	1.4	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1754	14281	26766	1.47	2.0E-63	BE410739.1	EST_HUMAN	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
3115	15668	28081	3.66	2.0E-63	4502168	NT	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
3247	15788	28216	2.38	2.0E-63	AF109718.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3917	16452	28859	2.14	2.0E-63	L39891.1	NT	Homo sapiens chromosome 3 subtelomeric region
4923	17434	29809	1.24	2.0E-63	AF111167.2	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
							Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5512	24588	30348	1.04	2.0E-63	11419428	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
6174	18742	31444	3.26	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6174	18742	31445	3.26	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6500	19054	31784	0.78	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6500	19054	31795	0.78	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S8/13S>
7073	19607	32402	0.84	2.0E-63	U66059.1	NT	Homo sapiens MIST mRNA, partial cds
7128	19661	32456	0.47	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7128	18681	32457	0.47	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7508	19711	32513	1.58	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7508	19711	32514	1.58	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
8339	20754	33049	0.95	2.0E-63	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
							Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
8417	20831	33728	0.54	2.0E-63	11421514	NT	(semaphorin) 3A (H. sapiens) (LOC63232), mRNA
9022	21455	34365	3.66	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9381	21813	34727	1.28	2.0E-63	11420849	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
9381	21813	34728	1.28	2.0E-63	11420849	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
9895	22397	35348	0.88	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10528	22975	35958	25.65	2.0E-63	N78945.1	EST_HUMAN	2b18b05.s1 Soares, fetal_lung_N9HIL18W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN);
10557	23004	36080	3.8	2.0E-63	AF069810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
10557	23004	35990	3.8	2.0E-63	AF069810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
11428	23787	36985	34.86	2.0E-63	AB040930.1	NT	Homo sapiens mRNA for KIAA1487 protein, partial cds
11545	23902	36985	22.19	2.0E-63	AF200344.1	NT	Homo sapiens aspartyl protease 3 mRNA, partial cds
11545	23902	36986	22.19	2.0E-63	AF200344.1	NT	Homo sapiens aspartyl protease 3 mRNA, partial cds
11807	24714	30671	7.12	2.0E-63	11418185	NT	Homo sapiens acaninase 2, mitochondrial (ACO2), mRNA
4364	16886	29267	2.47	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized Infant brain cDNA Homo sapiens cDNA clone c-zvd11
4364	16886	29268	2.47	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized Infant brain cDNA Homo sapiens cDNA clone c-zvd11
5608	18106	30561	1.88	1.0E-63	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6050	18622	31312	1.41	1.0E-63	AW562286.1	EST_HUMAN	QV0-ST0215-080100-083-009 ST0215 Homo sapiens cDNA
6728	19274	32034	0.76	1.0E-63	AW451950.1	EST_HUMAN	UI-H-BB-alk-h-02-0-UI.1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:30687/63 3'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6728	19274	32035	0.75	1.0E-63	AW451850.1	EST_HUMAN	U1-H-B18-alt-h-02-Q-U1.e1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
8981	21414		2.87	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12518	24836		8.41	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6268	18831	31544	0.55	9.0E-64	AW401433.1	EST_HUMAN	U1-HF-BKO-aad-b-09-Q-U1.f1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3053153 5'
8538	20973	33874	5.83	9.0E-64	AI478185.1	EST_HUMAN	U1-HF-BKO-aad-b-09-Q-U1.f1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:2161525 3'
1072	13618		4.69	8.0E-64	BE280786.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
8453	19009	31743	3.32	8.0E-64	BE885755.1	EST_HUMAN	601508968F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
11607	23940		5.55	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
11865	23978		2.99	8.0E-64	T60651.1	EST_HUMAN	Y499502.F1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:79179 5'
3511	16054		0.82	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4782	17286	29879	2.53	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4782	17286	29880	2.53	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
8389	20803	33700	0.71	7.0E-64	4508786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
10060	22461	35413	2.62	7.0E-64	Y07848.1	NT	Homo sapiens EWS, ger22, rp22 and bam22 genes
1719	14247	28729	2.78	6.0E-64	AI651992.1	EST_HUMAN	wb51607.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1719	14247	28730	2.78	6.0E-64	AI651992.1	EST_HUMAN	wb51607.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3083	15637	28043	4.97	8.0E-64	AW028445.1	EST_HUMAN	wy13603.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528436 3'
3083	15637	28044	4.97	8.0E-64	AW028445.1	EST_HUMAN	wy13603.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528436 3'
5889	18488	31146	2.54	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5889	18488	31147	2.54	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6910	18488	31170	5.1	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
6919	18497	31178	0.54	6.0E-64	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
6115	18684	31381	0.66	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
6115	18684	31382	0.66	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
7684	20129	32982	2.99	6.0E-64	11525878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7684	20129	32983	2.99	6.0E-64	11525878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
8570	21893	34922	8.29	6.0E-64	11420565	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
8695	22107	35035	1.97	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
9848	22251	35186	2.22	6.0E-64	S76475.1	NT	tAC [human, brain, mRNA, 2716 nt]
10552	22999	35982	5.19	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
10552	22999	35983	5.19	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10796	15637	28043	2.43	6.0E-64	AW028445.1	EST_HUMAN	w13e03.x1 NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2529436 3'
10796	15637	28044	2.43	6.0E-64	AW028445.1	EST_HUMAN	w13e03.x1 NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2529436 3'
11826	24079	30989	4.6	6.0E-64	11526198	NT	Homo sapiens Interleukin 10 receptor, beta (IL10RB), mRNA
843	13400	25840	2.84	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
843	13400	25841	2.84	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1370	13905	26361	1.01	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1453	13985	28446	1.6	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1453	13985	28447	1.6	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1709	14237	26722	1.13	5.0E-64	U89388.1	NT	Human (3 mbt) protein homolog mRNA, complete cds
2784	14041	26508	1.95	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2784	14041	26507	1.95	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3972	16507	28913	7.9	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR63 (CR63) mRNA, partial cds
4122	16861	29037	0.66	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
5394	17881	30242	1.09	5.0E-64	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
8432	20848	33747	0.89	4.0E-64	BE784607.1	EST_HUMAN	601590382F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944397 5'
10595	23040	36024	2.54	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
10595	23040	36025	2.54	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
2103	14617	27136	6.3	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (TFujikawa) Homo sapiens cDNA clone GEN-559E02 5'
3215	15767	28187	0.87	3.0E-64	BE794381.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3421	15985	28377	1.2	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3421	15985	28378	1.2	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6369	18946	31682	1.44	3.0E-64	Z26273.1	NT	H.sapiens isoform 1 gene for L-type calcium channel, exon 28
6871	19219	31865	0.77	3.0E-64	AW600861.1	EST_HUMAN	UJHF-BPOp-ab-c-05-Q-UJr NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3073181 5'
6842	19383	32158	2.93	3.0E-64	BF370000.1	EST_HUMAN	RC8-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
8978	21411	34325	2.16	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8978	21411	34326	2.16	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8998	21431	34339	3.55	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ
8998	21431	34340	3.55	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ
1115	13659	26100	1.71	2.0E-64	AA609940.1	EST_HUMAN	af08d08.a1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1429	13682	26418	1.06	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2430	14933		6.55	2.0E-64	A1927030.1	EST_HUMAN	wc87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2436	14938	27454	2.68	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2436	14938	27455	2.68	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3789	16326	28727	0.59	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGE resequences, MAGE Homo sapiens cDNA
3789	16326	28728	0.59	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGE resequences, MAGE Homo sapiens cDNA
6309	18870	31597	2.36	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
6563	19114	31858	0.82	2.0E-64	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6833	19374	32162	4.81	2.0E-64	BF668537.1	EST_HUMAN	602123474F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:4280395 5'
6947	19485	32264	1.15	2.0E-64	A076387.1	EST_HUMAN	oz29b03.x1 Soares fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676717 3'
7072	19606	32401	3.46	2.0E-64	M77185.1	NT	H1.sapiens dopamine receptor D5 pseudogene 1, partial cds
8407	20821	33718	0.6	2.0E-64	11431054	NT	Homo sapiens alaxin 2-binding protein 1 (AZBP1), mRNA
9116	21548	34451	1.63	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
9116	21548	34452	1.63	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
9498	21929	34853	1.51	2.0E-64	AU132570.1	EST_HUMAN	AU132570 NT2RP4 Homo sapiens cDNA clone NT2RP4000109 5'
10545	22992	35974	4.12	2.0E-64	BF628114.1	EST_HUMAN	602042882F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4180556 5'
10833	23268	36254	3.63	2.0E-64	A1922911.1	EST_HUMAN	wn81b08.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3'
10833	23288	36255	3.63	2.0E-64	A1922911.1	EST_HUMAN	wn81b08.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3'
11001	23430	36448	2.2	2.0E-64	AW864773.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
11260	23626	36674	3.31	2.0E-64	BE269880.1	EST_HUMAN	601185078F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3542922 5'
11260	23626	36675	3.31	2.0E-64	BE269880.1	EST_HUMAN	601185078F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3542922 5'
11741	24026	31014	1.63	2.0E-64	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
12212	24327		2.97	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
271	12869	25285	1.97	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1761	14288	28770	20.91	1.0E-64	A1928419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:121698_cds1 PROTHYMOSIN ALPHA (HUMAN):contains element MSR1 repetitive element ;
2869	15524	27946	0.84	1.0E-64	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
							Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel alpha
3491	16034	28456	6.02	1.0E-64	AF196779.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3576	16118	28533	1.43	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3576	16118	28534	1.43	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3910	16445	28652	0.85	1.0E-64	8922829	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11026), mRNA
10086	22487	35444	1.16	1.0E-64	AA042975.1	EST_HUMAN	zk63908.s1 Soares pregnant uterus_NHPU Homo sapiens cDNA clone IMAGE:486567 3'
11712	24011		2.02	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11290	23655		69.92	9.0E-65	BF330876.1	EST_HUMAN	QV4-BT0267-081199-017-e03 BT0267 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11282	23628	36877	8.88	8.0E-65	A1929244.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to
10163	22554	35522	1.92	7.0E-65	BE081653.1	EST_HUMAN	SW:RL21_HUMAN P48778 60S RIBOSOMAL PROTEIN L21.;
11498	23856	36930	2.03	7.0E-65	Z21378.1	EST_HUMAN	QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA
1082	13628	26088	1.72	6.0E-65	AV721898.1	EST_HUMAN	HSAAEA50W TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test346 (b)
1875	14397		20.82	6.0E-65	AA550929.1	EST_HUMAN	nt86d10.s1 NCL CGAP_P11 Homo sapiens cDNA clone HTBBZC06 5'
6922	19461	32239	1.08	6.0E-65	AA603892.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
							nt86d10.s1 NCL CGAP_P15 Homo sapiens cDNA clone IMAGE:954517
9172	21604	34514	2.04	6.0E-65	AW083252.1	EST_HUMAN	xc07b09.x1 NCL CGAP_Co21 Homo sapiens cDNA clone IMAGE:2683545 3' similar to TR:Q63306 Q63306
9348	21780	34987	4.86	6.0E-65	AA427878.1	EST_HUMAN	LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORFS.; contains L1.b2 L1 repetitive element;
9348	21780	34688	4.86	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
10655	23095	36076	2.7	6.0E-65	BE567816.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
10819	23255	36240	3.32	6.0E-65	BF340825.1	EST_HUMAN	601340485F1 NIH_MGC 63 Homo sapiens cDNA clone IMAGE:3682677 5'
11022	23449	38468	1.77	6.0E-65	AW206752.1	EST_HUMAN	602037721F1 NCL CGAP_Bmf64 Homo sapiens cDNA clone IMAGE:4185877 5'
650	13214	25624	0.89	5.0E-65	AF064604.1	NT	U-H-B11-efg-4-10-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722826 3'
1384	13919	26376	1.43	6.0E-65	7661951	NT	Homo sapiens KE03 protein mRNA, partial cds
1384	13919	26376	1.43	6.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
3216	16768	28188	1.98	5.0E-65	4507848	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
3216	16768	28189	1.98	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7272	19777	32585	0.59	6.0E-65	4504606	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10363	22763	35719	1.17	5.0E-65	AF009668.1	NT	Homo sapiens Interferon-related developmental regulator 1 (IFRD1), mRNA
189	12802	25219	1.94	4.0E-65	AL120418.1	EST_HUMAN	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
768	13328	25758	1.29	4.0E-65	A1266488.1	EST_HUMAN	DKFZp761G108.t1 761 (synonym: hemy2) Homo sapiens cDNA clone DKFZp761G108 5'
766	13326	25757	1.29	4.0E-65	A1266488.1	EST_HUMAN	qtm46e01.x1 Soares_placenta_8to9weeks_2NbHP8tc9w Homo sapiens cDNA clone IMAGE:1891800 3'
1105	13649	26091	1.42	4.0E-65	4826735	NT	qtm46e01.x1 Soares_placenta_8to9weeks_2NbHP8tc9w Homo sapiens cDNA clone IMAGE:1891800 3'
1514	14046	26511	9.08	4.0E-65	4506636	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
3961	16498	28905	0.93	4.0E-65	AW993185.1	EST_HUMAN	Homo sapiens ribosomal protein L34 (RPL34) mRNA
6469	18024	31759	4.24	4.0E-65	AB033093.1	NT	RC2-BN0033-160200-073-e03 BN0033 Homo sapiens cDNA
6469	18024	31760	4.24	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
7520	18971	32805	0.8	4.0E-65	AY006372.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
							Homo sapiens oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7556	20008	32848	0.93	4.0E-65	M19878.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
7687	20113	32868	2.04	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
8063	20494	33372	0.83	4.0E-65	U40372.1	NT	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
8083	20494	33373	0.88	4.0E-65	U40372.1	NT	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
8421	20835	33731	0.54	4.0E-65	U39556.1	NT	Human MAP kinase kinase 6 (MKK6) mRNA, complete cds
9436	21868	34783	0.89	4.0E-65	11428127	NT	Homo sapiens Janus Kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10419	22819		1.88	4.0E-65	AJ277548.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
10733	23171	36154	2.41	4.0E-65	AV738784.1	EST_HUMAN	AV738784 CB Homo sapiens cDNA clone CBCBCE05 5'
10883	23316	36313	9.78	4.0E-63	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12050	13849	26091	1.34	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
100	12718	25132	2.66	3.0E-65	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
101	12718	25132	2.4	3.0E-63	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1265	16263		9.2	3.0E-65	X78932.1	NT	H.sapiens HZF9 mRNA for zinc finger protein
1798	14323	26817	0.98	3.0E-65	AJ000692.1	EST_HUMAN	ov23703.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element;
2945	15500	27919	0.83	3.0E-65	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3239	15790	28209	1.22	3.0E-65	4504950	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3719	16259	28663	1.83	3.0E-65	AJ000692.1	EST_HUMAN	ov23703.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element;
4695	17211	29590	1.7	3.0E-65	6912385	NT	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
10089	22490	35447	1.86	3.0E-65	BE787368.1	EST_HUMAN	601479886F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3882405 5'
11142	22832	35802	8.24	3.0E-65	AA430008.1	EST_HUMAN	zw65a06.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3381	15927	28342	7.31	2.0E-65	BF680294.1	EST_HUMAN	602165062F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4295966 5'
6887	19427		4.44	2.0E-65	BE263373.1	EST_HUMAN	601190883F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3634741 5'
7572	20022	32865	28.69	2.0E-65	BF578922.1	EST_HUMAN	602134359F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4289285 5'
9249	21681	34591	1.24	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
9249	21681	34592	1.24	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
10449	22900	35878	2.88	2.0E-65	11419247	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependant regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA
11663	23978		4.64	2.0E-65	AA307604.1	EST_HUMAN	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus
12170	24691		2.68	2.0E-65	BF246086.1	EST_HUMAN	601854033F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4073769 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
83	12710		0.8	1.0E-65	BF125544.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
557	13128	25539	1.93	1.0E-65	7857495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3349	15895	28317	1.33	1.0E-65	BE466681.1	EST_HUMAN	h224a09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3208888 3'
4012	16545	28942	2.51	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
4012	16545	28943	2.51	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
4222	16747	29136	3.08	1.0E-65	AW029340.1	EST_HUMAN	wx08c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4222	16747	29137	3.08	1.0E-65	AW029340.1	EST_HUMAN	wx08c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
5537	18127	30482	0.48	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-09 BT0702 Homo sapiens cDNA
5537	18127	30483	0.48	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-09 BT0702 Homo sapiens cDNA
5737	18319	30764	0.65	1.0E-65	AJ243738.1	EST_HUMAN	qn88h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR-Q07823
8816	21250	34155	2.2	1.0E-65	AW620481.1	EST_HUMAN	Q07823 MAC30 PROTEIN;
8816	21250	34156	2.2	1.0E-65	AW620481.1	EST_HUMAN	QV2-ST0298-140200-042-112 ST0298 Homo sapiens cDNA
8865	21299	34208	2.59	1.0E-65	AU141295.1	EST_HUMAN	QV2-ST0298-140200-042-112 ST0298 Homo sapiens cDNA
8865	21299	34209	2.59	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYR01 Homo sapiens cDNA clone THYR01000356 5'
9244	21676	34585	1.2	1.0E-65	BF698707.1	EST_HUMAN	AU141295 THYR01 Homo sapiens cDNA clone THYR01000356 5'
9355	21787	34695	1.69	1.0E-65	AU129040.1	EST_HUMAN	602126239F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4283313 5'
9355	21787	34696	1.69	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9383	21795		3.22	1.0E-65	11431994	NT	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9876	22023	34952	6.42	1.0E-65	A191716.1	EST_HUMAN	Homo sapiens Inositol 1,4,5-trisphosphate receptor, type 1 (ITPR1), mRNA
9958	22360	35310	1.19	1.0E-65	AU163783.1	EST_HUMAN	qd56a02.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M28581 ZINC
10413	22813	35788	1.13	1.0E-65	AB037832.1	NT	FINGER PROTEIN 8 (HUMAN)/contains MER19.11 MER19 repetitive element;
10442	22893	35869	2.69	1.0E-65	M26167.1	NT	AU163783 NT2RP3 Homo sapiens cDNA clone NT2RP3004018 3'
10581	23008	35995	25.13	1.0E-65	4506660	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10908	23340	36346	3.85	1.0E-65	BF698707.1	EST_HUMAN	Human platelet factor 4 variation 1 (PF4var1) gene, complete cds
10986	23415	36429	3.24	1.0E-65	A1621017.1	EST_HUMAN	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11713	24012		2.78	1.0E-65	11418041	NT	602126239F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4283313 5'
11819	24075	30986	6.42	1.0E-65	11418322	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
12270	24364		1.91	1.0E-65	11418248	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
74	12693	25103	0.83	9.0E-68	AL160311.1	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
74	12693	25104	0.83	9.0E-68	AL160311.1	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1512	14044		5.72	9.0E-68	M87298.1	NT	Novel human gene mapping to chromosome 22
						NT	Human transposon-like element, partial

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3909	16444	28850	0.87	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3909	16444	28851	0.87	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4740	17254	29634	0.81	8.0E-66	AA424304.1	EST_HUMAN	z60c06.r1 Soares_NHMPu_ST Homo sapiens cDNA clone IMAGE:767048 5'
4387	16909	29292	1.01	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
4387	16909	29293	1.01	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
4387	16909	29294	1.01	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
10937	23398	36378	3.49	6.0E-66	X89181.1	NT	H. sapiens mRNA for ribosomal protein L31
1399	13933	26390	1.39	5.0E-66	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-H06 BT0311 Homo sapiens cDNA
9547	21982	34884	13.1	5.0E-66	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
813	13371	25803	1.04	4.0E-66	6879816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
2178	14689	27213	1.42	4.0E-66	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2369	14874		5.8	4.0E-66	AJ223394.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4836	17348		8.68	4.0E-66	9635487	NT	Human endogenous retrovirus, complete genome
5815	18395	31058	3.76	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate
6020	18594	31281	1.04	4.0E-66	AW939119.1	EST_HUMAN	cyclohydrolase (MTHFD2), mRNA
7255	18029	30412	5.18	4.0E-66	AW965473.1	EST_HUMAN	QV1-DT0069-110200-067-g10 DT0069 Homo sapiens cDNA
7571	20021	32884	8.37	4.0E-66	U78188.1	NT	EST377546 MAGI resequences, MAGI Homo sapiens cDNA
8160	18395	31058					Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
8690	21125	34025	1.13	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate
8726	21161	34087	1.06	4.0E-66	X57147.1	NT	cyclohydrolase (MTHFD2), mRNA
10452	22903	35882	4.34	4.0E-66	BF607493.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20119 (FLJ20119), mRNA
11133	23585	36626	2.57	4.0E-66	AB023215.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1458	13990	28453	4.81	3.0E-66	4502098	NT	UJH-BW1-amr-a-10-O-UJ.st NCL CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'
1489	13980	28454	4.81	3.0E-66	4502098	NT	Homo sapiens mRNA for KIAA0998 protein, partial cds
2857	15150	27861	7.2	3.0E-66	11141880	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5
3078	15632	28039	7.66	3.0E-66	7662223	NT	(SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
							Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5
							(SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
							Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
							Homo sapiens KIAA0649 gene product (KIAA0649), mRNA

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5726	18307	30738	0.79	3.0E-66	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5842	18422	31091	0.71	3.0E-66	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
6053	18825	31315	1.86	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6053	18826	31316	1.86	3.0E-66	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10093	22494	35453	0.95	3.0E-66	7019450	NT	Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
10388	22788	35768	1.08	3.0E-66	AF155659.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein E (MCBPE) mRNA, complete cds
11263	23629	36678	6.76	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
53	12674	25073	1.65	2.0E-66	7657334	NT	Homo sapiens Mieschep/NIK-related kinase (MINK), mRNA
53	12674	25074	1.65	2.0E-66	7657334	NT	Homo sapiens Mieschep/NIK-related kinase (MINK), mRNA
439	12617	25004	1.27	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
439	12617	25005	1.27	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1803	14326	28921	2.9	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2199	14652	27174	0.86	2.0E-66	X65859.1	NT	H. sapiens pseudogene for the low affinity L-8 receptor
2928	15483	27604	1.81	2.0E-66	X65859.1	NT	H. sapiens pseudogene for the low affinity L-8 receptor
3501	16044	28465	0.82	2.0E-66	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3765	16304	28704	0.79	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4080	16611	28999	0.68	2.0E-66	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4700	17216	28597	62.42	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4700	17216	28598	62.42	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
6100	18669	31363	0.94	2.0E-66	AW98854.1	EST_HUMAN	EST380930 MAGI resequences, MAGI Homo sapiens cDNA
6100	18669	31364	0.94	2.0E-66	AW98854.1	EST_HUMAN	EST380930 MAGI resequences, MAGI Homo sapiens cDNA
9251	21683	34594	2.72	2.0E-66	N45480.1	EST_HUMAN	y59c02.r1 Sources: multiple_sclerosis_2NbfHMSF Homo sapiens cDNA clone IMAGE:277826 5'
12057	24928		2.72	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
2847	15403	27822	1.77	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBAD007 5'
2847	15403	27823	1.77	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBAD007 5'
4407	15403	27822	4.02	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBAD007 5'
4407	15403	27823	4.02	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBAD007 5'
5637	18224	30824	5.72	1.0E-66	BF673088.1	EST_HUMAN	602162898F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4284151 5'
6061	18633	31326	0.89	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
6061	18633	31327	0.89	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
7349	19760	32567	1.55	1.0E-66	BF328623.1	EST_HUMAN	RC5-BN0193-010900-034-G08 BN0193 Homo sapiens cDNA

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8971	21404	34318	1.1	1.0E-66	AA668858.1	EST_HUMAN	aa80e04.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:827262 3'
10285	22686	35649	0.88	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10285	22686	35650	0.88	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10722	23160	36144	2.88	1.0E-66	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11277	23642	36894	1.97	1.0E-66	AW688744.1	EST_HUMAN	EST380820 MAGE resequences, MAGJ Homo sapiens cDNA
11553	23910	36995	1.78	1.0E-66	BE684346.1	EST_HUMAN	601343157F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3685143 5'
11553	23910	36996	1.78	1.0E-66	BE684346.1	EST_HUMAN	601343157F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3685143 5'
11824	24077		2.71	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
4987	17497		0.63	8.0E-67	M79158.1	EST_HUMAN	EST01750 Subtracted Hippocampus, Striatum (cat. #836206) Homo sapiens cDNA clone HHCNP31 similar to L1 repetitive element
395	13011	25434	1.2	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN); EST198812 Testis 1 Homo sapiens cDNA 5' and similar to similar to C. elegans hypothetical protein, cosmid ZK353
1414	13948	28404	1.5	7.0E-67	AA363416.1	EST_HUMAN	zh56b05.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1577	14108	28671	1.3	7.0E-67	W85947.1	EST_HUMAN	zh56b05.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1677	14108	28672	1.3	7.0E-67	W85947.1	EST_HUMAN	zh56b05.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1987	14485	26993	1.11	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-trisphosphate 5/6 kinase (ITPK1), mRNA
1987	14485	26994	1.11	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-trisphosphate 5/6 kinase (ITPK1), mRNA
2768	13011	25434	1.05	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);
6388	18945	31681	0.88	7.0E-67	10190695	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6594	18145	31893	1.98	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6594	19145	31894	1.98	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
7089	18932	32427	1.31	7.0E-67	4885084	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110T119K0) (ATP8B1A), mRNA
8162	20584	33483	1.14	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8162	20584	33484	1.14	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8869	21303	34213	0.93	7.0E-67	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
11410	23771	36830	5.95	7.0E-67	U82466.1	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
11688	23925	37004	1.19	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11588	23925	37005	1.19	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12084	24235	30962	3.22	7.0E-67	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12504	24508		1.2	7.0E-67	11421527	NT	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA

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676	13147	25564	2.2	6.0E-67	X88988.1	NT	H sapiens mRNA for acetyl-CoA carboxylase
818	13376	25813	1.54	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1306	13841	26290	1.08	6.0E-67	Y14320.1	NT	Homo sapiens PMP89 gene, exons 3, 4, 5, 6 & 7
3127	15680	28096	1.57	6.0E-67	4506434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3415	15859	28370	1.32	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3415	15859	28371	1.32	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4143	16671	29058	1.04	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4143	16671	29057	1.04	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4755	17269	28651	5.18	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4755	17269	28652	5.18	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5052	17562		0.81	6.0E-67	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5357	17582		0.71	6.0E-67	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3180	15733	28162	2.3	6.0E-67	AF009650.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
10765	23203		3.29	6.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1360	13895	26351	1.18	4.0E-67	BE0819.1	EST_HUMAN	Y022d11.1 Scores adult brain N264HB55Y Homo sapiens cDNA clone IMAGE:167263 5'
8918	21352		1.62	4.0E-67	BF357321.1	EST_HUMAN	RC0-HT0934-150900-028-c03 HT0934 Homo sapiens cDNA
2771	13216	25827	1.04	3.0E-67	AA333788.1	EST_HUMAN	EST37803 Embryo, 9 week Homo sapiens cDNA 5' end
3431	15975	28388	1.08	3.0E-67	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-H08 BT0311 Homo sapiens cDNA
4744	17258	28638	3.13	3.0E-67	AW869159.1	EST_HUMAN	MR3-SN0068-040500-008-f01 SN0068 Homo sapiens cDNA
4773	17287		1.46	3.0E-67	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
5290	17790	30155	4.27	3.0E-67	AA189735.1	EST_HUMAN	zq09a11.s1 Stratiens muscle 937209 Homo sapiens cDNA clone IMAGE:629180 3'
11026	23453		11.84	3.0E-67	AA827874.1	EST_HUMAN	om18b07.s1 Scores_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
193	12796	25211				EST_HUMAN	hw18g09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9
888	13423	25871	0.96	2.0E-67	BE348354.1	EST_HUMAN	CE09617
1132	13676		7.23	2.0E-67	AW816405.1	EST_HUMAN	QV4-ST0234-181189-037-f05 ST0234 Homo sapiens cDNA
2148	14681	27184	1.5	2.0E-67	AF167480.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
2148	14681	27185	6.33	2.0E-67	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
2283	14780	27311	6.33	2.0E-67	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
3444	15888	28408	1.09	2.0E-67	AF309561.1	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
4016	16549	28046	4.8	2.0E-67	AA825755.1	EST_HUMAN	zj91g01.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
6377	17876	30235	2.88	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6378	18835	31973	1.31	2.0E-67	BF108266.1	EST_HUMAN	601823462F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043295 5'
6437	18893	31724	0.77	2.0E-67	AL049784.1	NT	Novel human gene mapping to chromosome 13
			5.01	2.0E-67	BF240758.1	EST_HUMAN	601876351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6823	19172	31925	2.12	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6823	19172	31928	2.12	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
7005	19541	32325	0.68	2.0E-67	AL120542.1	EST_HUMAN	DKFZ761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
9042	21474	34386	1.07	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to cerebellin
9042	21474	34387	1.07	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to cerebellin
8339	21771	34874	0.92	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
8339	21771	34875	0.92	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
9842	22245	35181	1.02	2.0E-67	AW263824.1	EST_HUMAN	U1-H-B12-ahr-e-10-Q-U1.s1 NC1_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'
10884	23124	36104	3.04	2.0E-67	BF685788.1	EST_HUMAN	602140-470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301705 5'
10822	23258	36243	2.82	2.0E-67	BF034485.1	EST_HUMAN	601455282F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858975 5'
10838	25001		2.62	2.0E-67	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11017	23444	36462	5.78	2.0E-67	AA348111.1	EST_HUMAN	EST64790 Hippocampus II Homo sapiens cDNA 5' end
11206	22858	35832	1.66	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
11954	24773	30682	2.2	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P-1), mRNA
266	12884	25282	5.53	1.0E-67	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
728	13289	25713	1.16	1.0E-67	AA702794.1	EST_HUMAN	z69b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4762	17278	29859	0.71	1.0E-67	BF439247.1	EST_HUMAN	rab61f08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3'
11507	23866		3.66	9.0E-68	4508090	NT	Homo sapiens mitogen-activated protein kinase 6 (MAPK6), mRNA
2084	14598	27116	1.69	8.0E-68	BE870732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3877	16412	28815	7.07	8.0E-68	AA208456.1	EST_HUMAN	zq82h10.r1 Stratagene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07690 SAV PROTEIN.;
3877	16412	28816	7.07	8.0E-68	AA208456.1	EST_HUMAN	zq82h10.r1 Stratagene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07690 SAV PROTEIN.;
1855	14377		1.09	6.0E-68	AW503842.1	EST_HUMAN	U1-HF-BN0-alb-p-07-Q-U1.r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078924 5'
8058	20489	33364	0.5	6.0E-68	AW953543.1	EST_HUMAN	EST366613 MAGC resequences, MAGC Homo sapiens cDNA
8058	20489	33365	0.5	6.0E-68	AW953543.1	EST_HUMAN	EST366613 MAGC resequences, MAGC Homo sapiens cDNA
10340	22740	35709	2.97	6.0E-68	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
12283	24374		1.61	6.0E-68	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
825	15259	25821	0.81	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
825	15259	25822	0.81	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
842	13399	25838	5.56	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
842	13399	25839	5.66	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3107	15660	28072	3.25	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7103	19636	32430	0.66	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab3)-like 1 (RAB3IL1), mRNA
7103	19636	32431	0.66	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab3)-like 1 (RAB3IL1), mRNA
2432	14935	27449	3.09	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2432	14935	27450	3.09	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
5071	17581		4.94	4.0E-68	P04408	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6264	18828	31542	0.66	4.0E-68	AF157063.1	NT	Homo sapiens sedlin (SEDL) gene, exon 4
7156	19898	32691	6.66	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7156	19898	32692	6.66	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
8220	20639	33528	0.76	4.0E-68	7681693	NT	Homo sapiens DKFZP686L0724 protein (DKFZP686L0724), mRNA
9369	21801	34709	6.77	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9369	21801	34710	6.77	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9459	21890	34811	3.61	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
10783	23221	36203	2.27	4.0E-68	4508282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
10783	23221	36204	2.27	4.0E-68	4508282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
3660	16200	28608	3.32	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9660	20951		3.82	3.0E-68	A1342323.1	EST_HUMAN	q38h02.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR12 THR repetitive element;
10377	22777	35745	1.8	3.0E-68	F28794.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
12608	24689		1.49	3.0E-68	AW839485.1	EST_HUMAN	QV1-DT0072-010200-056-h06 DT0072 Homo sapiens cDNA
2815	17991		31.74	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4037	16570	28962	0.76	2.0E-68	BE875766.1	EST_HUMAN	771602.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:O80828 O80828
4726	17244	29626	2.34	2.0E-68	AB008681.1	NT	HYPOTHETICAL 88.8 KD PROTEIN, ;
7279	19784		11.82	2.0E-68	R45088.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
7495	19889	32497	4.44	2.0E-68	BF036316.1	EST_HUMAN	y938g04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34898 3'
7663	20109		0.55	2.0E-68	11525737	NT	601458514F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5'
7843	20283	33145	0.58	2.0E-68	BF338745.1	EST_HUMAN	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetyl-galactosaminyltransferase 8 (GalNAc-7B) (GALNT8), mRNA
11706	24847		2.15	2.0E-68	BE897376.1	EST_HUMAN	IL3-CT0634-180900-273-A01 CT0534 Homo sapiens cDNA
82	12899	25113	1.2	1.0E-68	4506222	NT	601437397F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922192 5'
310	12905	25326	13.18	1.0E-68	AW816405.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
2157	14670	27192	0.97	1.0E-68	AB011149.1	NT	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
2157	14670	27193	0.97	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2115	15205	27722	2.16	1.0E-68	AW461832.1	EST_HUMAN	Homo sapiens mRNA for KIAA0577 protein, complete cds
							UI-H-B13-alk-f-01-0-U1.e1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5133	17638	30000	1.07	1.0E-68	AA897343.1	EST_HUMAN	al47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
5201	17704	30088	2.05	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632344 5'
5575	18163	30528	2.03	1.0E-68	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0888), mRNA
8213	20633	33522	0.73	1.0E-68	11436716	NT	Homo sapiens senf1n/SUMO-specific protease (SENP1), mRNA
10828	23070	36055	1.75	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
10828	23070	36056	1.75	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
10855	23126	36105	3.97	1.0E-68	L76416.1	NT	Homo sapiens MIF2 suppressor (HSMT3) mRNA, complete cds
10866	23395	36407	2.3	1.0E-68	11433277	NT	Homo sapiens myosin IC (MYO1C), mRNA
11029	23456	36476	2.16	1.0E-68	AF043129.1	NT	Homo sapiens Interleukin-7 receptor precursor (IL7R) gene, exons 7 and 8 and complete cds
11089	23494	36521	5.48	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11089	23494	36522	5.48	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11402	23763	36823	2.99	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
11402	23763	36824	2.99	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12263	12699	25113	1.96	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12500	24876	30573	1.44	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12564	24546		1.45	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
21	12641	25028	12.26	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
21	12641	25029	12.26	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1053	13599	26038	0.84	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1053	13599	26039	0.84	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4146	16874	29061	0.78	9.0E-69	4757867	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
5371	17869	30229	0.9	9.0E-69	AF05177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
10872	23112		3.45	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5'
3364	15910		1.55	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
6883	19231	31981	5.84	7.0E-69	8966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
8535	20970	33871	5.82	6.0E-69	AI182764.1	EST_HUMAN	qe2h01.x1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11668 60S RIBOSOMAL PROTEIN L18 (HUMAN);
8535	20970	33872	5.82	6.0E-69	AI192764.1	EST_HUMAN	qe2h01.x1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11668 60S RIBOSOMAL PROTEIN L18 (HUMAN);
9323	21755	34663	1.24	5.0E-69	AA826039.1	EST_HUMAN	cd60a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1372300 3'
538	13110		1.54	4.0E-69	AI873630.1	EST_HUMAN	wm28h11.x1 NCI_CGAP_Uk4 Homo sapiens cDNA clone IMAGE:2437125 3'
6041	24598	31302	1.68	4.0E-69	BE561063.1	EST_HUMAN	601344705F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677641 5'
							wh57b08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137
6130	18699	31398	5.04	4.0E-69	AI764973.1	EST_HUMAN	O55137 ACYL-COA THIOESTERASE.1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6989	19528	32308	2.98	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6989	19528	32310	2.98	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
401	13017	25441	3.78	3.0E-69	BE268012.1	EST_HUMAN	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
631	13195	25601	2.42	3.0E-69	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
2271	14779		0.89	3.0E-69	5728910	NT	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
6492	18002	36999	1.83	3.0E-69	11418185	NT	Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
7180	19801		0.84	3.0E-69	AJ27557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
7257	18031	30414	0.54	3.0E-69	11428786	NT	Homo sapiens sperm surface protein (HSS), mRNA
7845	20285	33147	0.85	3.0E-69	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7802	20341	33209	1.43	3.0E-69	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurotrophin (CTNND2) mRNA, partial cds
8066	20497	33378	9.34	3.0E-69	AF268075.1	NT	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
8910	21344	34281	0.88	3.0E-69	AW138846.1	EST_HUMAN	UI-H-B1-acw-g-01-0-U1.s1 NCJ CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716840 3'
9189	21621		1.74	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' and similar to similar to ribosomal protein S18
9930	22045	34976	2.32	3.0E-69	X13223.1	NT	H. sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase
9717	22140	35097	2.6	3.0E-69	X06233.1	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
10437	22889	35865	10.88	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
10619	23062		10.26	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
11728	24018		6.32	3.0E-69	11419167	NT	Homo sapiens HGC8.2 protein (HGC8.2), mRNA
133	12995	25420	0.88	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
133	12995	25421	0.88	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
421	12995	25420	5.03	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
421	12995	25421	5.03	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
2799	16366		2.97	2.0E-69	AA431157.1	EST_HUMAN	zw71g02.r1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:781882 5'
9038	21470	34380	0.97	2.0E-69	AA114270.1	EST_HUMAN	zm28g01.r1 Striatogene pancreas (#937208) Homo sapiens cDNA clone IMAGE:527088 5'
1700	14228	26710	1.99	1.0E-69	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
6128	17634		0.85	1.0E-69	BE409094.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635781 5'
6358	18914	31647	0.73	1.0E-69	BE902501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
6356	18914	31648	0.73	1.0E-69	BE902501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
6960	19497	32276	4.28	1.0E-69	AW393989.1	EST_HUMAN	QV0-TT0010-031195-045-c07 TT0010 Homo sapiens cDNA
7210	18921	32750	1.44	1.0E-69	7662283	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7210	18921	32751	1.44	1.0E-69	7662283	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7229	19841	32658	3.45	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7229	19841	32669	3.45	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7286	19791	32601	0.55	1.0E-69	BE531007.1	EST_HUMAN	G01278532F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3610614 5'
7286	19791	32602	0.55	1.0E-69	BE531007.1	EST_HUMAN	G01278532F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3610614 5'
10160	22561	35528	4.74	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10160	22561	35529	4.74	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10222	22823	35580	1.13	1.0E-69	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
10654	23094		41.63	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
11658	23975	36553	1.78	1.0E-69	BF125887.1	EST_HUMAN	G01762802F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:4025785 5'
12094	24244		3.34	1.0E-69	AB090994.1	EST_HUMAN	wf64e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23600390 3' similar to contains Alu repetitive element; contains element M1R repetitive element;
2227	15331	27257	1.45	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.1 NCI CGAP P1 Homo sapiens cDNA clone IMAGE:1008023
4365	16917	28302	1.93	8.0E-70	L77608.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1789	14314	26807	1.35	7.0E-70	A1497807.1	EST_HUMAN	tm89f01.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1789	14314	26808	1.35	7.0E-70	A1497807.1	EST_HUMAN	tm89f01.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1881	14403	26897	1.18	7.0E-70	AA282955.1	EST_HUMAN	z15h04.1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
1988	14504		4.01	7.0E-70	5031668	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4242	18767	29153	5.34	7.0E-70	4757723	NT	Homo sapiens adenylyate cyclase 3 (ADCY3) mRNA
5743	18325	30761	5.27	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5743	18325	30762	5.27	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7334	19748	32549	1.84	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding epigenetic factor SF1, exons 2-8
8324	20739	33634	1	7.0E-70	11417306	NT	Homo sapiens titin immunoglobulin domain protein (myotilin) (TTID), mRNA
8408	20822	33719	0.47	7.0E-70	11419404	NT	Homo sapiens cerebral cavernous malformations 1 (CCM1), mRNA
8953	21388	34297	3	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8953	21388	34298	3	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
9152	21584	34491	4.61	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
9152	21584	34492	4.61	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
9444	21875	34763	4.62	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9444	21875	34794	4.62	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9644	20935	33832	1.37	7.0E-70	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9664	20854	33854	2.45	7.0E-70	11525984	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9664	20854	33855	2.45	7.0E-70	11525984	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10240	22841	35603	0.91	7.0E-70	AB036428.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10240	22841	35604	0.91	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10856	23289	36281	2.12	7.0E-70	11429985	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA
10856	23289	36282	2.12	7.0E-70	11429985	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA
11346	23710	38766	2.11	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11346	23710	36767	2.11	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
12381	24858	30587	6.28	7.0E-70	Z00040.1	NT	Human kappa-immunoglobulin germ line pseudogene variable region (subgroup V kappa I)
12578	24558	30845	9.1	7.0E-70	Z00040.1	NT	Human kappa-immunoglobulin germ line pseudogene variable region (subgroup V kappa I)
894	13448	25887	3	6.0E-70	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2053	14568	27083	4.57	6.0E-70	M30338.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2463	15338	27474	1.58	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2463	15338	27475	1.58	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
11669	23982		2.68	5.0E-70	BE186034.1	EST_HUMAN	MR3-HT0487-150200-115-a08 HT0487 Homo sapiens cDNA
7135	19687	32462	0.84	4.0E-70	T06037.1	EST_HUMAN	EST03926 Fetal brain, Stratagens (cat#836206) Homo sapiens cDNA clone HFBND25
7179	19892	32716	0.7	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
7179	19892	32717	0.7	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
1608	14137	28604	1.17	3.0E-70	BE071786.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
1606	14137	26605	1.17	3.0E-70	BE071786.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
5887	18466	31143	0.65	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5887	18466	31144	0.65	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
6243	18807	31620	1.19	3.0E-70	A1831975.1	EST_HUMAN	wh90cd03.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2388005 3'
6706	19253	32005	2.01	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302808 5'
6706	19253	32006	2.01	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302808 5'
40	12660	26052	0.66	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
709	13271	25688	15.45	2.0E-70	N42161.1	EST_HUMAN	W07a10.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
709	13271	25689	15.45	2.0E-70	N42161.1	EST_HUMAN	W07a10.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
725	13288	25712	3.32	2.0E-70	A1246899.1	EST_HUMAN	W07a10.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to W07a10.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to
1047	13593	26033	1.7	2.0E-70	8923668	NT	W07a10.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to W07a10.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to
1215	13755	26200	2.14	2.0E-70	7661983	NT	Homo sapiens hypophthalmin protein FLJ20768 (FLJ20768), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1215	13755	26201	2.14	2.0E-70	7661983	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1734	14261	26746	1.9	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2214	14724		7.52	2.0E-70	AA054010.1	EST_HUMAN	z48g04.r1 Soares refina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
3623	16163	28573	0.68	2.0E-70	H37988.1	EST_HUMAN	P03345 GAG POLYPROTEIN ;
3628	16365	28764	0.61	2.0E-70	AL133207.2	EST_HUMAN	yp58b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:191599 5'
3955	18490	28899	1.68	2.0E-70	AJ246003.1	NT	Novel human gene mapping to chromosome X
4061	18592	28994	5.24	2.0E-70	M69181.1	NT	Homo sapiens Spast gene for spastin protein
6777	18358	30818	10.01	2.0E-70	X72682.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5777	18358	30818	10.01	2.0E-70	X72682.1	NT	H. sapiens gene for schwannomin (CS8)
6518	18071	31814	1.48	2.0E-70	AF310105.1	NT	H. sapiens gene for schwannomin (CS8)
6997	18533	32316	2.17	2.0E-70	D12625.1	NT	Homo sapiens NALP1 mRNA, complete cds
7035	19570	32359	12.52	2.0E-70	AF123074.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
7035	19570	32360	12.52	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7415	18084	30378	1.99	2.0E-70	11422642	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
7883	20322	33187	0.67	2.0E-70	AF288207.1	NT	Homo sapiens cysteinyl-tRNA synthetase mRNA, complete cds, alternatively spliced
8574	21009	33908	5.68	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
9112	21544		1.02	2.0E-70	H47959.1	EST_HUMAN	yp78g02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193682 5'
9453	21864	34804	1.34	2.0E-70	11626365	NT	Homo sapiens dynactin p62 subunit (LOC51184), mRNA
10142	22543	35512	1.02	2.0E-70	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10851	23284	38274	3.67	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
10851	23284	38275	3.67	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11368	23748	38807	24.19	2.0E-70	4503620	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
12082	24233	30959	2.39	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12082	24233	30960	2.39	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3371	15917		2.99	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
10711	23148	36132	8.47	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLBGB10 5'
6242	18808	31518	5.77	9.0E-71	AI143870.1	EST_HUMAN	qo04f01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6242	18808	31519	5.77	9.0E-71	AI143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE ;
							qo04f01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
							O14045 PHOSPHOTRANSFERASE ;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptar
7459	19982	32798	2.31	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.;
11278	19982	32798	3.6	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.;
9390	21822		2.74	8.0E-71	AA171451.1	EST_HUMAN	z021d11.1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:810101 5' similar to TR:G1143081 G1143081 STRAIN XA34 POL.;
7849	20289	33152	8.71	7.0E-71	AA442230.1	EST_HUMAN	z60h06.f1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:768075 5'
9120	21662	34456	1.37	7.0E-71	AA705457.1	EST_HUMAN	z191a08.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
2118	14628	27152	7.93	5.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4138	16885	28052	1.55	5.0E-71	AW818405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
6169	18737	31438	1.59	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 8 (CDK8) mRNA
7028	18684	32351	1.31	5.0E-71	11641408	NT	Homo sapiens keratin, hair, acidic, 7 (KRT47), mRNA
7329	18741	32544	1	5.0E-71	7662209	NT	Homo sapiens KIAA0823 gene product (KIAA0823), mRNA
7391	18060	30400	0.48	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
7391	18060	30401	0.48	5.0E-71	AB033108.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
7586	20035	32883	1.01	5.0E-71	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
8018	20448	33319	1.69	5.0E-71	M38108.1	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
8251	20688	33558	0.88	5.0E-71	11526445	NT	Homo sapiens MAGUK protein p55T; Protein Associated with Lins 2 (LOC51878), mRNA
8285	20701	33595	26	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
9977	22379		2.13	5.0E-71	X13467.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
10490	22840	35920	1.78	5.0E-71	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
10490	22940	35921	1.78	5.0E-71	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
10762	23200	36186	9.06	5.0E-71	11436514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
11983	24176		1.26	5.0E-71	11418039	NT	Homo sapiens RNA binding motif protein 9 (RBM9), mRNA
107	12724	28138	3.38	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
384	12954	28370	25.68	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
384	12934	28371	25.68	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2840	15395	27810	1.56	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4457	16977	29363	7.34	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5084	17594	29901	7.78	4.0E-71	7687602	NT	Homo sapiens putative home-binding protein (SOUL), mRNA
8658	21091		1.22	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone IMAGE:1043083 similar to contains PTR5.13 PTR5
10480	22830	35908	2.52	3.0E-71	AA557683.1	EST_HUMAN	n145h10.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043083 similar to contains PTR5.13 PTR5 repetitive element;

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1263	13800	26249	4.46	2.0E-71	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
5573	18161	30526	8.45	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5573	18161	30527	8.45	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
7383	18053	30391	0.56	2.0E-71	AL042439.1	EST_HUMAN	DKFZp434D1721.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1721.5'
10422	22822	35791	2.85	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10422	22822	35792	2.85	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10482	22832	36809	6.13	2.0E-71	BE018477.1	EST_HUMAN	bb81a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048764 5' similar to SW.R238_HUMAN P64727 UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B ;
11330	23694	36746	3.94	2.0E-71	R56628.1	EST_HUMAN	y17g11.r1 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:154772 5'
11740	24027		7.69	2.0E-71	T89489.1	EST_HUMAN	y943e09.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120520 5'
657	13222	25633	1.4	1.0E-71	AI077627.1	EST_HUMAN	oy15b03.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element ;
965	13518	25962	1.49	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1127	13871	26110	5.24	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1372	13907	26363	19.3	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2007	14523	27036	1.59	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2007	14523	27037	1.59	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2841	15136	27646	6.76	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3479	16022	28443	1.78	1.0E-71	AF119685.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3590	16132	28544	7.23	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3590	16132	28545	7.23	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3648	16188	28594	0.78	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3648	16188	28595	0.78	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3740	16280	28693	1.97	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4504	17022	29404	1.85	1.0E-71	D28478.1	NT	Human mRNA for KIAA0045 gene, complete cds
4631	17147	29527	0.69	1.0E-71	H23176.1	EST_HUMAN	ym56h10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52528 5'
7122	19655	32451	1.23	1.0E-71	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
7523	18974	32808	1.55	1.0E-71	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
7776	20217	33079	89.54	1.0E-71	U80753.1	NT	Homo sapiens CAC179 mRNA, partial cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8763	21187	34088	2.2	1.0E-71	11428430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8960	21393	34304	5.1	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
8960	21393	34305	5.1	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
10039	22441	35388	7.1	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
10088	22489		3.82	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10398	22798	35773	1.28	1.0E-71	11433142	NT	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
10566	23013		2.68	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10665	23105	36086	3.79	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
10926	23358	36368	2.09	1.0E-71	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
10926	23358	36369	2.09	1.0E-71	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
12137	24270		9.64	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
424	12998	25423	0.92	9.0E-72	AB057635.1	EST_HUMAN	wk85g03.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.8 KD PROTEIN; contains Alu repetitive element;
424	12998	25424	0.92	9.0E-72	AB057635.1	EST_HUMAN	wk85g03.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.8 KD PROTEIN; contains Alu repetitive element;
11489	23857	36931	6.71	9.0E-72	BF573955.1	EST_HUMAN	602131973F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271155 5'
11489	23857	36932	6.71	9.0E-72	BF573955.1	EST_HUMAN	602131973F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271155 5'
6422	18979	31712	0.82	8.0E-72	BF035762.1	EST_HUMAN	601458747F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862451 5'
10893	23325	36324	3.63	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
10893	23325	36325	3.63	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
10893	23325	36326	3.63	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
4129	16657	28041	1.63	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4129	16657	29042	1.63	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4129	16657	29043	1.63	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7594	20014	32858	2.84	7.0E-72	S41694.1	NT	(pseudogene) PTMAP2-prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
12271	24385		1.34	7.0E-72	F26259.1	EST_HUMAN	HSPD13670 HM3 Homo sapiens cDNA clone s4000051 G02
8920	21354		4.41	6.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
65	12685	25093	1.35	6.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
65	12685	25094	1.35	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
66	12685	25093	3.57	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
66	12685	25094	3.57	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1168	13709		2.2	5.0E-72	L11845.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7361	10818	32832	1.86	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8166	21628	34538	4.12	6.0E-72	AW161274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782584 5' similar to
11011	23438	36455	5.18	6.0E-72	BF331571.1	EST_HUMAN	TR-Q99785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN ;contains element MSR1 repetitive element ;
11011	23438	36456	5.18	6.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-405 BT0598 Homo sapiens cDNA
11817	24916		2.98	5.0E-72	BE926645.1	EST_HUMAN	MR4-BT0598-010600-005-405 BT0598 Homo sapiens cDNA
4878	17391		1.14	4.0E-72	11034944	NT	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA
5723	18305	30736	0.98	4.0E-72	AF170025.1	NT	Homo sapiens hypothetical protein J1057B20.2 (J1057B20.2), mRNA
6910	19449	32228	0.91	4.0E-72	T87947.1	EST_HUMAN	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds
7889	20328	33194	1.93	4.0E-72		NT	y493a01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to
							SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
							Homo sapiens heet domain and RLD 2 (HERC2), mRNA
							q167c02.x1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1849730 3' similar to
							TR:Q14498 Q14498 SPLICING FACTOR. [1]; contains Alu repetitive element; contains element L1 repetitive element ;
10316	22716	35683	0.84	4.0E-72	A1248786.1	EST_HUMAN	yu28a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:236084 5'
11284	23849	36696	7.9	4.0E-72	H79421.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11384	23746	36803	1.94	4.0E-72	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11384	23746	36804	1.94	4.0E-72	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11413	23774	36833	4.21	4.0E-72	T81910.1	EST_HUMAN	y429d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
12185	24314	30913	6.83	4.0E-72	AJ277646.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
20	12840	25027	3.94	3.0E-72	5031978	NT	Homo sapiens pro-B-cell colony-enhancing factor (PBEF) mRNA
926	13480		1.53	3.0E-72	AA723823.1	EST_HUMAN	ah63a03.s1 Soares testis_NHT Homo sapiens cDNA clone 1310290 3'
1184	13726	26166	8.44	3.0E-72	U16308.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1184	13726	26167	8.44	3.0E-72	U16308.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1224	13764	26208	1.72	3.0E-72	U60226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1224	13764	26209	1.72	3.0E-72	U60226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
3036	15591	28003	14.28	3.0E-72	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3241	15782	28210	3.17	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3832	16369	28788	2.55	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction) [human, precursor B-cell line REH, mRNA Partial, 211 nt]

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4446	18966	29353	0.94	3.0E-72	AF143892.1	NT	Homo sapiens thioredoxin-like protein (TXNL) gene, exon 3
4448	18968	29354	0.94	3.0E-72	AF143892.1	NT	Homo sapiens thioredoxin-like protein (TXNL) gene, exon 3
4581	17097	29485	3.51	3.0E-72	11418186	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
5282	17763	30132	4.84	3.0E-72	AW959877.1	EST_HUMAN	EST371747.MAGE resequences, MAGF Homo sapiens cDNA
5782	18963		1.18	3.0E-72	4755093	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6281	18843	31561	1.89	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6281	18843	31562	1.89	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6480	18035	31774	4.95	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6480	18035	31775	4.95	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6970	19507	32287	4.32	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
8104	20530	33407	1.64	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
8759	21183	34095	1.48	3.0E-72	5031892	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
10325	22725	35692	1.36	3.0E-72	X98289.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
10374	23021	36008	2.39	3.0E-72	AB030074.1	NT	Homo sapiens mRNA for K-sam-1H2, partial cds
11332	23896	36748	7.94	3.0E-72	11424091	NT	Homo sapiens CD37 antigen (CD37), mRNA
11332	23896	36749	7.94	3.0E-72	11424091	NT	Homo sapiens CD37 antigen (CD37), mRNA
11470	23828	36895	13	3.0E-72	4506052	NT	Homo sapiens primase, polypeptide 2A (58kD) (PRIM2A) mRNA
11470	23828	36896	13	3.0E-72	4506052	NT	Homo sapiens primase, polypeptide 2A (58kD) (PRIM2A) mRNA
12101	24250	30927	2.48	3.0E-72	AB011389.1	NT	Homo sapiens gene for AF-9, complete cds
6257	18821	31536	1.58	2.0E-72	11426671	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
10523	22970	36950	2.02	2.0E-72	AA789277.1	EST_HUMAN	aj28b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:X02087 H.septens mRNA for 7SL RNA pseudogene (HUMAN);
12180	24310	30910	8.34	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
1989	14515	27025	3.4	1.0E-72	AA846225.1	EST_HUMAN	al83d02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395 3'
6047	18618	31308	4.37	1.0E-72	7657678	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6912	19451	32228	1.49	1.0E-72	11321678	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6912	19451	32230	1.49	1.0E-72	11321678	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6995	24620	32314	1.37	1.0E-72	AV751818.1	EST_HUMAN	AV751818.NPD Homo sapiens cDNA clone NPDAIE11 5'
7813	20255	33116	0.42	1.0E-72	BE761978.1	EST_HUMAN	60155588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940460 5'
8168	20590	33471	4.32	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
8168	20590	33472	4.32	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9759	22102	35095	7	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9769	22162	36098	7	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1488	14020	26484	1.26	9.0E-73	AW374988.1	EST_HUMAN	MRO-CT00683-071089-002-h11 CT00683 Homo sapiens cDNA
6344	18902	31636	0.91	9.0E-73	11525983	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
10729	23167		143.76	9.0E-73	11424098	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1063	13608	26048	0.93	8.0E-73	AW071755.1	EST_HUMAN	ws55c08.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2601088 3' similar to TR:Q59050
3256	15907	28223	0.59	8.0E-73	11435180	NT	Homo sapiens gephyrin (GPH), mRNA
6945	18426	31096	0.78	8.0E-73	4505788	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
6926	19484	32242	-5.45	8.0E-73	11428469	NT	Homo sapiens lysozyme homolog (LOC57151), mRNA
8700	21135	34039	2	8.0E-73	AF113129.1	NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9585	22008	34936	9.85	8.0E-73	BE018900.1	EST_HUMAN	bb82a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
9860	22263	35200	1.57	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9860	22263	35201	1.57	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
11327	23691	36744	2.19	8.0E-73	11418786	NT	Homo sapiens DEAD-box protein (HAGE), mRNA
12020	24187	30861	1.18	8.0E-73	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12268	24356	30901	3.69	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
1161	13704	26144	1.17	7.0E-73	8923260	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3264	15815	28232	0.74	7.0E-73	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
5026	17536		1.84	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
162	12767		2.66	8.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7616	20065	32917	4.08	8.0E-73	BE166574.1	EST_HUMAN	QV0-HT0494-020300-137-403 HT0494 Homo sapiens cDNA
5504	18095	30339	2.28	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM44A1), mRNA
1834	14356	28856	1.21	3.0E-73	11435913	NT	Homo sapiens home-binding protein (HEBP), mRNA
1834	14356	28857	1.21	3.0E-73	11435913	NT	Homo sapiens home-binding protein (HEBP), mRNA
7068	19802	32397	0.95	3.0E-73	AA136403.1	EST_HUMAN	z085e04.s1 Stratagene fetal retina 537202 Homo sapiens cDNA clone IMAGE:566950 3' similar to
10478	22928		2.41	3.0E-73	X99660.1	NT	gb:Z23064_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
10790	23228	36211	1.71	3.0E-73	BE711238.1	EST_HUMAN	H. sapiens SH3GLP2 pseudogene, 5' end
10790	23228	36212	1.71	3.0E-73	BE711238.1	EST_HUMAN	RC8-HT0878-290600-013-H10 HT0878 Homo sapiens cDNA
11357	23720		1.73	3.0E-73	AI004040.1	EST_HUMAN	RC8-HT0878-290600-013-H10 HT0878 Homo sapiens cDNA
12516	24616		1.58	3.0E-73	AL183246.2	NT	out1102.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1625955 3'
						NT	Homo sapiens chromosome 21 segment HS21C046

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12520	24518		1.84	3.0E-73	AW898081.1	EST_HUMAN	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA
874	13429	25877	2.09	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
1897	14417		2.88	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA
2192	14703		0.89	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3138	15691	28109	1.8	2.0E-73	4502682	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3535	16078	28494	0.76	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3535	16078	28495	0.76	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4463	16983		1.01	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6777	19320	32085	0.51	2.0E-73	AF086824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
6777	19320	32086	0.51	2.0E-73	AF086824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
6828	19369	32147	6.22	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7071	19805	32399	1.31	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7071	19805	32400	1.31	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
8985	20799	33697	0.58	2.0E-73	M04048.1	NT	Human peripheral myelin protein 22 mRNA, complete cds
8392	20806	33705	0.46	2.0E-73	AB037760.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
10318	22718	35698	1.52	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10372	22772	35741	1.67	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10372	22772	35742	1.67	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10536	22983	35963	2.35	2.0E-73	11431598	NT	Homo sapiens KIAA1080 protein; Golgi-associated, gamma-adenin ear containing, ARF-binding protein 2 (KIAA1080), mRNA
10837	23272	36281	7.2	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
10837	23272	36282	7.2	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
12021	14417		2.18	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA
1764	14291	29774	2.72	1.0E-73	AU121695.1	EST_HUMAN	AUT121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2385	14889	27409	2.66	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
6692	18239	31989	1.21	1.0E-73	BE151283.1	EST_HUMAN	CM1-HT0282-111199-042-h10 HT0282 Homo sapiens cDNA
9692	22104	35031	1.18	1.0E-73	AI147427.1	EST_HUMAN	qg61b07.r1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element
11200	22852	35825	6.24	1.0E-73	BE385477.1	EST_HUMAN	MER22 repetitive element;
11462	23820	36692	1.79	9.0E-74	X77225.1	NT	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5'
11462	23820	36693	1.79	9.0E-74	X77225.1	NT	H. sapiens mRNA for TFIIA
761	13321	25750	1.2	8.0E-74	4557426	NT	H. sapiens mRNA for TFIIA
							Homo sapiens CD39-like 4 (CD39L4) mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6209	18775	31480	2	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3429 nt]
6209	18775	31481	2	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3429 nt]
1800	14419	26917	4.2	7.0E-74	AJ001689.1	NT	Homo sapiens NK62D gene, exon 10
3298	15847	28265	1.44	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
9508	21989	34892	2.4	7.0E-74	BE967432.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3932997 5'
12257	24355	30900	4.05	7.0E-74	BE266305.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3535855 5'
1149	13693	26134	3.91	6.0E-74	AF108907.1	NT	Homo sapiens S164 gene, partial cds, PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
2210	14720	27241	32.73	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2210	14720	27242	32.73	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
3710	16250	26654	1.61	6.0E-74	BE048846.1	EST_HUMAN	h64e11.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3710	16250	26655	1.61	6.0E-74	BE048846.1	EST_HUMAN	h64e11.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5621	18208	30607	4.67	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
928	13482	25928	2.53	6.0E-74	AY020986.1	EST_HUMAN	h17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2651	15144		10.45	6.0E-74	AW362756.1	EST_HUMAN	PMO-C70289-271089-001-h07 C70289 Homo sapiens cDNA
5663	18248	30648	2.18	6.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
6073	18646	31340	15.53	6.0E-74	X89870.1	NT	H. sapiens mRNA for TPCR18 protein
6125	18894	31391	7.42	6.0E-74	4507868	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6201	18767	31470	2.04	6.0E-74	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
6201	18767	31471	2.04	6.0E-74	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
7301	19805	32617	2.43	6.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8206	19805	32617	0.67	6.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8658	21093	33999	1.87	6.0E-74	11345483	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
10518	22967	35946	5.36	6.0E-74	Y09420.1	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10619	22967	35947	5.36	6.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
10629	23071	36057	2.37	6.0E-74	5729768	NT	H. sapiens mRNA for HIP-1
293	12889	26310	2.32	4.0E-74	D87676.1	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
876	13430	25878	7.28	4.0E-74	AB028942.1	NT	Homo sapiens DNA for anyfold precursor protein, complete cds
							Homo sapiens mRNA for KIAA1019 protein, partial cds
1911	14430	26927	1.52	4.0E-74	AB028998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1911	14430	26928	1.52	4.0E-74	AB028998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1988	14612	27021	4.67	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
1996	14512	27022	4.67	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2050	14566	27080	1.66	4.0E-74	AB032994.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
3053	15607	28017	5.56	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3509	16052	28473	1.21	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4078	16809	28997	1.01	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4593	17109	29498	1.68	4.0E-74	7602183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4656	17172	29553	0.97	4.0E-74	Z1727.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5124	17631	29992	0.79	4.0E-74	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
5444	17838	30288	6.64	4.0E-74	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
8036	21468		5.58	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
8600	22080	35007	2.36	3.0E-74	M78984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Striatum (cat. #836205) Homo sapiens cDNA clone HHCPF91
10267	22668	35631	2.58	3.0E-74	AA601493.1	EST_HUMAN	no17q05.s1 NCI CGAP Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
882	13535	25976	31.87	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
882	13535	25978	31.87	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1208	13747	28192	1.09	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T47D
1277	13813	26267	2.3	2.0E-74	AI950528.1	EST_HUMAN	wx51e07.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
1612	14143	26812	3.31	2.0E-74	4885198	NT	Q08379 GOLGIN-95, contains element MER22 repetitive element;
1612	14143	26613	3.31	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblast leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2528	15027	27543	3.97	2.0E-74	AI557280.1	EST_HUMAN	Homo sapiens epidermal growth factor receptor (avian erythroblast leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
5108	17616	28978	2.85	2.0E-74	AL355092.1	NT	PT2.1_15_G11.r tumor2 Homo sapiens cDNA 3'
5112	17620	29983	1.55	2.0E-74	J02963.1	NT	Novel human gene mapping to chromosome 22
5432	17827	30278	0.98	2.0E-74	BE409494.1	EST_HUMAN	Novel human gene mapping to chromosome 22
5432	17827	30279	0.98	2.0E-74	BE409494.1	EST_HUMAN	Human platelet glycoprotein IIb mRNA, 3' end
6082	24599	31346	1.95	2.0E-74	BE711134.1	EST_HUMAN	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
6187	24602	31454	2.13	2.0E-74	11439587	NT	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
6187	24602	31455	2.13	2.0E-74	11439587	NT	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
6266	24602	31454	2.92	2.0E-74	11439587	NT	RC8-HT0878-220500-011-C03 HT0878 Homo sapiens cDNA
6266	24602	31455	2.92	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
6266	24602	31455	2.92	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7542	19992	32831	0.92	2.0E-74	BF030788.1	EST_HUMAN	601557524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
8592	21027	33928	1.69	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
8607	22087	35015	6.12	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
11953	24156		2.78	2.0E-74	AA196181.1	EST_HUMAN	z996a06.s1 Stielagen muscle 897209 Homo sapiens cDNA clone IMAGE:628018 3'
55	12876	25077	2.23	1.0E-74	7657334	NT	Homo sapiens Missheper/NIK-related kinase (MINK), mRNA
351	12841	25355	5.24	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
617	13090	25503	1	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
624	13098	25508	3.97	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
618	13188	25590	1.7	1.0E-74	4508020	NT	Homo sapiens zho finger protein 259 (ZNF259) mRNA
1028	13577	28018	1.92	1.0E-74	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
2132	14846	27169	3.48	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3100	15683	28065	2.87	1.0E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3934	16488	28878	0.65	1.0E-74	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3934	16489	28879	0.65	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3982	16517	28922	5.98	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
4079	16610	28988	1.06	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0842-270300-019-06 BT0842 Homo sapiens cDNA
					h273h08.x1 NCL_CGAP_Lu24	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:B0511.12
4284	16809	29193	0.68	1.0E-74	BE467769.1	EST_HUMAN	CE17351
5366	17864	30223	0.94	1.0E-74	8659564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
5366	17864	30224	0.94	1.0E-74	8659564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
7077	19811	32404	0.91	1.0E-74	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
8157	20580	33458	1	1.0E-74	11417977	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
8410	20824	33721	0.48	1.0E-74	9506658	NT	Homo sapiens hypothetical protein similar to tumor suppressor p33ING1 (FLJ20089), mRNA
8874	21108	34011	1.36	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8874	21109	34012	1.36	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
9218	21650	34562	5.49	1.0E-74	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (FLUNC) gene, complete cds
10384	22784	35732	1.74	1.0E-74	11420549	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
11536	23893	36976	4.78	1.0E-74	D26181.1	NT	Human mRNA for novel protein kinase PKN, complete cds
11573	23918	37002	1.58	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
11659	23976		3.83	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
11813	14645	27169	1.55	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2580	15076		8.42	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
11977	24171		2.26	8.0E-76	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2215	14725	27248	1.82	6.0E-75	AB17415.1	EST_HUMAN	wk38a08.x1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cd84
11245	23611	36656	1.87	6.0E-75	BE781831.1	EST_HUMAN	RETROVIRUS-RELATED POL POL YPROTEIN (HUMAN);
7031	19567	32354	0.5	5.0E-75	BF211517.1	EST_HUMAN	601686109F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940130 5'
8382	20777	33678	0.41	5.0E-75	AA573446.1	EST_HUMAN	601812201F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048497 5'
8382	20777	33677	0.41	6.0E-75	AA573446.1	EST_HUMAN	nk89d03.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:1028933 3'
9285	21717	34828	1.14	5.0E-75	BE272325.1	EST_HUMAN	nk89d03.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:1028933 3'
9601	22081	35008	1.19	5.0E-75	BF690264.1	EST_HUMAN	601128088F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989865 5'
10201	22602	35586	3.1	5.0E-75	AI638623.1	EST_HUMAN	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
11515	23873	36953	3.09	6.0E-75	BE789623.1	EST_HUMAN	tt31c12.x1 NCL CGAP_GC08 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361
116	12728	25141	1.75	4.0E-75	BE081333.1	EST_HUMAN	HYPOTHETICAL 20.1 KD PROTEIN;
476	13050	26764	0.92	4.0E-75	N38757.1	EST_HUMAN	601692016F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3948227 5'
1753	14280	26764	0.91	4.0E-75	AW997230.1	EST_HUMAN	QV1-BT0632-210200-078-e02 BT0632 Homo sapiens cDNA
2804	15361	27778	5.68	4.0E-75	BE409464.1	EST_HUMAN	yx30r08.r1 Scarses melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:268055 5'
5791	18372	31030	0.68	4.0E-75	11417946	NT	CMO-NN0057-150400-335-at11 NN0057 Homo sapiens cDNA
5791	18372	31030	0.68	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5593	19144	31892	6.25	4.0E-75	5579457	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
7140	19871	32467	1.66	4.0E-75	11417946	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (10KD) (EIF3S8), mRNA
7140	19871	32468	1.66	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10478	22926	35906	22.48	4.0E-75	7689505	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
1029	13680	26021	3.85	3.0E-75	AF157623.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
1030	13580	26021	2.77	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1811	14334	26828	1.43	3.0E-75	AB011153.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2323	14830	27344	4.73	3.0E-75	4759153	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2981	15536	27663	0.96	3.0E-75	AL163201.2	NT	Homo sapiens synaptsomal-associated protein, 29KD (SNAP29) mRNA
3146	15699	28117	1.06	3.0E-75	AB011153.1	NT	Homo sapiens chromosome 21 segment HS21C001
3323	15870	28280	0.98	3.0E-75	MT2393.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3323	15870	28291	0.98	3.0E-75	MT2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3738	16276	28681	0.63	3.0E-75	MT2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4184	16711	28102	1.95	3.0E-75	D87675.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
5501	18092	30333	1.21	3.0E-75	11420956	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
5501	18092	30334	1.21	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6858	19398	32174	0.86	3.0E-75	AF123074.1	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
						NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6858	19398	32175	0.68	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7152	19885	32885	1.66	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7152	19885	32886	1.66	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7575	20025	32868	4.68	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7575	20025	32869	4.69	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
8163	20576	33451	3.18	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
8163	20576	33452	3.18	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
9330	21762	34669	1.54	3.0E-75	11420804	NT	Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNAIL), mRNA
5942	18520		1.16	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cDNA Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q66386 Q66386
9176	21607	34517	1.7	2.0E-75	AI311783.1	EST_HUMAN	q991e02.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:728485 3' similar to TR:Q66386 Q66386
2197	14708	27229	5.44	1.0E-75	AW168135.1	EST_HUMAN	POL/ENV GENE ;
2800	15455	27982	2.22	1.0E-75	X62221.1	NT	hg60d02.x1 NCL CGAP_U44 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.t1
4741	17253	29635	0.9	1.0E-75	BE276301.1	EST_HUMAN	H.sapiens ERCC2 gene, exons 1 & 2 (partial)
8109	20535	33412	0.81	1.0E-75	BE082528.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
8109	20535	33413	0.81	1.0E-75	BE082528.1	EST_HUMAN	RC05-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
8941	21374		4.94	1.0E-75	AA389270.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
9638	22053	34983	4.49	1.0E-75	BF313645.1	EST_HUMAN	z457h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728485 3' similar to gb:U13932 40S
9638	22053	34984	4.49	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
10686	23106		3.57	1.0E-75	AA664377.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129878 5'
10675	23308	36304	2.55	1.0E-75	AF223391.1	NT	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129878 5'
11868	18014	30446	2.22	1.0E-75	BE694192.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129878 5'
46	12667	25091	1.19	9.0E-78	AI652648.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129878 5'
46	12667	25092	1.19	9.0E-78	AI652648.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129878 5'
2315	14822		3.99	9.0E-78	AA702415.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129878 5'
9970	22372	35320	29.07	9.0E-78	M12937.1	NT	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129878 5'
982	13516	25958	1.51	8.0E-78	4504374	NT	Human ferritin Heavy subunit mRNA, complete cds
							Homo sapiens H factor 1 (complement) (HF1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
982	13515	28569	1.51	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HFI) mRNA
2446	14947	27464	4.94	8.0E-76	AF228180.1	NT	Homo sapiens alpha-aminoacidic semialdehyde synthase mRNA, complete cds
2884	15419	27842	1.38	8.0E-76	7706724	NT	Homo sapiens mediator (Sur2), mRNA
6485	19040	31780	5.73	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7992	20428	39292	1.73	8.0E-76	11435215	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
8082	20510	33389	0.97	8.0E-76	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55872), mRNA
10281	22692	35658	1.27	8.0E-76	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
10459	22810	35890	4.97	8.0E-76	10442821	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
12236	24343		1.65	8.0E-76	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12341	24821	30589	1.63	8.0E-76	AL365515.1	NT	Novel human gene mapping to chromosome 22
798	13356	25762	1.11	7.0E-76	5016092	NT	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3257	15808	28224	3.43	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3263	15814	28231	8.24	7.0E-76	4505082	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3308	16856	28278	2.74	7.0E-76	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
4393	16915	29289	3.77	7.0E-76	4507194	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4393	16915	29300	3.77	7.0E-76	4507194	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1287	13803		21.63	6.0E-76	BE308263.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3688787 5'
11217	22869	35943	2.2	6.0E-76	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'
1894	14414	26911	8.99	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1894	14414	26912	8.99	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1894	14414	26913	8.99	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3165	15718	28139	0.71	4.0E-76	BE814096.1	EST_HUMAN	QV3-BN0047-270700-283-q06 BN0047 Homo sapiens cDNA
5521	18111	30355	1.12	4.0E-76	BE783412.1	EST_HUMAN	601471725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874470 5'
10053	22454	35403	6.49	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TF-ujlwara) Homo sapiens cDNA clone GEN-178G01 5'
10053	22454	35404	6.49	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TF-ujlwara) Homo sapiens cDNA clone GEN-178G01 5'
648	13212	25621	2.07	3.0E-76	BF516262.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
648	13212	25622	2.07	3.0E-76	BF516262.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1616	14147	26917	4.36	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1616	14147	26918	4.36	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3406	15951	28363	5.17	3.0E-76	BF375889.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3406	15951	28364	5.17	3.0E-76	BF375889.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4094	18825	29016	4.83	3.0E-76	BE348693.1	EST_HUMAN	h107H12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151823 3' similar to TR:O94886 O94886
5487	17899	36998	2.47	3.0E-76	Z41314.1	EST_HUMAN	KIAA0792 PROTEIN.;
							HSCZQD042 normalized Infant brain cDNA Homo sapiens cDNA clone c-zq04 3'
6008	18582	31268	0.88	3.0E-76	AA180611.1	EST_HUMAN	z073c07.11 Stratigene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592524 5' similar to
6280	18852	31573	0.65	3.0E-76	AW027705.1	EST_HUMAN	gbL32976 MIXED LINEAGE KINASE 1 (HUMAN);
6701	19248	31899	10.1	3.0E-76	AF286598.1	NT	w075c05.x1 Soares_thymus_NHFT Homo sapiens cDNA clone IMAGE:2535368 3'
8738	21170	34075	1.18	3.0E-76	N42671.1	EST_HUMAN	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
9846	22249	35184	3.99	3.0E-76	AW288353.1	EST_HUMAN	yy20g10.11 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:271842 5'
9861	22284	35202	0.83	3.0E-76	AA442309.1	EST_HUMAN	xs49h01.x1 NCL CGAP_K1011 Homo sapiens cDNA clone IMAGE:2773009 3'
9861	22284	35203	0.83	3.0E-76	AA442309.1	EST_HUMAN	z54411.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:767461 5'
11563	24729	30878	1.92	3.0E-76	AW867884.1	EST_HUMAN	z54411.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
11673	24861	30450	3.49	3.0E-76	AW958455.1	EST_HUMAN	EST380059 MAGI2 resequences; MAGJ Homo sapiens cDNA
295	12891	25312	1.22	2.0E-76	D84295.1	NT	EST386525 MAGI2 resequences; MAGD Homo sapiens cDNA
356	12946	25359	2.81	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
356	12946	25359	2.81	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
478	13052	26360	0.83	2.0E-76	4557662	NT	Human mRNA for possible protein TPRDII, complete cds
607	13175	26578	1.18	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1056	13602	26044	1.04	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1558	14080	26552	1.92	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1558	14080	26553	1.92	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
2787	15354	27774	2.93	2.0E-76	P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F6
3260	15811	28228	2.39	2.0E-76	AA445992.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
							P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.;
3260	15811	28229	2.39	2.0E-76	AA445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.;
4153	12891	25312	0.72	2.0E-76	D84295.1	NT	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
4532	17050	29433	0.95	2.0E-76	11545921	NT	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.;
							Human mRNA for possible protein TPRDII, complete cds
4567	17084	29471	1	2.0E-76	AL163283.2	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
5031	17541	29913	7.23	2.0E-76	AW879618.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
5582	18151		1.64	2.0E-76	AF127845.1	NT	GV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
5718	18300	30730	0.5	2.0E-76	9968846	NT	Gorilla grilla olfactory receptor (GGO18) gene, partial cds
5886	18465	31142	5.23	2.0E-76	AB029004.1	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7893	20332	33199	0.57	2.0E-76	11421326	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
							Homo sapiens KIAA0783 gene product (KIAA0783), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7819	20357	33224	0.74	2.0E-76	11426908	NT	Homo sapiens A Kinase (PRKA) anchor protein 10 (AKAP10), mRNA
8194	20816	33503	2.11	2.0E-76	11427410	NT	Homo sapiens TPCR88 protein (HSTPCR88P), mRNA
10232	22833	35597	2.23	2.0E-76	11437211	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63160), mRNA
10699	23138	36119	2.48	2.0E-76	7649807	NT	Homo sapiens HIRA interacting protein 4 (dnaj-like) (HIRIP4), mRNA
11535	23892	36975	68.87	2.0E-76	AF200345.1	NT	Homo sapiens aspartyl protease 4 mRNA, complete cds
4316	16840	29230	6.48	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4316	16840	29231	6.48	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5705	18289	30715	7.08	1.0E-76	BE798537.1	EST_HUMAN	601589886F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6665	19116	32548	0.59	1.0E-76	AA333207.1	EST_HUMAN	EST37301 Embryo, 8 week Homo sapiens cDNA 5' end
7333	19745	32548	3.95	9.0E-77	BE889525.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
12411	24443		1.28	9.0E-77	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638753 5'
192	12784	26209	1.02	8.0E-77	R83144.1	EST_HUMAN	y01102.1 Scores breast 3NbhBst Homo sapiens cDNA clone IMAGE:187165 5' similar to SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;
4558	17075	29460	1.18	8.0E-77	BF205181.1	EST_HUMAN	601868926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4108503 5'
5710	18294	30721	1.62	8.0E-77	4506230	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) mRNA
12389	24430	30898	12.2	8.0E-77	R00245.1	EST_HUMAN	y66904.s1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element ;
1880	14402	26896	1.58	7.0E-77	AA625755.1	EST_HUMAN	zu91g01.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:746392 3'
2311	14818	27337	3.28	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kd) (POLR2E) mRNA
2311	14818	27338	3.28	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kd) (POLR2E) mRNA
278	12873	26280	4.71	6.0E-77	4504600	NT	Homo sapiens Interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1189	13712	26152	2.81	6.0E-77	AW957763.1	EST_HUMAN	EST369823 IMAGE resequences, IMAGE Homo sapiens cDNA
1586	14098	26561	1.22	6.0E-77	A1204068.1	EST_HUMAN	qe77h12.x1 Scores fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:1745063 3'
1269	13805	26254	2.02	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1392	13926	26384	1.47	5.0E-77	4557260	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2632	15127	27640	2.1	5.0E-77	AF162866.1	NT	Homo sapiens tau-like kinase 1 (TLK1) mRNA, complete cds
3603	16046	28468	0.88	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
4753	17267	29948	1.54	6.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4753	17267	29949	1.54	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4763	17307	29686	3.82	5.0E-77	4507636	NT	Homo sapiens nuclear receptor subfamily 2, group E, member 1 (NR2E1), mRNA
5017	17527	29801	2.89	6.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G1728 5'
7168	19881	32705	0.69	5.0E-77	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7791	20233	33093	0.54	5.0E-77	X98296.1	NT	H. sapiens mRNA for ubiquitin hydrolase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8115	20233	33083	0.73	5.0E-77	X98298.1	NT	H.sapiens mRNA for ubiquitin hydrolase
8906	21340	34254	2.4	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8906	21340	34255	2.4	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9745	22113	35040	2.84	5.0E-77	11421828	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9745	22113	35041	2.84	5.0E-77	11421828	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10369	22768	35736	1.05	5.0E-77	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
10369	22768	35737	1.05	5.0E-77	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
11628	23887	36989	1.57	5.0E-77	7692041	NT	Homo sapiens KIAA0284 gene product (KIAA0284), mRNA
1917	14436	28937	1.18	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1917	14436	28938	1.18	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10857	23097	36078	5.72	3.0E-77	BF359917.1	EST_HUMAN	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA
1383	13918	26374	1.5	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBT10 5'
1462	13995	28460	3.03	2.0E-77	AW967712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2015	14531	27045	1.55	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2024	14540	27063	1.88	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2516	15339	27629	4.01	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2516	15339	27530	4.01	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4046	18578	28967	1.74	2.0E-77	BE044316.1	EST_HUMAN	ho43b05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4440	18960	28947	0.71	2.0E-77	AI613519.1	EST_HUMAN	fw22g02.x1 NCL_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4440	18960	28948	0.71	2.0E-77	AI613519.1	EST_HUMAN	fw22g02.x1 NCL_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4636	17152		1.2	2.0E-77	4504068	NT	Homo sapiens glutamyl-oxaloacetyl transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4820	17332	29711	6.14	2.0E-77	AA653025.1	EST_HUMAN	ns68g12.e1 NCL_CGAP_P2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29, [1]; contains element MSR1 repetitive element ;
6253	18817	31532	2.17	2.0E-77	BE288940.1	EST_HUMAN	601118852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
6486	19041	31781	1.92	2.0E-77	BE787143.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
7618	20067	32919	17.18	2.0E-77	AI839003.1	EST_HUMAN	at74a09.x1 Barleed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311
9713	22136	35063	6.28	2.0E-77	U50321.1	NT	Q13311 TAX1-BINDING PROTEIN TXBP151, [1]; Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
9713	22136	35064	6.28	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7

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11533	18817	31532	2.23	2.0E-77	BE288940.1	EST_HUMAN	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
45	12665	25057	1.19	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
45	12665	25058	1.19	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
286	12883	25301	3.34	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
286	12883	25302	3.34	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	15296	25902	4.58	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	15296	25903	4.58	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2343	14849	27367	0.88	1.0E-77	AB028024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3005	16560	27972	2.45	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DEC1), mRNA
4375	16597	29278	3.76	1.0E-77	7706289	NT	Homo sapiens CGI-80 protein (LOC51628), mRNA
4560	17077	29462	19.11	1.0E-77	AJ228041.1	NT	Homo sapiens 958 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4606	17212	29591	2	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
5195	17698	30062	1.15	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5195	17698	30063	1.15	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
6226	18791	31498	1.58	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6226	18791	31499	1.58	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6353	18911	31644	1.59	1.0E-77	M25944.1	NT	Human von Willebrand factor gene, exon 20
6760	19333	32103	0.78	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
7484	19688	32484	14.17	1.0E-77	5881412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
8200	20621	33508	1.03	1.0E-77	11420159	NT	Homo sapiens cullin 1 (CUL1), mRNA
8310	20734	33628	0.9	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
10389	22789	35759	1.03	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10389	22789	35760	1.03	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10859	23262	36285	3.43	1.0E-77	11433426	NT	Homo sapiens meningioma expressed antigen 6 (colled-coil praline-rich) (MGEA6), mRNA
10404	22804	35761	2.98	9.0E-78	AW753032.1	EST_HUMAN	RC3-CT0254-280999-011-b05 CT0254 Homo sapiens cDNA
6788	18331	32100	2.67	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
6788	19331	32101	2.67	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
88	12705	25119	1.56	8.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
88	12705	25120	1.56	8.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3280	15829	28247	0.85	6.0E-78	BF344101.1	EST_HUMAN	602016926F1 NCI_CGAP_Brl84 Homo sapiens cDNA clone IMAGE:4152511 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5187	17691	30052	5.78	6.0E-78	BF380870.1	EST_HUMAN	IL2-UT0074-170900-163-F08 UT0074 Homo sapiens cDNA
6913	19452		3.04	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRAL1), mRNA
225	12827	25241	1.11	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2475	14976	27490	3.42	5.0E-78	AW673424.1	EST_HUMAN	bas4h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800405 5' similar to WP:Y48B6A.6
3363	16909	28331	4.44	5.0E-78	M65586.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5668	18263	30853	2.93	5.0E-78	AF038536.1	NT	Homo sapiens Bcl-2 macular dystrophy related protein mRNA, partial cds
5840	18420	31088	14.84	5.0E-78	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68KD (TGFB1), mRNA
7595	20044	32894	2.45	5.0E-78	AW953120.1	EST_HUMAN	EST365190 MAGE resequences, MAGE Homo sapiens cDNA
9395	21827	34742	7.87	5.0E-78	U60889.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
9398	21828	34743	3.49	5.0E-78	BE960836.1	EST_HUMAN	601649061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 6'
1164	13707	26147	1.3	4.0E-78	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
1544	14075	26536	1.63	4.0E-78	AL355841.1	NT	Novel human gene mapping to chromosome 22
2212	14722	27244	5.12	4.0E-78	AF107405.1	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4344	16866	29248	1.72	4.0E-78	7658876	NT	Homo sapiens synectin (LOC30816), mRNA
4826	17338	29718	1.17	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4826	17338	29719	1.17	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
6048	18620	31309	1.15	4.0E-78	11420732	NT	Homo sapiens SFRS protein kinase 2 (SRPK2), mRNA
6487	18042	31782	0.62	4.0E-78	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
6487	18042	31783	0.62	4.0E-78	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
6926	19465	32243	0.64	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7994	20428	33265	0.65	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
9256	21688	34599	1.35	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
9256	21688	34600	1.35	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
10335	22735	35702	2.04	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10335	22735	35703	2.04	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10544	22891	35973	2.54	4.0E-78	11426610	NT	Homo sapiens regulatory factor X-associated ankyrin-containing protein (RXANK), mRNA
11172	23562	36593	2.27	4.0E-78	AF169149.1	NT	Homo sapiens s-CaBP1 (CaBP1) mRNA, complete cds
11309	23673	36723	14.29	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
11530	23888	36970	2.78	4.0E-78	10880123	NT	Homo sapiens pleckstrin homology, Sec7 and coiled/coiled domains 2 (cytohesin-2) (PSCD2), transcript variant 2, mRNA
12268	24363	30905	3.54	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
165	12770	25183	1.86	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
165	12770	25184	1.86	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3764	16303		1.31	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLAGE3 Homo sapiens cDNA clone PLACE3000373 5'
3823	16360	28760	0.93	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4121	16360	28760	1.09	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
5345	17844	30202	3.65	3.0E-78	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
10235	22636		5.47	3.0E-78	BE144758.1	EST_HUMAN	CMO-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA
3082	15636		2.63	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4027	16560		2.13	2.0E-78	AA311872.1	EST_HUMAN	EST182683 Jurkat T-cells VI Homo sapiens cDNA 5' end
5347	17846		1.96	2.0E-78	BE069220.1	EST_HUMAN	QV3-BT0380-171299-041-502 BT0380 Homo sapiens cDNA
7960	20396	33264	1.13	2.0E-78	AW402306.1	EST_HUMAN	UHF-BK0-aal-g-10-0-UI17 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7960	20396	33265	1.13	2.0E-78	AW402306.1	EST_HUMAN	UHF-BK0-aal-g-10-0-UI17 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
8280	20697	33588	3.68	2.0E-78	BF689800.1	EST_HUMAN	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298669 5'
8661	21096	34002	3.33	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBRAWF08 5'
8965	21398	34309	1.18	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07: tumor2 Homo sapiens cDNA 3'
8965	21398	34310	1.18	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07: tumor2 Homo sapiens cDNA 3'
10882	23285	36289	2.85	2.0E-78	AI197837.1	EST_HUMAN	q150h05.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859961 3' similar to WP:R90.1
10881	23314		2.1	2.0E-78	BE439409.1	EST_HUMAN	CE06325 PROTEIN KINASE ;
10903	23335	36339	3.28	2.0E-78	NG6951.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
5367	17885	30225	2.12	1.0E-78	4769843	NT	z44812.s1 Sceres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295623 3'
5558	18147	30509	3.57	1.0E-78	11417304	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
7367	18037	30421	0.74	1.0E-78	AV648699.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
8424	20838	33735	0.48	1.0E-78	AI631520.1	EST_HUMAN	AV648699 GLC Homo sapiens cDNA clone GLCBMCO1 3'
8424	20838	33736	0.48	1.0E-78	AI631520.1	EST_HUMAN	wa99a04.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2304270 3' similar to contains L1.B3 L1
8744	21178		2.92	1.0E-78	U52373.1	NT	repetitive element ;
11849	24098	30995	1.57	1.0E-78	11435903	NT	repetitive element ;
4748	17262	28642	3.95	9.0E-79	11525891	NT	Human serine/threonine kinase MNB (mnrb) mRNA, complete cds
4921	17432	28806	4.18	9.0E-79	BE000837.1	EST_HUMAN	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC33140), mRNA
6689	18274	30695	18.65	9.0E-79	AB028070.1	NT	Homo sapiens peptide YY (PYY), mRNA
6670	19218	31964	2.77	8.0E-79	5454145	NT	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
6976	19513	32263	0.96	9.0E-79	11430822	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
							Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
							Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF/SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7819	24637		1.02	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
8144	20587	33444	0.53	9.0E-79	D30688.1	NT	Human T-cell mRNA for glycyl RNA synthase, complete cds
8388	21820	34736	5.98	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
8388	21820	34737	5.98	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
10314	22714	36678	1.78	9.0E-79	AF082346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10314	22714	36680	1.76	9.0E-79	AF082346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10848	23281	36271	4.33	9.0E-79	AY088273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
11266	23632	36882	6.16	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
11266	23632	36883	6.16	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
12482	24501	30882	1.82	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3741	16281	28684	1.08	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4528	17047	29428	5.56	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4529	17047	29429	5.56	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
5198	17701	30066	2.25	8.0E-79	AF064755.1	NT	Homo sapiens nuclear inhibitor of protein phosphatase-1 (PPP1R8) gene, exon 5
11860	18011	30443	1.25	8.0E-79	8587387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
3213	16765	28185	14.6	7.0E-79	BE619648.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
							zfp4e04.s1 Soares fetal liver spleen INFIL S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to
11588	23926		3.56	6.0E-79	AA689829.1	EST_HUMAN	TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
11252	23618	36665	2.22	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
327	12820	25338	1.15	3.0E-79	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
1003	13554	25998	1.49	3.0E-79	AF232708.1	NT	Homo sapiens cell-line taA201a chloride ion current inducer protein (Cln) gene, complete cds
3060	15614	28023	1.93	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5617	18204	30601	5.81	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5898	18572	31258	1.55	3.0E-79	AB020689.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
6026	18600	31287	0.96	3.0E-79	BE789470.1	EST_HUMAN	601492143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
6026	18600	31288	0.96	3.0E-79	BE789470.1	EST_HUMAN	601492143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
6048	18621	31310	4.03	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6049	18621	31311	4.03	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
7125	19858	32453	0.86	3.0E-79	BE255893.1	EST_HUMAN	601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'
7492	19896	32492	3.76	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
7492	19896	32493	3.76	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
8482	20875	33775	0.59	3.0E-79	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
9749	21163	34084	1.21	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
10642	23063	36067	5.1	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds

Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10842	23083	38068	5.1	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
11521	23879	38882	1.62	3.0E-79	F05701.1	EST_HUMAN	HSC0JE081 normalized infant brain cDNA Homo sapiens cDNA clone c-0j808
301	12897		1.2	2.0E-79	H63129.1	EST_HUMAN	y48f03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208541 3'
653	13218	28629	1.31	2.0E-79	BE378926.1	EST_HUMAN	601189415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
952	13504	25949	0.9	2.0E-79	475784.1	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1009	13560	28004	1.22	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1009	13560	26005	1.22	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1080	13608		1.51	2.0E-79	AE23747.1	EST_HUMAN	th18h07.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2118685 3'
1846	14398	26863	1.03	2.0E-79	7692255	NT	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA
2080	14576	27091	3.44	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2080	14576	27092	3.44	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2098	14612	27131	3.54	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2688	15161	27672	2.84	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0937 protein, partial cds
3926	16461	28869	0.74	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4181	16708	28098	1.36	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4759	17263	28633	0.61	2.0E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5308	17808	30173	0.69	2.0E-79	7692357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
5940	18518		1.04	2.0E-79	AA312223.1	EST_HUMAN	EST182826 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid B0303.15
6001	18575	31261	0.79	2.0E-79	11181769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6584	19115	31859	1.27	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
7376	18046	30430	0.79	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7610	20059	32911	2.53	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7610	20059	32912	2.53	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
8704	21139	34042	1.2	2.0E-79	4508442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
9010	21443	34355	2	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11005 (FLJ11005), mRNA
10109	22510	35473	1.94	2.0E-79	S72869.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10109	22510	35474	1.94	2.0E-79	S72869.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10808	23242	36223	3.15	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
10806	23242	36224	3.15	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
11628	17808	30173	4.22	2.0E-79	7692357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
11719	24014	31008	7.46	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
11857	24169	30975	2.73	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6940	24818		3.73	1.0E-79	BF363071.1	EST_HUMAN	MRO-NN0087-280600-017-b10 NN0087 Homo sapiens cDNA
7064	19598	32393	0.48	1.0E-79	AI613480.1	EST_HUMAN	U37608.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623 TEKTIN C1.1
7064	19598	32394	0.48	1.0E-79	AI613480.1	EST_HUMAN	U37608.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623 TEKTIN C1.1
11372	23734	36702	4.48	1.0E-79	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-e05 HT0540 Homo sapiens cDNA
11749	24888		1.57	1.0E-79	AI460115.1	EST_HUMAN	ar79a04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151438 3'
3108	15659	28070	9.53	9.0E-80	AA725848.1	EST_HUMAN	el23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343848 3'
3106	15659	28071	9.53	9.0E-80	AA725848.1	EST_HUMAN	el23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343848 3'
10042	22444	35392	1.49	9.0E-80	BE798603.1	EST_HUMAN	601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936061 5'
11046	23472	36497	7.06	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
11046	23472	36498	7.06	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
3596	16137		1.03	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
8131	20554	33430	3.01	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
8131	20554	33431	3.01	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
9821	22036	34987	1.8	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9821	22036	34988	1.8	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7390	18059	30399	0.63	7.0E-80	AF127892.1	NT	Callithrix jacchus olfactory receptor (CJA80) gene, partial cds
923	13477	25624	0.87	6.0E-80	AI422187.1	EST_HUMAN	ff58d02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN
1649	14180	26849	1.71	6.0E-80	U64898.1	NT	Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 99 KD SUBUNIT PRECURSOR :
6085	18635	31349	1.92	6.0E-80	11421462	NT	Homo sapiens NAD convertase mRNA, complete cds
6383	18940	31677	3.61	6.0E-80	AJ404488.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
6547	19099	31841	4.57	6.0E-80	11436736	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6536	19147		0.99	6.0E-80	7662393	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6651	19189	31949	0.89	6.0E-80	MT8533.1	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA
9233	21665	34674	3.63	6.0E-80	11526464	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
9233	21665	34675	3.53	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 61 (GPR51), mRNA
9354	21788	34694	1.82	6.0E-80	AL163301.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9590	22013	34943	0.87	6.0E-80	AF161495.1	NT	Homo sapiens chromosome 21 segment HS21C101
						NT	Homo sapiens HSPC146 mRNA, complete cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9939	22341	35290	1.66	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
10721	23159	36143	3.3	6.0E-80	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
10895	23424	36441	25.86	6.0E-80	AF228730.1	NT	Homo sapiens Cyt19 mRNA, complete cds
11495	23853	36924	6.68	6.0E-80	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11495	23853	36925	6.68	6.0E-80	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11730	24757		2.31	6.0E-80	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11939	24149		6.26	6.0E-80	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
12487	24897		2.74	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
12595	24571	30852	1.25	6.0E-80	AF105658.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
605	13173	25578	1.55	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
858	13414	25859	1.92	6.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
858	13414	25860	1.92	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
1220	13760		1.27	6.0E-80	X91647.1	NT	H. sapiens next gene (exon 12)
1485	14017		3.52	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2330	14837	27362	7.22	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2763	15243	27758	2.77	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
5041	17551	28922	1.29	5.0E-80	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8489	20901	33795	0.42	5.0E-80	AW028576.1	EST_HUMAN	w33e09.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531272 3' similar to TR:O35085.
8489	20901	33796	0.42	5.0E-80	AW028575.1	EST_HUMAN	O35085 ARX HOMEOPROTEIN.; contains TAR1.11 TAR1 TAR1 repetitive element;
8896	21330	34241	0.92	5.0E-80	9910293	NT	w32e09.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531272 3' similar to TR:O35085
9519	21982	34908	12.57	4.0E-80	F25915.1	EST_HUMAN	O35085 ARX HOMEOPROTEIN.; contains TAR1.11 TAR1 TAR1 repetitive element;
224	12828		12.5	3.0E-80	AL163210.2	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
4978	17489		8.1	3.0E-80	BE817465.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03
6105	18674	31369	2.19	3.0E-80	AI091676.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1776	14300	26787	3.2	2.0E-80	R35321.1	EST_HUMAN	QV4-BN0263-040800-241-g10 BN0263 Homo sapiens cDNA
1832	14354	26854	0.9	2.0E-80	AI444821.1	EST_HUMAN	cc23et12.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1667054 3' similar to
1981	14497	27006	4.16	2.0E-80	AL043116.2	EST_HUMAN	TR:O35780 O35780 PIG-L;
5251	17752	30120	7.74	2.0E-80	AI979276.1	EST_HUMAN	y956a08.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:38060 5'
6567	19118	31881	0.87	2.0E-80	AI923972.1	EST_HUMAN	RET487 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7
6567	19118	31882	0.87	2.0E-80	AI923972.1	EST_HUMAN	DKFZp434D1323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1323 5'
							wu03a04.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2555854 3'
							wu48c10.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448788 3'
							wu48c10.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448788 3'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7195	19906	32736	0.93	2.0E-80	AA592952.1	EST_HUMAN	nm80401.s1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:1090177 3'
7321	19733	32536	2.66	2.0E-80	11421830	NT	Homo sapiens Golgi transport complex protein (90 kDa) (GTC90), mRNA
7701	20146	33004	0.77	2.0E-80	T75215.1	EST_HUMAN	yc86f12.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:22851 5' similar to SP:K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B ;
8515	20927	33823	0.43	2.0E-80	AL041469.1	EST_HUMAN	DKFZp434E2217_s1 434 (synonym: hss3) Homo sapiens cDNA clone DKFZp434E2217 3'
9446	21877	34786	0.93	2.0E-80	AW964270.1	EST_HUMAN	EST376343 IMAGE resequences, MAGH Homo sapiens cDNA
9878	22281	36221	1.09	2.0E-80	AJ007378.1	NT	Homo sapiens GGT gene, exon 6
10651	23091	36074	22.36	2.0E-80	AA393392.1	EST_HUMAN	z70f12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191315
11481	23839	36908	2.67	2.0E-80	BE253522.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
11481	23839	36907	2.67	2.0E-80	BE253522.1	EST_HUMAN	601108820F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344692 5'
354	12944		1.99	1.0E-80	AL163303.2	NT	601108820F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344692 5'
822	13380	25817	1	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 segment HS21C103
1904	14423		1.45	1.0E-80	A1732658.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
4877	17389	29761	0.7	1.0E-80	N99520.1	EST_HUMAN	nm01112.x5 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR repetitive element ;
5580	18168		4.1	1.0E-80	BE386615.1	EST_HUMAN	za39g07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294972 5' similar to contains Alu repetitive element
6273	18836	31551	6.53	1.0E-80	L10347.1	NT	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
6847	19388	32163	1.73	1.0E-80	5174540	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
7652	20098	32950	1	1.0E-80	AJ224172.1	NT	Homo sapiens melate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
8060	20517	33398	2.86	1.0E-80	A1948731.1	EST_HUMAN	Homo sapiens mRNA for lipophilin B
8090	20517	33397	2.88	1.0E-80	A1948731.1	EST_HUMAN	wq25cd05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
8802	21236	34143	1.05	1.0E-80	11421211	NT	wq25cd05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
9136	21667	34473	0.98	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9136	21667	34474	0.98	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9539	21954	34877	1.34	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10321	22721	35689	0.88	1.0E-80	D63479.2	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10444	22895	35871	4.3	1.0E-80	11641276	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10444	22895	35872	4.3	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
12015	24193	30949	1.87	1.0E-80	11417901	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
12277	24370		1.86	1.0E-80	AB011399.1	NT	Homo sapiens meningo (disrupted in balanced translocation) 1 (MN1), mRNA
							Homo sapiens gene for AF-6, complete cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10475	22926	35904	1.89	8.0E-81	AI251752.1	EST_HUMAN	q190g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854288 3'
10475	22925	35905	1.89	8.0E-81	AI251752.1	EST_HUMAN	q190g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854288 3'
10933	23365	36375	8.92	8.0E-81	BE394525.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
							ze21d10.1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:359635 5' similar to SW:KRHA_RABIT_Q02957 KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. [1]; contains element MER22 repetitive element;
2112	14625	27147	1.25	7.0E-81	AA011080.1	EST_HUMAN	
7702	20147	33005	3.12	7.0E-81	AB22115.1	EST_HUMAN	za91c08.x5 Soares_fetal_lung_NbH19W Homo sapiens cDNA clone IMAGE:289918 3'
4409	16930	29320	4.92	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4409	16930	29321	4.92	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5534	18124	30479	1.69	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5534	18124	30480	1.69	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8111	20537	33415	1.11	6.0E-81	AF038660.1	NT	Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
9502	21883	34857	1.55	6.0E-81	AA360017.1	EST_HUMAN	EST09128 Fetal lung II Homo sapiens cDNA 5' end
12169	24292	30936	1.5	6.0E-81	BF876022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
12169	24292	30937	1.5	6.0E-81	BF876022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2122	14635	27160	3.64	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8939	21373	34286	1.76	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8939	21373	34287	1.76	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9797	22200	35136	1.08	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
9797	22200	35137	1.08	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11331	23695	38747	2.16	5.0E-81	8506834	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
228	12830	25243	0.84	4.0E-81	AF252257.1	NT	Homo sapiens GRP2 binding protein mRNA, partial cds
						EST_HUMAN	th60e12.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
722	13283	25708	1.02	4.0E-81	AI521435.1	EST_HUMAN	
3130	15683	28089	4.48	4.0E-81	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3626	16169	28576	0.76	4.0E-81	AW004608.1	EST_HUMAN	ws90h03.x1 NCI_CGAP_Oc3 Homo sapiens cDNA clone IMAGE:2805269 3' similar to TR:O43815 O43815 STRIATIN.;
4177	16704	28092	2.9	4.0E-81	AF263308.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4177	16704	28093	2.6	4.0E-81	AF263308.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4415	16936	29327	1.25	4.0E-81	8923206	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
7731	20175	33034	1.05	4.0E-81	4757863	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2) mRNA
7879	20318	33183	0.54	4.0E-81	11420544	NT	Homo sapiens ets variant gene 1 (ETV1), mRNA
8842	21276	34186	2.73	4.0E-81	X06989.1	NT	Human mRNA for amyloid A4(751) protein

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9033	21465	34373	3.35	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9033	21466	34374	3.35	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9498	21927	34851	4.33	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10117	22518	35483	1.71	4.0E-81	11425281	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10980	23389	36399	4.42	4.0E-81	4768085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
10960	23389	36400	4.42	4.0E-81	4768085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
11620	24827	30593	4.77	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
11620	24827	30594	4.77	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12365	24418	30894	5.1	4.0E-81	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1300	13835	26282	11.15	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1300	13835	26283	11.16	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2265	14773	27294	1.17	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2948	15501	27920	6.76	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2948	15501	27921	6.76	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
5104	17613		2.45	3.0E-81	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6381	17878	30240	1.13	3.0E-81	6382070	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 12C, mRNA
2790	16347	27768	2.29	2.0E-81	BE784638.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2790	16347	27769	2.29	2.0E-81	BE784638.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3774	16312	28713	0.86	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
4722	17238	29819	1.78	2.0E-81	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
12631	16312	28713	3.01	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
3652	16192	28569	1.58	1.0E-81	AW900558.1	EST_HUMAN	EST372729 MAGe resequences, MAGF Homo sapiens cDNA
4552	17069	29451	3.71	1.0E-81	AA040370.1	EST_HUMAN	ZK45108.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to
4691	17207	29585	6.79	1.0E-81	BE047986.1	EST_HUMAN	PIR:S52437 S52437 CDP-diacetylglucuronidase - fruit fly
5486	17998	36987	3.56	1.0E-81	U97928.1	NT	t245c04.y1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291628 5'
5609	18197	30562	5.71	1.0E-81	11432866	NT	Human acylate hydratase (ACO2) gene, exon 3
5609	18197	30563	5.71	1.0E-81	11432866	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
							Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5784	18345	30801	0.74	1.0E-81	AA256669.1	EST_HUMAN	zr85c06.r1 Soares_NbHPu_S1 Homo sapiens cDNA clone IMAGE:682475 5' similar to SW:PR12_HUMAN
6923	18501	31182	2.99	1.0E-81	U52351.1	NT	P49643 DNA PRIMASE 68 KD SUBUNIT
6923	18501	31183	2.99	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds
							Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6459	18015	31749	1.48	1.0E-81	BF674641.1	EST_HUMAN	602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
6900	19440	32215	0.84	1.0E-81	11420885	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
6900	19440	32216	0.84	1.0E-81	11420885	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7118	19651	32447	1.08	1.0E-81	AJ133289.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
8329	20744	33639	8.77	1.0E-81	11432868	NT	Homo sapiens polymerase (DNA directed), gamma (POL.G), mRNA
8360	20775	33973	0.57	1.0E-81	AJ250408.1	NT	Homo sapiens GLI3 gene for GLI3 protein
9882	22285	35225	1.13	1.0E-81	BE958278.1	EST_HUMAN	601646051F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3830228 5'
9882	22285	35226	1.13	1.0E-81	BE958278.1	EST_HUMAN	601646051F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3830228 5'
10010	22412	35361	5.73	1.0E-81	BE984367.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3688483 5'
10119	22520	35485	0.95	1.0E-81	AA630784.1	EST_HUMAN	act14d06.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:856427 3' similar to SW:YB38_YEAST P38126 HYPOTHETICAL 80.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION.
10121	22522	35487	2.98	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10121	22522	35488	2.98	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10381	22781	35749	1.59	1.0E-81	AW897560.1	EST_HUMAN	CM3-NN0059-140400-147-a12 NN0059 Homo sapiens cDNA
10720	23158	36142	3.27	1.0E-81	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
10871	23304	36298	2.87	1.0E-81	AW844986.1	EST_HUMAN	MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA
10871	23304	36299	2.87	1.0E-81	AW844986.1	EST_HUMAN	MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA
10876	23309	36305	7.78	1.0E-81	AW798187.1	EST_HUMAN	RC3-UM0046-280200-011-a08 UM0048 Homo sapiens cDNA
10876	23309	36306	7.78	1.0E-81	AW798187.1	EST_HUMAN	RC3-UM0046-280200-011-a08 UM0048 Homo sapiens cDNA
11042	18192	28589	16.39	1.0E-81	AW960858.1	EST_HUMAN	EST372729 MAGC resequences, MAGF Homo sapiens cDNA
11275	23641	36893	5.13	1.0E-81	BF204253.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
11843	24093	30983	4.61	1.0E-81	11418138	NT	Homo sapiens phorbol (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
12	12632	25019	3.58	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
110	12632	25019	1.74	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
277	12874	25891	1.64	8.0E-82	U09888.1	NT	Human CRFB4 gene, partial cds
837	13394	25832	3.01	8.0E-82	U09888.1	NT	Human CRFB4 gene, partial cds
910	13464	25912	1.5	8.0E-82	U09888.1	NT	Human CRFB4 gene, partial cds
1519	14051	26515	1.18	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1659	14180	26662	1.18	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epitaxial androgen-related protein) (GPX6), transcript variant 2, mRNA
4260	16785	29170	1.6	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1478	14011		1.31	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2724	15214	27729	1.62	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
1970	14201	26875	13.64	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5758	18339	30794	0.74	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-708 HT0540 Homo sapiens cDNA
6768	18339	30795	0.74	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-708 HT0540 Homo sapiens cDNA
6036	18810	31298	0.68	4.0E-82	M25833.1	NT	Human von Willebrand factor gene, exon 9
11438	23798	36867	19.7	4.0E-82	AI937300.1	EST_HUMAN	wp75e09.x1 NCL CGAG_Brn26 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:O75276
12105	24251		4.67	4.0E-82	AF029701.2	NT	O75276 PKD1 ;
291	12888	25308	20.1	3.0E-82	4502168	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
723	13284	25709	2.19	3.0E-82	BE005705.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
810	13368	25805	6.01	3.0E-82	5174702	NT	RC2-BN0120-010400-013-702 BN0120 Homo sapiens cDNA
893	13448	25896	5.23	3.0E-82	4502168	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
1087	13633		21.18	3.0E-82	AA725848.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1385	13920	26377	1.35	3.0E-82	AW875073.1	EST_HUMAN	al23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343848 3'
1495	14027	26490	2.68	3.0E-82	AL163285.2	NT	RC8-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1862	14384	26875	1.12	3.0E-82	BE813232.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
3234	15786		2.77	3.0E-82	5453811	NT	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
8738	21172	34076	2.68	3.0E-82	11425208	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
9040	21472	34383	1.02	3.0E-82	11432889	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9040	21472	34384	1.02	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
9911	22313	35268	6	3.0E-82	AB029000.1	NT	Homo sapiens contactin 6 (CNTN6), mRNA
9911	22313	35259	6	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
614	13182	25585	1.71	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
614	13182	25586	1.71	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0899 protein, partial cds
1884	14213	26693	1.24	2.0E-82	AL046390.1	EST_HUMAN	Homo sapiens mRNA for KIAA0899 protein, partial cds
2933	15488	27809	0.71	2.0E-82	AL163201.2	NT	DKFZp434M117_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M117 5'
3853	16389	28789	1.37	2.0E-82	D87675.1	NT	Homo sapiens chromosome 21 segment HS21C001
4034	16567	28959	0.62	2.0E-82	U76833.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4250	16775	29161	1.25	2.0E-82	4504116	NT	Human integral membrane serine protease Sepsase mRNA, complete cds
4594	17110	29499	1.29	2.0E-82	AB028019.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4594	17110	29500	1.29	2.0E-82	AB028019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4929	17440	29817	2.58	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSR1) and wbscr5 (WBSR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5210	17713	30077	1.48	2.0E-82	4507680	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5210	17713	30078	1.48	2.0E-82	4507680	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5729	18311	30742	4.25	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6489	19044	31784	5.08	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
8219	24994		1.22	2.0E-82	AI478428.1	EST_HUMAN	hm21g05.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2157272 3'
8401	20815	33713	0.99	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8855	21289	34200	1.83	2.0E-82	11321670	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
10123	22524	35490	1.8	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10123	22524	35491	1.8	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11039	23486	36487	10.04	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11039	23486	36488	10.04	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11077	23502	36531	2.48	2.0E-82	U60736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11077	23502	36532	2.48	2.0E-82	U60736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11464	23822	36886	2.34	2.0E-82	5031660	NT	Homo sapiens EGF-like repeats and discolidin-like domains 3 (EDIL3), mRNA
11850	23971		2.88	2.0E-82	N64950.1	EST_HUMAN	zb31d10.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'
12228	24338		3.52	2.0E-82	AA011278.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_epilepsy_1NFSL_S1 Homo sapiens cDNA clone IMAGE:429868 5'
608	13177	25580	1.48	1.0E-82	11645921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1239	13777		2.68	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1318	13853	26302	1.99	1.0E-82	BE094386.1	EST_HUMAN	RC4-BT0310-110300-016-110 BT0310 Homo sapiens cDNA
1319	13854	26303	2.26	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0638 protein, partial cds
9302	21734	34641	0.86	1.0E-82	AB037838.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
10208	22609		1.39	1.0E-82	BF616938.1	EST_HUMAN	UIH-BW1-ae04-03-0-UI.s1 NCI_CGAP_Sub07 Homo sapiens cDNA clone IMAGE:3084053 3'
5374	17872	30233	1.08	9.0E-83	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9145	21677	34483	9.07	9.0E-83	BE672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561 5'
10228	22629	35595	1.05	9.0E-83	BE263347.1	EST_HUMAN	601117160F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357734 5'
1445	13977	26436	2.19	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614382 5'
1680	15264	26687	4.88	8.0E-83	N66951.1	EST_HUMAN	ze4812.s1 Soares_fetal_liver_epilepsy_1NFSL Homo sapiens cDNA clone IMAGE:295823 3'
1387	13922	26378	0.86	7.0E-83	AW385529.1	EST_HUMAN	QV4-LT0016-271299-069-h11 L70016 Homo sapiens cDNA
2818	16374		1.33	7.0E-83	AA584655.1	EST_HUMAN	no12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4872	17384		7.81	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3847893 3' similar to TR:Q9Y318 Q9Y318
6357	18915	31649	0.71	7.0E-83	11426657	NT	DJ207H1.1 ;
420	12994	25419	1.72	6.0E-83	M33320.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2977	15532	27951	0.85	8.0E-83	AW816405.1	EST_HUMAN	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-28
3011	15586		0.73	6.0E-83	AF231918.1	NT	QV4-ST0234-181198-037-003 ST0234 Homo sapiens cDNA
3030	15585	27995	1.15	6.0E-83	AA701457.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3550	16092	28509	1.05	8.0E-83	11430241	NT	z15905.s1 Soares_fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:435080 3'
5545	18135	30492	1.97	6.0E-83	4507866	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6327	18886	31617	1.37	6.0E-83	AJ010770.1	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
8007	20440	33308	1.84	6.0E-83	11422024	NT	Homo sapiens hyperion gene, exons 1-50
9817	22220	35156	2.66	6.0E-83	4505314	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
9878	22282	35222	0.85	6.0E-83	11430647	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
9879	22282	35223	0.85	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prip18 (PRP18), mRNA
11598	23933		4.05	6.0E-83	AF240786.1	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prip18 (PRP18), mRNA
970	13523		1.39	5.0E-83	U17883.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1977	15267		1.86	5.0E-83	AF006305.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
3638	16178	28588	0.85	5.0E-83	AL133207.2	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3918	16453	28660	0.82	5.0E-83	4885180	NT	Novel human gene mapping to chromosome X
5208	17711	30075	14.25	5.0E-83	4557013	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
5208	17711	30076	14.25	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5324	17824	30183	1.1	5.0E-83	AF083827.1	NT	Homo sapiens catalase (CAT) mRNA
659	13224	25635	1.28	4.0E-83	AF224689.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 11
1024	13575		4.89	3.0E-83	AA368311.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
2736	15226		3.81	3.0E-83	AA632654.1	EST_HUMAN	EST178542 Placenta [Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
6931	19470		0.86	3.0E-83	AI217223.1	EST_HUMAN	np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR12 THR repetitive element;
1777	14302	28789	1.03	2.0E-83	AA993492.1	EST_HUMAN	q164g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1765882 3'
1777	14302	28790	1.03	2.0E-83	AA993492.1	EST_HUMAN	q164g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92814
							Q92814 MYELOBLAST KIAA0216 ;
							Q92814 MYELOBLAST KIAA0216 ;
							Q92814 MYELOBLAST KIAA0216 ;

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1878	14400	26894	5.29	2.0E-83	N6951.1	EST_HUMAN	z48f12.81 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:285623 3'
2087	14601	27118	1.16	2.0E-83	AB033088.1	NT	Homo sapiens mRNA for KIAA1272 protein, partial cds
2807	15384	27780	1.36	2.0E-83	BE828694.1	EST_HUMAN	RC6-ET0046-280600-013-H12 ET0046 Homo sapiens cDNA
3231	15783		2.57	2.0E-83	11430834	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3775	16313		0.84	2.0E-83	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4359	16881	29284	8.37	2.0E-83	AF202878.1	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34), mRNA, partial cds
4897	17213	29592	2.42	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
4697	17213	29593	2.42	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5522	18112	30469	0.99	2.0E-83	U06678.1	NT	Human carcinoembryonic antigen gene family member 18 (CGM18), gene, exons A1 and B1
5730	18312	30743	0.8	2.0E-83	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6730	18312	30744	0.8	2.0E-83	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6132	18701	31397	0.89	2.0E-83	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
6265	18829	31543	1.44	2.0E-83	BE885401.1	EST_HUMAN	601507482F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908088 5'
7126	19659	32454	0.54	2.0E-83	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B), mRNA, partial cds
7920	20358	33225	5.45	2.0E-83	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B), mRNA, partial cds
8398	20812	33710	0.76	2.0E-83	BF105097.1	EST_HUMAN	601822090F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042318 5'
8624	21059	33987	1.59	2.0E-83	U66707.1	NT	Rattus norvegicus dentin-180 mRNA, complete cds
8861	21295	34203	2.05	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8861	21295	34204	2.05	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
10061	22462	35414	2.42	2.0E-83	M22084.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10061	22462	35415	2.42	2.0E-83	M22084.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10128	22529	35497	1.6	2.0E-83	AU117659	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001810 6'
10170	22571	35537	1.21	2.0E-83	AW505800.1	EST_HUMAN	UJ-HF-BNO-and-h-07-q-J1.1 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:3081852 5'
10625	23067	36052	3.97	2.0E-83	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
10705	23144	36126	2.1	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 6'
10705	23144	36127	2.1	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 6'
12274	24367		3.49	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
1443	13975	26433	1.39	1.0E-83	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB), mRNA
1443	13975	26434	1.39	1.0E-83	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB), mRNA
2593	15089	27604	4.93	1.0E-83	BE883690.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3876	16411	28814	4.27	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4201	16786	29171	1.67	1.0E-83	Z25822.1	NT	H.sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3

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4851	17462	28838	3.44	1.0E-83	4502186	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nadn-11, Alzheimer disease) (APP), mRNA
7066	18600	32396	1.79	1.0E-83	A1027614.1	EST_HUMAN	ov89b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M84241 QM
3789	18336	28738	3.73	7.0E-84	BE901209.1	EST_HUMAN	PROTEIN (HUMAN);
1327	13862	26310	3.6	6.0E-84	BE838864.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1327	13862	26311	3.6	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2297	14804	27322	3.45	6.0E-84	AA776574.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
5429	17824	30275	4.27	6.0E-84	R05659.1	EST_HUMAN	ae86a03.s1 Stralagene schizoa brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5489	18000		1.91	6.0E-84	AL042863.2	EST_HUMAN	ye83a04.r1 Soares fetal liver spleen 'INFLS Homo sapiens cDNA clone IMAGE:125262 5'
5780	18361	30822	1.92	6.0E-84	AA897339.1	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0322 5'
5929	18507	31191	1.14	6.0E-84	11426718	NT	ai47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338
5929	18507	31191	1.14	6.0E-84	11426718	NT	VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
5929	18507	31191	1.14	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
5929	18507	31192	1.14	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
7973	20409	33278	3.48	6.0E-84	BE810371.1	EST_HUMAN	PM0-LT0019-190600-004-F02 LT0019 Homo sapiens cDNA
8230	20649	33541	0.89	6.0E-84	AF038391.1	NT	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
8688	21123	34023	2.37	6.0E-84	BE770189.1	EST_HUMAN	PM4-FT0054-160600-004-e10 FT0054 Homo sapiens cDNA
734	13295	25720	1.08	5.0E-84	AA382811.1	EST_HUMAN	EST98094 Testis 1 Homo sapiens cDNA 5' end
2972	15527		1.33	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
6417	18974	31708	0.49	5.0E-84	AA167678.1	EST_HUMAN	zq39e07.r1 Stralagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632100 5' similar to
11298	23663	38708	2.56	5.0E-84	11426740	NT	TR:G483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q. ;
11392	23754	36811	2.77	5.0E-84	AB032857.1	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11392	23754	36812	2.77	5.0E-84	AB032857.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1442	13974	28432	1.92	4.0E-84	AB85321.1	EST_HUMAN	Homo sapiens mRNA for KIAA1131 protein, partial cds
5036	17546	29917	0.65	4.0E-84	4505928	NT	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to
5037	17547	29918	1.49	4.0E-84	AF068601.2	NT	SW:NPDC_HUMAN O43847 NARDILYSIN PRECURSOR ;
5326	17825	30184	3.43	4.0E-84	AA401549.1	EST_HUMAN	Homo sapiens polymerase (DNA-directed), alpha (70kd) (POLA2), mRNA
5513	18103	30347	0.61	4.0E-84	AF022835.1	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
							zu62a07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742648 5' similar to WP:F22B5.1
							CE02195 GTP-BINDING ADP-RIBOSYLATION FACTOR ;
							Homo sapiens multidrug resistance protein (MRP), exon 13

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5827	18407	31073	1.83	4.0E-84	11386188	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5827	18407	31074	1.83	4.0E-84	11386188	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6592	19143	31891	2.25	4.0E-84	AF058650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
8178	20600	33488	15.23	4.0E-84	11421328	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
9287	21719	34628	1.27	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9287	21719	34628	1.27	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
10697	23136	36118	6.43	4.0E-84	AB032956.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
330	12923	25341	2.03	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1182	13724	26163	1.08	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1909	14428	26825	1.93	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1947	14466	26970	2.14	3.0E-84	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3583	16125	28537	0.97	3.0E-84	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3748	16287	28691	4.49	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRSP1) mRNA, complete cds
10881	23101		12.28	3.0E-84	AI983801.1	EST_HUMAN	wu20d05.x1 Soares Dieckgraeft_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gbl.L05093 80S RIBOSOMAL PROTEIN L18A (HUMAN);
2026	14542	27058	4.74	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-508 BT0795 Homo sapiens cDNA
2026	14542	27057	4.74	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-508 BT0795 Homo sapiens cDNA
2897	15452	27878	10.73	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
2915	15470	27893	1.17	2.0E-84	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
4844	17356	29741	5.54	2.0E-84	BF308518.1	EST_HUMAN	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
4844	17356	29742	5.54	2.0E-84	BF308518.1	EST_HUMAN	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
5788	18389	30831	0.94	2.0E-84	BF511575.1	EST_HUMAN	UI-H-BI4-ec-a-02-Q-JI.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084983 3'
5788	18389	30832	0.94	2.0E-84	BF511575.1	EST_HUMAN	UI-H-BI4-ec-a-02-Q-JI.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084983 3'
7000	19536	32320	0.98	2.0E-84	H63370.1	EST_HUMAN	y56e11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208324 3'
8875	21110		1.61	2.0E-84	AI288874.1	EST_HUMAN	qm87c09.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1896728 3'
9581	22004	34931	1.2	2.0E-84	AU120280.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'
11876	24116	31001	2.04	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupskl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756323.1;
11876	24116	31002	2.04	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupskl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756323.1;
326	12919	25337	1.78	1.0E-84	AF114488.1	NT	Homo sapiens intractin short isoform (ITSN) mRNA, complete cds
566	13137	25547	8.97	1.0E-84	4507962	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
740	13301		1.5	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5), mRNA
1325	13860	26308	2.64	1.0E-84	AA984379.1	EST_HUMAN	am85b11.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628885 3'
1980	14498	27005	2.94	1.0E-84	BE392137.1	EST_HUMAN	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3828267 5'
2129	14642	27185	1.81	1.0E-84	11427187	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3761	16290	28683	3.02	1.0E-84	AA720851.1	EST_HUMAN	hw12e08.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4444	16864	29350	8.04	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4749	17263	29843	3.62	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4749	17263	29844	3.52	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4983	16864	29350	2.21	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6217	18783	31488	0.97	1.0E-84	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
6504	19058	31801	1.44	1.0E-84	S73482.1	NT	uterine water channel=28 kda erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
7285	19780	32659	1.46	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7285	19790	32660	1.46	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7546	19996	32638	1.94	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7987	20403	33273	2.8	1.0E-84	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
8080	20508	33387	0.65	1.0E-84	11430846	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
8127	20508	33387	2.03	1.0E-84	11430846	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
9719	22142		2.44	1.0E-84	6031894	NT	Homo sapiens nuclear transport factor 2 (placental protein 16) (PP16), mRNA
9892	18007	30440	1.95	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
9892	18007	30441	1.95	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
11748	24031		2.35	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
11887	24111	30998	4.12	1.0E-84	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
891	13543		1.26	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1099	13844	28083	3.13	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skp mRNA, complete cds
1099	13844	26084	3.13	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skp mRNA, complete cds
1595	14127	26592	1.16	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1595	14127	26593	1.16	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1674	14204	26680	2.46	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
4288	16783	29176	1.24	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4984	17494	28871	1.08	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C088
12450	14204	26680	1.96	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
1103	13706	26148	5.8	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11388	23750		10.09	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11108	23548	36588	2.76	6.0E-85	11438573	NT	Homo sapiens DEAD/1H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11168	23548	36588	2.76	6.0E-85	11438573	NT	Homo sapiens DEAD/1H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2228	14737	27258	3.18	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4461	16981		0.65	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
5708	18292	30718	1.6	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
5708	18292	30719	1.8	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
10899	23331	36333	1.75	6.0E-85	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12528	16981		4.09	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
6461	19017	31760	1.53	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6461	19017	31751	1.53	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
7231	19843	32681	0.64	4.0E-85	AI828119.1	EST_HUMAN	1984g01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285808 3'
10414	22814		1.51	4.0E-85	BE079283.1	EST_HUMAN	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA
1331	13867	26317	0.83	3.0E-85	AF096157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 8
1762	14288	26771	3.44	3.0E-85	T97495.1	EST_HUMAN	ye53g09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'
4967	17478	29855	0.93	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4967	17478	29856	0.93	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5557	18243	30841	0.74	3.0E-85	11436001	NT	Homo sapiens lactoferrin proline rich protein (LPRP), mRNA
6393	18950	31685	0.65	3.0E-85	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6447	19003	31734	6.02	3.0E-85	7662309	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6447	19003	31735	6.02	3.0E-85	7662309	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7363	19820		7.47	3.0E-85	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7875	20314	33180	0.84	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0821 protein (KIAA0821), mRNA
8542	20977	33877	1.29	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
9326	21758	34665	3.18	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
12407	24439		2.15	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
987	13639	25963	1	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Mac2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1065	13611	26052	2.31	2.0E-85	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1451	13983	28443	8.1	2.0E-85	5174776	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1451	13983	28444	6.1	2.0E-85	5174776	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2137	14650	27172	1.36	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2782	13904		7.2	2.0E-85	7667468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
4387	16879	28282	6.28	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4982	17493	29870	1.27	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9530	21945	34868	1.15	2.0E-85	A1760820.1	EST_HUMAN	MSR1 repetitive element;
9798	22201	35138	1.06	2.0E-85	A1914459.1	EST_HUMAN	w449d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331481 3'
10217	22618	35586	1.2	2.0E-85	A1886384.1	EST_HUMAN	w194d12.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443607 3'
2183	14694		5.84	1.0E-85	BE794306.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2281	14798	27316	4.8	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2291	14798	27317	4.8	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
8383	20797	33695	0.52	1.0E-85	BE062951.1	EST_HUMAN	MRO-B170264-221199-002-403 BT0284 Homo sapiens cDNA
9885	22288	33229	2.18	1.0E-85	BE257917.1	EST_HUMAN	601109738F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33505653 5'
10702	23141	36122	3.75	1.0E-85	AA778785.1	EST_HUMAN	z45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
10702	23141	36123	3.75	1.0E-85	AA778785.1	EST_HUMAN	z45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
10778	23216	36198	2.26	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
10778	23216	36199	2.26	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
11753	24198	30662	3.48	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12023	24198	30652	4.72	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1480	13992		6.38	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
6439	18995	31726	0.71	8.0E-86	11424140	NT	Homo sapiens similar to CDC28 protein kinase 1 (H. sapiens) (LOC63041), mRNA
11424	23785	36846	1.72	8.0E-86	4503224	NT	Homo sapiens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA
234	12835	25246	1.26	7.0E-86	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
961	13513	25955	1.23	7.0E-86	AA808001.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
961	13513	25956	1.23	7.0E-86	AA808001.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6510	18084	31805	1.19	7.0E-86	9966886	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6510	18084	31806	1.19	7.0E-86	9966886	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7394	18093	30404	7.55	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
9170	21602	34512	3.95	7.0E-86	L38657.1	NT	Homo sapiens galactose oxidase (GALC) gene, exon 15
9834	22237		1.44	7.0E-86	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9871	22274	35215	1.86	7.0E-86	11626307	NT	Homo sapiens D1George syndrome critical region gene 6 (DGCR6), mRNA
10742	23180	36164	2.64	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10742	23180	38165	2.64	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CAT160 (H. sapiens) (LOC63170), mRNA
1326	13861	26309	1.95	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA
218	12820	25238	1.6	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
6339	18897	31628	12.45	4.0E-86	BE295843.1	EST_HUMAN	601176865F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
11008	12820	25238	3.7	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4306	16831	29220	0.59	3.0E-86	BE867703.1	EST_HUMAN	601443262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847455 5'
5853	18442	31117	6.37	3.0E-86	AW340948.1	EST_HUMAN	x282h12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
8823	21257	34162	1.2	3.0E-86	AV722329.1	EST_HUMAN	AV722329 HTB Homo sapiens cDNA clone HTBBS04 5'
10192	22593	35559	4.47	3.0E-86	BE886478.1	EST_HUMAN	601508696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
10192	22593	35560	4.47	3.0E-86	BE886479.1	EST_HUMAN	601508696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
11185	22837	35808	4.55	3.0E-86	AI69240.1	EST_HUMAN	tu18b02.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:2251371 3'
11267	23633	36684	2.04	3.0E-86	AV690499.1	EST_HUMAN	AV690469 GRK Homo sapiens cDNA clone GKCBSE02 5'
11721	24765		1.61	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
280	12877	25293	2.11	2.0E-86	AA306284.1	EST_HUMAN	EST177232 Jurkat T-cells V1 Homo sapiens cDNA 5' end
431	13005		2.8	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1221	13761	28205	2.71	2.0E-86	N58977.1	EST_HUMAN	yz19a08.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:283478 5'
2097	14611	27130	4.13	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
3393	16939	28351	1.67	2.0E-86	AW666142.1	EST_HUMAN	EST378215 MAGI resequences, MAGI Homo sapiens cDNA
3745	16284	28687	2.76	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3745	16284	28688	2.76	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4052	16584		2.62	2.0E-86	AW616742.1	EST_HUMAN	hd87g08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2916542 3'
4841	17353	29738	2.91	2.0E-86	AF050490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5180	17684	30043	2.67	2.0E-86	4505778	NT	Homo sapiens phosphotyrosine kinase, alpha 1 (muscle) (PHKA1), mRNA
6160	18728	31431	211.07	2.0E-86	Z16411.1	NT	H.sapiens mRNA encoding phosphidipase c
6160	18728	31432	211.07	2.0E-86	Z16411.1	NT	H.sapiens mRNA encoding phosphidipase c
7507	24625	32512	1.1	2.0E-86	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
9053	21485	34396	2.42	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
9053	21485	34397	2.42	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
9280	21712	34623	1.5	2.0E-86	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9563	21686	34913	1.86	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA
10338	22738	35708	2.97	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10338	22738	35707	2.97	2.0E-96	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10378	22778	35746	1.35	2.0E-96	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
12199	24318	30915	2.77	2.0E-96	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12390	24431		3.74	2.0E-96	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12602	24711	30783	1.79	2.0E-96	11417883	NT	Homo sapiens adrenoleuc, beta, receptor kinase 2 (ADRBK2), mRNA
1614	14145	26615	0.88	1.0E-96	48268855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
3121	15874	28087	3.06	1.0E-96	5453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3194	15747	28168	3.37	1.0E-96	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3259	15810	28226	1.17	1.0E-96	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3259	15810	28227	1.17	1.0E-96	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4281	16806	29180	6.24	1.0E-96	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5817	18397	31060	2.18	1.0E-96	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5812	18200		1.9	9.0E-87	AI150703.1	EST_HUMAN	q577c09.x1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
7933	20370	33236	1.88	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7933	20370	33236	1.88	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
497	13070	25489	57	8.0E-87	X52245.1	NT	O.cuniculus mRNA for elongation factor 1 alpha
2191	14702	27221	2.21	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
2191	14702	27222	2.21	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
6738	19283	32044	0.99	7.0E-87	AW890336.1	EST_HUMAN	MRO-NT00339-020500-004-a11 NT00339 Homo sapiens cDNA
8787	21201	34102	3.03	7.0E-87	BF352776.1	EST_HUMAN	IL3-HT0619-080700-198-D10 HT0619 Homo sapiens cDNA
10091	22492	35449	4.2	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
10091	22492	35450	4.2	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
10673	23113	36087	28.92	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
10873	23113	36088	28.92	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
3508	16051	28472	0.89	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
6760	19303	32068	1.62	6.0E-87	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
10510	22959		5.17	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1188	13730	26172	1.75	5.0E-87	AA382811.1	EST_HUMAN	EST98094 Testis 1 Homo sapiens cDNA 5' end
12025	19730	26172	1.57	5.0E-87	AA382811.1	EST_HUMAN	EST98094 Testis 1 Homo sapiens cDNA 5' end
990	13542	25985	1.5	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1203	13744	26188	16.22	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1965	14483	26992	1.88	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
2004	14520	27031	1.25	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element
2004	14520	27032	1.25	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element
2322	14829	27342	1.86	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
2322	14829	27343	1.86	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
3441	15985	28402	2.3	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
5703	18287	30712	7.5	4.0E-87	000321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLLOCATION VARIANT 2)
6029	18603	31290	1.27	4.0E-87	U85429.1	NT	Human transcription factor NFATX3 mRNA, complete cds
6351	18909	31642	4.26	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4031 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4031
8206	20628	33513	0.67	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
8206	20628	33514	0.67	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
8330	20745	33640	0.94	4.0E-87	L48524.1	NT	Homo sapiens tuberlin (TSC2) gene, exon 10
10942	23374	36384	5.2	4.0E-87	M60678.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
10979	23408	36418	1.77	4.0E-87	AB040537.1	NT	Homo sapiens DDX10 mRNA for RNA helicase, complete cds
10979	23408	36419	1.77	4.0E-87	AB040537.1	NT	Homo sapiens DDX10 mRNA for RNA helicase, complete cds
12131	24811	30582	1.36	4.0E-87	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12131	24811	30583	1.36	4.0E-87	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12304	24384		25.1	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2735	16226	27737	3.11	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
2802	16487		0.97	2.0E-87	BF327920.1	EST_HUMAN	QVO-BN0148-050600-264-a03 BN0148 Homo sapiens cDNA
3788	16323	28724	0.9	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
4955	17495	29872	1.2	2.0E-87	BF376311.1	EST_HUMAN	GM0-TN0038-150800-652-108 TN0038 Homo sapiens cDNA
5048	17558	29928	0.71	2.0E-87	BE175478.1	EST_HUMAN	RC6-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA
5930	18508	31193	8.69	2.0E-87	BE734190.1	EST_HUMAN	601568041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5930	18508	31194	8.69	2.0E-87	BE734190.1	EST_HUMAN	601568041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
6656	19204		3.94	2.0E-87	BE587183.1	EST_HUMAN	601341383F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3883348 5'
7069	19803	32398	0.83	2.0E-87	N48128.1	EST_HUMAN	y21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243398 5'
7165	19878	32701	0.74	2.0E-87	AV654143.1	EST_HUMAN	AV654143 GLC Homo sapiens cDNA clone GLCDS604 3'
7617	20068	32918	1.31	2.0E-87	BE294432.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
7874	20120	32975	0.81	2.0E-87	11433048	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7938	20375	33242	42.84	2.0E-87	N48128.1	EST_HUMAN	y21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243398 5'
8225	20844	33535	40.45	2.0E-87	N48128.1	EST_HUMAN	y21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243398 5'
8928	21363	34276	6.52	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
8887	22280		5.42	2.0E-87	BE531136.1	EST_HUMAN	801278315F1 NIH MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5'
1213	15262		2.28	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
3707	16248	28652	8.41	1.0E-87	Y00062.1	NT	Human mRNA for T-cell cyclophilin
3732	16272	28676	3.02	1.0E-87	4788827	NT	Homo sapiens neuroxin III (NRXN3), mRNA
5313	17813		0.61	1.0E-87	4605256	NT	Homo sapiens moesin (MSN), mRNA
6544	19086	31837	7.29	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6544	19086	31838	7.29	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7621	20070	32922	0.72	1.0E-87	AF039517.1	NT	Homo sapiens corticotropin-releasing factor type 1 receptor gene, exon 8
7621	20070	32923	0.72	1.0E-87	AF039517.1	NT	Homo sapiens corticotropin-releasing factor type 1 receptor gene, exon 8
7627	20075	32928	1.06	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7878	20317	33182	1.05	1.0E-87	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
8048	20480	33354	0.75	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
8348	20763	33660	0.41	1.0E-87	4505626	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
8714	21149	34053	11.22	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9788	22189	35126	4.59	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
9788	22189	35127	4.59	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
10287	22688	35651	1.29	1.0E-87	M34428.1	NT	Human L-plastin mRNA, 5' end
10516	22894	35943	5.77	1.0E-87	5728867	NT	Homo sapiens lect domain and RLD 2 (HERC2), mRNA
10780	23218		2.36	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10816	23261	36235	2.12	1.0E-87	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
10815	23251	36236	2.12	1.0E-87	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
12127	24988		1.23	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1133	13677	28116	8.77	9.0E-88	AF187465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1381	13916	28372	3.72	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1381	13916	28373	3.72	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
2040	14556	27067	3.01	9.0E-88	7681701	NT	Homo sapiens DKFZP586P1622 protein (DKFZP586P1522), mRNA
3624	16184	28574	1.37	9.0E-88	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
4286	16811	29195	3.51	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
4286	16811	29196	3.51	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8356	21768	34697	3.77	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1804	14327		1.54	5.0E-88	7661887	NT	Homo sapiens KIAA00683 gene product (KIAA00683), mRNA
2576	15072	27591	4.51	5.0E-88	N89399.1	EST_HUMAN	K07105 Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
2868	15511	27931	0.91	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN), complete cds
2968	15523	27944	0.67	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN), complete cds
2968	15523	27945	0.67	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN), complete cds
3367	15913		2.88	5.0E-88	AF693217.1	EST_HUMAN	w68h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338799 3' similar to contains Alu repetitive element; contains element MER22 MER22 repetitive element;
3518	16061	28483	0.67	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN), complete cds
7153	18868	32687	2.7	5.0E-88	H10932.1	EST_HUMAN	ym06b10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:47129 5'
8583	21018	33917	1.9	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
11868	14327		1.27	5.0E-88	7661887	NT	Homo sapiens KIAA00683 gene product (KIAA00683), mRNA
1361	13896	26352	1.58	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-F10 TN0028 Homo sapiens cDNA
1361	13898	26353	1.58	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-F10 TN0028 Homo sapiens cDNA
7692	20137	32993	1.31	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kd (TGFB1), mRNA
11244	23610	36854	2.67	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11244	23610	36855	2.67	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
752	13312	25739	1.07	3.0E-88	11545600	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1788	14313		1.59	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259), mRNA
2801	15458	27883	8.04	3.0E-88	N69951.1	EST_HUMAN	ze48f12.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:295823 3'
4257	16782	29164	0.88	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA
4257	16782	29165	0.88	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA
4514	17032		3.9	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5454	17949		0.95	3.0E-88	Z21378.1	EST_HUMAN	HSAAAEAVO TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test346 (b)
5552	18142	30502	2.77	3.0E-88	11428567	NT	Homo sapiens valsin-containing protein (VCP), mRNA
5852	18431	31103	4.96	3.0E-88	9868888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5975	18551	31236	4.02	3.0E-88	11420697	NT	Homo sapiens vral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
6475	19030	31767	0.67	3.0E-88	11417370	NT	Homo sapiens interleukin 13 (IL13), mRNA
6752	24814	32089	0.83	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6752	24814	32090	0.83	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7497	19701	32500	16.31	3.0E-88	AF279285.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
8053	20485	33360	6.23	3.0E-88	11438400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8576	21011	33911	8.56	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA
8773	21207	34109	1.49	3.0E-88	AF034374.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds
9843	20934	33831	1.25	3.0E-88	11526262	NT	Homo sapiens t-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
9888	22390	35340	0.95	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9988	22390	35341	0.95	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
11851	24100	-	5.53	3.0E-88	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1081	13607	28048	1.79	2.0E-88	7305198	NT	Homo sapiens Caldesin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1836	14167	28837	1.05	2.0E-88	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1741	14268	28763	3.89	2.0E-88	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4463	16973	28360	2.79	2.0E-88	5031666	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAI4), mRNA
6204	18770	31474	5.53	1.0E-88	AW139565.1	EST_HUMAN	UI-H-B11-aca-d04-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6204	18770	31475	5.53	1.0E-88	AW139565.1	EST_HUMAN	UI-H-B11-aca-d04-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
7009	19546	32329	28.4	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7009	19545	32330	28.4	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7661	20011	32854	1.48	1.0E-88	AI989034.1	EST_HUMAN	wq70a12.t1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2476603 3'
7628	20076	32829	3.82	1.0E-88	AA488981.1	EST_HUMAN	aa54a11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B02722 CE00851
9505	21068	34891	0.93	1.0E-88	AA190368.1	EST_HUMAN	zp87c02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627170 5' similar to SW:POL.1_HUMAN P10266 RETROVIRUS-RELATED POLYPROTEIN ;
9761	22154	35085	2.94	1.0E-88	AL043314.2	EST_HUMAN	DKFZp434N0323.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
11194	22846	35810	4.74	1.0E-88	AA991479.1	EST_HUMAN	os91g03.s1 NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb.M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
12085	24230	-	4.46	1.0E-88	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10730	23168	36151	75.02	9.0E-89	11421238	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA
2691	15182	27694	5.69	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508188 5'
7342	19754	32559	1.27	8.0E-89	11421514	NT	Homo sapiens similar to serpin domain, immunoglobulin domain (Ig), short basic domain, secreted, (serpinophin) 3A (H. sapiens) (LOC63232), mRNA
450	13025	25449	1.45	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
450	13025	25450	1.45	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4848	17459	29835	1.99	7.0E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B), mRNA
5009	17519	29993	6.42	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E246.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E246 5'
5687	18272	30592	1.28	7.0E-89	X98932.1	NT	H. sapiens CLN3 gene, complete CDS

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5687	18272	30693	1.28	7.0E-89	X99832.1	NT	H.sapiens CLN3 gene, complete CDS
6673	19221	31968	0.85	7.0E-89	7549808	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
6673	19221	31968	0.85	7.0E-89	7549808	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
8003	20436	33303	1.79	7.0E-89	11420754	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
8987	21420	34331	1.65	7.0E-89	J02923.1	NT	Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds
10394	22794	35766	1.17	7.0E-89	X62048.1	NT	H.sapiens Wee1 hu gene
10394	22794	35766	1.17	7.0E-89	X62048.1	NT	H.sapiens Wee1 hu gene
10403	22803	35779	1.57	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
10403	22803	35780	1.57	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
11008	23434	36452	3.29	7.0E-89	M59783.1	NT	Human aldose reductase (AR) gene, segment 2
12545	24766		1.31	7.0E-89	J06235.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
12568	24548		1.25	7.0E-89	U87927.1	NT	Human aconitase hydratase (ACO2) gene, exon 2
1048	13595	26035	0.99	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
2118	14632	27165	1.07	6.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
2332	14839	27353	1.89	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2332	14839	27354	1.89	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
3508	16049	28470	0.82	6.0E-89	7681817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4683	17199	29576	3.26	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
4683	17199	29577	3.26	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
5356	17855	30212	0.76	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
6386	17855	30213	0.76	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5204	17707	30070	2.72	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5204	17707	30071	2.72	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
8108	20634	33411	0.65	4.0E-89	BE762749.1	EST_HUMAN	QV3-NT0022-080600-219-g03 NT0022 Homo sapiens cDNA
2831	15387	27800	1.83	3.0E-89	AW876181.1	EST_HUMAN	EST388290 IMAGE resequences, MAGN Homo sapiens cDNA
7580	20028	32876	1.37	3.0E-89	AI217359.1	EST_HUMAN	qht17003.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844915.3
10582	23029	36012	2.6	3.0E-89	N57357.1	EST_HUMAN	yw86e11.r1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:259148.5 similar to SW:P14K_HUMAN_P42366 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA ;
131	12899	25425	0.85	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
131	12899	25426	0.85	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
425	12899	25425	0.66	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
425	12998	25426	0.66	2.0E-89	7706070	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
548	13120	25529	0.82	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2835	15381	27804	1.78	2.0E-89	A1222095.1	EST_HUMAN	qg86c08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
3538	16081	28498	0.87	2.0E-89	AA758149.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
3538	16081	28500	0.87	2.0E-89	AA759149.1	EST_HUMAN	ah70e03.s1 Soares testis_NHT Homo sapiens cDNA clone 1320988 3'
4164	16991	29077	1.37	2.0E-89	AF089897.1	NT	ah70e03.s1 Soares testis_NHT Homo sapiens cDNA clone 1320988 3'
4170	16997	29086	5.04	2.0E-89	X58742.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4170	16997	29087	5.04	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4371	16993	29274	0.75	2.0E-89	AL163203.2	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4534	17052	29435	0.98	2.0E-89	AJ007378.1	NT	Homo sapiens chromosome 21 segment HS21C003
5117	17924	29986	1.75	2.0E-89	11545821	NT	Homo sapiens GGT gene, exon 5
5597	18185	30759	1.56	2.0E-89	BE641744.1	EST_HUMAN	Homo sapiens melanoma differentiation associated protein-6 (MDA5), mRNA
5741	18323	30759	3.57	2.0E-89	AB007646.1	NT	601065996F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
6072	18644	31339	1.54	2.0E-89	U03985.1	NT	Homo sapiens gene for LECT2, complete cds
6527	18078	31819	0.71	2.0E-89	AL163286.2	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
8203	20624	33511	5.67	2.0E-89	U81004.1	NT	Homo sapiens chromosome 21 segment HS21C085
8587	21022	33923	2.64	2.0E-89	11428801	NT	Human GT24 (GT24) mRNA, partial cds
8944	21377	34289	0.92	2.0E-89	AJ245503.1	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
11130	23682	36623	8.79	2.0E-89	11434411	NT	Homo sapiens partial mRNA for PEX5 related protein
11222	22874	35849	2.43	2.0E-89	5729867	NT	Homo sapiens Integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
11320	23684	36733	3.36	2.0E-89	11433673	NT	Homo sapiens hec domain and RLD 2 (HERC2), mRNA
11439	23789	36858	2.63	2.0E-89	U10892.1	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
11325	23689	36740	5.04	1.0E-89	BF196052.1	EST_HUMAN	Human MAG-7 antigen (MAGE7) pseudogene, complete cds
11325	23689	36741	5.04	1.0E-89	BF196052.1	EST_HUMAN	hr81d09.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:054778 054778
8798	21232	34139	1.28	9.0E-90	AL163246.2	NT	SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN;
8798	21232	34140	1.28	9.0E-90	AL163246.2	NT	hr81d09.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:054778 054778
1089	13635	26073	2.71	8.0E-90	AL163246.2	NT	SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN;
						NT	hr81d09.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:054778 054778
						NT	Homo sapiens chromosome 21 segment HS21C046
						NT	Homo sapiens chromosome 21 segment HS21C046

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1090	13635	26073	2.63	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1362	15307	26354	4.58	8.0E-90	BE670561.1	EST_HUMAN	7c36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1362	15307	26355	4.58	8.0E-90	BE670561.1	EST_HUMAN	7c36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
10487	22937	35915	1.7	8.0E-90	A1222095.1	EST_HUMAN	qq96c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
10487	22937	35916	1.7	8.0E-90	A1222095.1	EST_HUMAN	qq96c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
859	13415		3.82	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8949	21382		2.09	7.0E-90	AA782977.1	EST_HUMAN	ai63d08.s1 Scores_testis_NHT Homo sapiens cDNA clone 1375503 3'
9317	21749	34657	2.4	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
9317	21749	34658	2.4	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
10141	22542	35510	2.42	7.0E-90	H68849.1	EST_HUMAN	yr86e04.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11588 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10141	22542	35511	2.42	7.0E-90	H68849.1	EST_HUMAN	yr86e04.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11588 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10344	22744	36711	0.91	7.0E-90	BF526089.1	EST_HUMAN	602071208F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214257 5'
3028	15583	27693	2.15	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
3028	15583	27694	2.15	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
4244	18769	29155	8.87	6.0E-90	8922398	NT	H. sapiens ECE-1 gene (exon 6)
4244	18769	29156	8.87	6.0E-90	8922398	NT	H. sapiens ECE-1 gene (exon 6)
6285	18947	31566	3.37	6.0E-90	U17700.1	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6285	18947	31567	3.37	6.0E-90	U17700.1	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
8285	18847	31567	3.37	6.0E-90	U17700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
8872	21306	34217	3.65	6.0E-90	4504794	NT	Homo sapiens HsGCN1 mRNA, partial cds
8872	21306	34218	3.65	6.0E-90	4504794	NT	Homo sapiens Inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
159	12764		23.82	5.0E-90	AB038344.1	NT	Homo sapiens Inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
1223	13763	26207	2.94	5.0E-90	U80226.1	NT	Homo sapiens TCE6 gene, exon 1-10b
						NT	Human germin-aminobutylic acid transaminase mRNA, partial cds
1786	14321	26814	0.92	6.0E-90	A1222095.1	EST_HUMAN	qq96c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1766	14321	26815	0.92	5.0E-90	AI222095.1	EST_HUMAN	q98608.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
2468	14989	27482	1.6	5.0E-90	AF114487.1	NT	Homo sapiens interseitin long isoform (ITSN) mRNA; complete cds
4576	17092	29480	12.38	5.0E-90	4508354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4598	17114	29502	0.68	5.0E-90	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4652	17168	29548	1.37	5.0E-90	AA705222.1	EST_HUMAN	z82g10.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
4652	17168	29549	1.37	5.0E-90	AA705222.1	EST_HUMAN	z82g10.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
5858	18437	31112	3.29	5.0E-90	Z18411.1	NT	H. sapiens mRNA encoding phospholipase C
5878	18455		0.61	5.0E-90	AF008915.1	NT	Homo sapiens EVI5 homolog mRNA; complete cds
5963	18639	31225	1.2	5.0E-90	AB015817.1	NT	Homo sapiens ELKS mRNA; complete cds
6046	18437	31112	2.38	5.0E-90	Z18411.1	NT	H. sapiens mRNA encoding phospholipase C
7109	18642	32437	0.76	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7109	18642	32438	0.76	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7661	20107	32869	1.53	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA; partial cds
7661	20107	32860	1.53	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA; partial cds
8079	20507	33386	5.49	5.0E-90	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
8846	21280	34193	5.37	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
8819	22222	35168	1.29	5.0E-90	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10337	22737	35705	6.97	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type BA, member 2 (ATP8A2), mRNA
11317	23681	36731	1.78	5.0E-90	AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene; partial cds
12359	24451		1.7	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-8; complete cds
12408	24440		2.35	5.0E-90	AI523366.1	EST_HUMAN	ar78r05.x1 Barehead actin HPLRB0 Homo sapiens cDNA clone IMAGE:2128761 3'
316	12911	25330	2.6	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
316	12911	25331	2.6	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1113	13657	26098	3.91	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1687	14216	26697	8.53	4.0E-90	X98033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 18
4701	17217	29599	4.9	4.0E-90	ID87875.1	NT	Homo sapiens DNA for amyloid precursor protein; complete cds
4852	17384	29747	1.81	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein; partial cds
4875	17387	29759	1.63	4.0E-90	M95967.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 8
5051	17561		0.64	3.0E-90	AI30786.1	EST_HUMAN	q28608.x1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2041743 3' similar to gb:U31470 RAS-LIKE PROTEIN TC10 (HUMAN);

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8529	20964	33866	0.89	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-any-b-04-0-UI.at NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
8529	20964	33866	0.89	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-any-b-04-0-UI.at NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11378	23740	36799	72.49	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
221	12823	25240	5.04	2.0E-90	BE537913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1204	13745	26189	8.44	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1204	13745	26189	8.44	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
2276	14784		4.81	2.0E-90	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3852	16388	28798	2.33	2.0E-90	AI139213.1	EST_HUMAN	qc54c02.x1 Scareea_placenta 81cd9weeks 2NBHP869W Homo sapiens cDNA clone IMAGE:1713410 3'
4737	17261	29632	1.03	2.0E-90	AB006827.1	NT	similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3.;
4981	17492	29869	10.77	2.0E-90	5729855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
6056	18628	31319	0.54	2.0E-90	11525901	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
6056	18628	31320	0.54	2.0E-90	11525901	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
6065	18637	31331	4.04	2.0E-90	AW672686.1	EST_HUMAN	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
8891	22284	35233	2.73	2.0E-90	11427320	NT	be49405.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 5' similar to Trc075208 O75208 HYPOTHETICAL 35.5 KD PROTEIN.;
8991	22284	35234	2.73	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10003	22405	35354	1.67	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10003	22405	35355	1.67	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
11221	22873	35848	2.6	2.0E-90	11024711	NT	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
280	12987	25307	4.03	1.0E-90	4502166	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
389	15256	25397	1.38	1.0E-90	AF231920.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
380	15256	25397	1.14	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
715	13276	25697	2.42	1.0E-90	AJ237589.1	NT	Homo sapiens chromosome 21 unknown mRNA
715	13276	25698	2.42	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
750	13310	25736	17.97	1.0E-90	AF264750.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
750	13310	25737	17.97	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1137	13681		3.72	1.0E-90	4507828	NT	Homo sapiens ALR-like protein mRNA, partial cds
1338	13874	26326	3.38	1.0E-90	AF096154.1	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1338	13874	26327	3.38	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1687	14198		1.46	1.0E-90	BE379884.1	EST_HUMAN	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
							601165653F2 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3511116 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1883	14385	28876	1.94	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57187), mRNA
2808	15365	27781	6.31	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3858	16394	28799	0.93	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3858	16394	28797	0.93	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4451	16971	28358	1.2	1.0E-90	AF167340.1	NT	Homo sapiens soluble Interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5944	18521	31204	2.21	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
6123	18692	31389	1.13	1.0E-90	11426910	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7508	19710	32511	0.81	1.0E-90	U91934.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7767	20210	33073	0.66	1.0E-90	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
8208	20828	33517	2.97	1.0E-90	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
9231	21663	34572	3.66	1.0E-90	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9548	21891		1.14	1.0E-90	AF163804.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9562	21895	34911	1.33	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9562	21895	34912	1.33	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
10453	22804	35883	3.28	1.0E-90	R25688.1	EST_HUMAN	y844d11.2 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35477 5'
10817	23253	36238	2.02	1.0E-90	J04474.1	NT	Human branched chain alpha-keto acid dehydrogenase mRNA, 3' end
12347	24409	30891	1.89	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2X4, complete cds
12347	24409	30892	1.89	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2X4, complete cds
4212	16737	29128	6.97	8.0E-91	D12234.1	EST_HUMAN	HUJ0005381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
8856	21290	34201	1.78	7.0E-91	11419234	NT	Homo sapiens makofin, ring finger protein, 1 (MKRN1), mRNA
3450	16994	28413	1.28	5.0E-91	AA702784.1	EST_HUMAN	z60b04.s1 Soares fetal liver spleen_1N1S1 Homo sapiens cDNA clone IMAGE:448015 3'
4553	17070	28452	1.07	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y78AA1 Homo sapiens cDNA clone Y78AA1002087 5'
4553	17070	28453	1.07	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y78AA1 Homo sapiens cDNA clone Y78AA1002087 5'
4868	17378	28754	0.81	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4868	17378	28755	0.81	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6974	19511	32292	1.28	5.0E-91	AI879995.1	EST_HUMAN	su4909.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to SW ASPG FLAME Q47898 N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR:
8782	21216	34120	1.19	5.0E-91	BF314682.1	EST_HUMAN	601901624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130833 5'
9183	21615	34525	1.95	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
9183	21615	34526	1.95	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12380	24424		1.7	6.0E-01	AI183568.1	EST_HUMAN	q970f11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744385 3' similar to contains
3158	15711	28131	1.4	4.0E-01	AF156776.1	NT	MIR.b2 MIR MIR repetitive element ;
3158	15711	28132	1.4	4.0E-01	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
10707	23146	38130	2.71	4.0E-01	AL183284.2	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
11803	24085	30982	2.42	4.0E-01	M77994.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
11803	24085	31028	2.42	4.0E-01	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #336205) Homo sapiens cDNA clone HHCMC60 similar to
12107	24253	30928	1.35	4.0E-01	M77994.1	EST_HUMAN	Retrovirus-related gag polyprotein
12107	24253	30929	1.35	4.0E-01	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #336205) Homo sapiens cDNA clone HHCMC60 similar to
1630	14182	26632	1.13	3.0E-01	11430193	NT	Retrovirus-related gag polyprotein
1630	14182	26633	1.13	3.0E-01	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
2598	15092	27607	1.65	3.0E-01	AF169555.1	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
2598	15092	27608	1.65	3.0E-01	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
3312	15880	28278	1.21	3.0E-01	AL163283.2	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
3439	15983	28399	3.98	3.0E-01	AB033104.1	NT	Homo sapiens chromosome 21 segment HS21C083
3439	15983	28400	3.98	3.0E-01	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3790	16327	28729	0.95	3.0E-01	AF084530.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4630	17146	29528	4.76	3.0E-01	M30638.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
5075	17585	29852	1.18	3.0E-01	AL163285.2	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5075	17585	29853	1.18	3.0E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5956	18532	31214	1.72	3.0E-01	11434964	NT	Homo sapiens epidermal secretory protein (19.5kD) (HE1), mRNA
6632	19181		2.75	3.0E-01	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6936	19475	32264	3.45	3.0E-01	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6936	19475	32255	3.45	3.0E-01	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
8169	20591	33473	4.69	3.0E-01	U96959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8169	20591	33474	4.69	3.0E-01	U96959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
9182	21624	34534	3.34	3.0E-01	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
10976	23405	36414	4.03	3.0E-01	AB028003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10976	23405	36415	4.03	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11506	23894	36941	2.79	3.0E-91	AF180864.1	NT	Homo sapiens ADP-ribosylation factor binding protein GGA3 (GGA3) mRNA, complete cds
12081	24223	30957	1.68	3.0E-91	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12440	15092	27607	4.28	3.0E-91	AF168555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
12440	15092	27608	4.28	3.0E-91	AF168555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
10926	23367	36367	1.71	2.0E-91	BE794237.1	EST_HUMAN	601471469F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874648 5'
11528	23886	36968	2.08	2.0E-91	6871607	NT	Mus musculus BTB and CNC homology 2 (Bach2), mRNA
50	12671	25069	2.97	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1278	13814	26268	9.3	1.0E-91	AW449746.1	EST_HUMAN	UI-H-B13-aks-d01-Q-U1.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2735280 3'
6669	18254	30654	0.82	1.0E-91	11434402	NT	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
7238	19850	32669	2.17	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157804 5'
7238	19850	32670	2.17	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157804 5'
8498	20908	33803	0.56	1.0E-91	M20453.1	NT	Human nucleus-encoded mitochondrial aldehyde dehydrogenase 2 (ALDH2) gene, exon 10
11966	24896		1.81	1.0E-91	H16212.1	EST_HUMAN	ym30e03.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:49587 5'
1274	13811	26262	9.51	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1274	13811	26263	9.51	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
5721	18303	30735	4.31	9.0E-92	J03007.1	NT	Human Na ⁺ K ⁺ ATPase alpha-subunit mRNA, partial cds
5872	18461	31126	2.75	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
6766	16339	32110	4.47	9.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
8912	21346	34262	1.93	9.0E-92	AB040946.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8912	21346	34263	1.93	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9531	21846	34869	1.74	9.0E-92	11422086	NT	Homo sapiens brafordin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
10977	23408		3.02	9.0E-92	7706889	NT	Homo sapiens RNBB6 (RNBB6), mRNA
95	12712	26125	5.47	8.0E-92	W26387.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
299	12895	26315	3.91	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
5244	17745	30112	0.62	8.0E-92	AW157571.1	EST_HUMAN	au83108.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
5648	18235	30634	0.85	8.0E-92	AB049820.1	NT	TR-Q60302 O60302 KIAA0555 PROTEIN; contains element MER22 repetitive element;
5760	18341	30797	0.68	8.0E-92	AF264717.1	NT	Homo sapiens FVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6868	19438	32214	1.27	8.0E-92	AJ000979.1	NT	Homo sapiens MCP-4 gene
6802	19442	32219	1.1	8.0E-92	AF179428.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
8328	20743	33637	0.48	8.0E-92	X69636.1	NT	H. sapiens gene for Inter-alpha-trypsin inhibitor heavy chain H1, exons 7-8

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8328	20743	33638	0.48	8.0E-92	X89536.1	NT	H.sapiens gene for Inter-alpha-trypsin inhibitor heavy chain H1, exons 7-8
8950	21383	34294	3.63	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8950	21383	34295	3.63	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8387	21819	34735	2.95	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10064	22495	35405	1.2	8.0E-92	Y13828.1	NT	Homo sapiens mRNA for MBNL protein
10687	23033	36016	1.99	8.0E-92	AF074393.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11118	23571	36614	4.19	8.0E-92	4503340	NT	Homo sapiens dihydropyrimidinase S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
28	12646	26034	1.6	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
69	12688	25097	3.71	7.0E-92	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
249	15279	25266	8.05	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
249	15279	25267	6.05	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
608	13176		1.21	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Sepsis truncated isoform mRNA, complete cds
1313	13848	26289	1.67	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2092	14606	27123	3.64	7.0E-92	5031570	NT	Homo sapiens ARP2 (ectin-related protein 2, yeast) homolog (ACTR2), mRNA
2092	14606	27124	3.64	7.0E-92	5031570	NT	Homo sapiens ARP2 (ectin-related protein 2, yeast) homolog (ACTR2), mRNA
2477	14978	27492	3.32	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2678	15171	27679	4.49	7.0E-92	6006798	NT	Homo sapiens NRAS-related gene (D1S159E), mRNA
2710	15200	27716	9.15	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3318	17863	28283	0.85	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3318	17863	28284	0.85	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4626	17142	28523	1.25	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2860 nt]
4626	17142	28524	1.25	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2860 nt]
5511	18102	30345	5.93	7.0E-92	AA446206.1	EST_HUMAN	zw66d12.r1 Squares, testis, NHT Homo sapiens cDNA clone IMAGE:781175 5'
2723	15213	27728	2.44	3.0E-92	BE009714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902839 5'
6164	18732	31436	6.18	3.0E-92	AA378336.1	EST_HUMAN	EST01020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
10547	22894	35676	10.35	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
10547	22894	35677	10.35	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
27	12847	25035	1.21	2.0E-92	4501898	NT	Homo sapiens actinin A receptor, type IIB (ACV2B) mRNA
163	12785	25169	3.61	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA
183	12785	25200	3.61	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
770	13330	25762	2.97	2.0E-92	BE299180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
770	13330	25763	2.97	2.0E-92	BE299180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1712	14240		1.13	2.0E-92	S78653.1	NT	mig-mas-related [human, Genomic, 2416 nt]
1887	14408	26804	1.94	2.0E-92	A1818119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1887	14408	26905	1.94	2.0E-92	A1818119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1976	14493	27003	8.95	2.0E-92	4508860	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2595	15091	27608	15.08	2.0E-92	6912457	NT	Homo sapiens syndecan 4 (emphiglycan, ryudocan) (SDC4) mRNA
3607	16147	28554	0.89	2.0E-92	AF231919.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3607	16147	28555	0.89	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3685	16225	28633	5.49	2.0E-92	5803180	NT	Homo sapiens chromosome 21 unknown mRNA
4305	16830	29219	1.47	2.0E-92	MT0976.1	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4809	17321	29700	0.59	2.0E-92	AF139523.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5093	17603		3.69	2.0E-92	AL040437.1	EST_HUMAN	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
5482	17957		0.87	2.0E-92	AL163201.2	NT	DKFZp434C0414_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0414 5'
6039	18813	31301	0.65	2.0E-92	AF016535.1	NT	Homo sapiens chromosome 21 segment HS21C001
6629	19178		1.07	2.0E-92	4504786	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6971	19508	32288	2.35	2.0E-92	AB028991.1	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
7856	20393		0.74	2.0E-92	U87780.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
7891	20393		0.68	2.0E-92	U87780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
9258	21690	34802	1.3	2.0E-92	AW340174.1	EST_HUMAN	Human NPY Y1-like receptor pseudogene mRNA, complete cds
10541	22988	35988	2.41	2.0E-92	11434900	NT	hcd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711
10831	23268	36252	3.58	2.0E-92	5803103	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
10921	23353	36361	2.54	2.0E-92	AW836290.1	EST_HUMAN	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
10921	23353	36382	2.64	2.0E-92	AW836290.1	EST_HUMAN	Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA
12179	24299	30942	2.93	2.0E-92	AB028016.1	NT	CM4-L T0026-161299-062-g06 L T0026 Homo sapiens cDNA
12475	15091	27608	38.96	2.0E-92	6912457	NT	CM4-L T0026-161299-062-g06 L T0026 Homo sapiens cDNA
12599	24903	30469	1.18	2.0E-92	AF106656.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
1822	14344	26842	1.27	1.0E-92	R78078.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1822	14344	26843	1.27	1.0E-92	R78078.1	EST_HUMAN	Homo sapiens adenylysuccinate lyase gene, complete cds
							y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145674 5'
							y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145674 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1997	14513	27023	38.76	1.0E-92	4506688	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
9449	21880	34798	3.66	1.0E-92	A380356.1	EST_HUMAN	tg01b02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1; contains Alu repetitive element; contains element
9449	21880	34798	3.66	1.0E-92	A380356.1	EST_HUMAN	tg01b02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1; contains Alu repetitive element; contains element
1963	14481	26980	2.02	9.0E-93	AU121681.1	EST_HUMAN	MER17 repetitive element;
1973	14491		21.15	9.0E-93	AA316723.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2583	15079		1.58	9.0E-93	AF223301.1	NT	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
3609	16149	28557	1.04	9.0E-93	BE386571.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11390	23762		31.68	9.0E-93	11478526	NT	601281837F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
6946	19484	32263	3.56	8.0E-93	BF036384.1	EST_HUMAN	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
8519	24997		0.44	8.0E-93	AA777071.1	EST_HUMAN	601460521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
259	12857	25274	20.03	7.0E-93	AF231918.1	NT	z24504.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377839 3' similar to SW:POL_SMSAV_P03359 POL POL YPRROTEIN;
3037	15582	28004	0.74	6.0E-93	11526176	NT	Homo sapiens chromosome 21 unknown mRNA
7050	19594	32379	1.07	6.0E-93	AB033093.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
7325	19737	32541	1.24	6.0E-93	AF095771.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
1413	13947	28403	1.08	5.0E-93	AB014511.1	NT	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds
1439	13971	26427	5.49	5.0E-93	AI674184.1	EST_HUMAN	wd09c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
1503	14035	26429	5.49	5.0E-93	AI674184.1	EST_HUMAN	wd09c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
1799	15322	26918	0.99	5.0E-93	AJ297710.1	NT	Homo sapiens chromosome 21 segment HS21C001
3182	15745	28106	3.51	5.0E-93	X04201.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 2
8083	18653	31347	1.2	5.0E-93	M22878.1	NT	Human skeletal muscle 1.3 kb mRNA for topomycin
6420	18977		1.58	5.0E-93	AF045553.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
8259	20876	33566	3.76	5.0E-93	AF067136.1	NT	Homo sapiens wbscr1 (WBSOR1) and wbscr5 (WBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
9779	22182	35117	2.32	5.0E-93	AF274863.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
							Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9897	22289	35241	1.26	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
10090	22491	35448	1.84	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
10607	23051	36036	1.9	6.0E-93	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2) mRNA
12069	24578	30837	1.87	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
80	12707		6.41	4.0E-93	AA459833.1	EST_HUMAN	z50609.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795988 3' similar to SW:CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM;
462	13036	25469	2.31	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
462	13036	25460	2.31	4.0E-93	4557878	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
764	13362	25787	1.22	4.0E-93	7657464	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
764	13362	25788	1.22	4.0E-93	7657464	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
1214	13764	26189	2.18	4.0E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
1922	14441	26944	2.98	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in Intron 5
2163	14666	27189	1.59	4.0E-93	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
2535	15033	27549	3.9	4.0E-93	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3555	16097	28514	0.83	4.0E-93	7705398	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4000	16591	28983	2.15	4.0E-93	4504654	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5127	16097	28514	0.83	4.0E-93	7705398	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5912	18490	31173	4.72	4.0E-93	T46864.1	EST_HUMAN	y584c12.11 Striatogene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN
10911	23343	36351	39.14	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GKc Homo sapiens cDNA clone GKDRF07 5'
3651	16191	28597	7	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332038 5'
3651	16191	28598	7	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332038 5'
4252	16777		6.32	3.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
6067	18639	31333	0.54	3.0E-93	AI553853.1	EST_HUMAN	tr29g03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2169078 3'
6067	18639	31334	0.54	3.0E-93	AI553853.1	EST_HUMAN	tr29g03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2169078 3'
6916	19455	32234	1.12	3.0E-93	11426182	NT	Homo sapiens GON5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GON5L2), mRNA
10583	23030	36013	2.2	3.0E-93	AI624629.1	EST_HUMAN	w602405.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304489 3'
196	12789	25214	19.65	2.0E-93	AB015910.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
196	12789	25215	19.65	2.0E-93	AB015910.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
337	12930	25347	10.9	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
338	12930	25347	7.49	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1629	14161	26631	2.63	2.0E-93	AF225898.1	NT	Homo sapiens tensin mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2049	14665	27079	1.39	2.0E-93	U40763.1	NT	Human Cdk-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2388	14892	27411	3.27	2.0E-93	BE262982.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3398220 5'
5673	18258	30858	4.32	2.0E-93	AW964386.1	EST_HUMAN	EST376458 MAGE resequences, MAGE Homo sapiens cDNA
5684	18289	30889	0.77	2.0E-93	4758153	NT	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA
5806	18386		0.91	2.0E-93	BF351459.1	EST_HUMAN	QV3-HT0513-290300-128-h04 HT0613 Homo sapiens cDNA
5905	18483	31165	1.07	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
5920	18498	31179	0.73	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-86
7053	19587		1.25	2.0E-93	AW602002.1	EST_HUMAN	U1HF-BNO-ake-g-09-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone 1-86
10860	23293	36288	2.01	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
10860	23293	36287	2.01	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
11952	24155		1.56	2.0E-93	AA126735.1	EST_HUMAN	229c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3'
12044	24213		2.53	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
12337	24404		4.77	2.0E-93	BF035327.1	EST_HUMAN	601485531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3962086 5'
106	12723	25136	2.07	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
106	12723	25137	2.07	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
536	13108	25519	7.02	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (D328E19.C1.1), mRNA
617	13185	25589	3.81	1.0E-93	AI148755.1	EST_HUMAN	Q84808.X1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q82384 Q62384
895	13450	25898	6.82	1.0E-93	D87676.1	NT	ZINC FINGER PROTEIN ;
1198	13739	26182	0.98	1.0E-93	4503872	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1270	13808	26255	8.58	1.0E-93	8923270	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD67, mRNA
1270	13808	26255	8.58	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1377	13912	26367	1.32	1.0E-93	AF167706.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
2231	14740	27260	1.85	1.0E-93	AF231981.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
2360	14865	27386	10.69	1.0E-93	AF050068.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2781	13803	26312	1.72	1.0E-93	BE297369.1	EST_HUMAN	Homo sapiens MHC class 1 region
2781	13863	26313	1.72	1.0E-93	BE297369.1	EST_HUMAN	60117766F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3932865 5'
2887	15442	27855	4.38	1.0E-93	D87675.1	NT	60117766F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3932865 5'
3174	15727		1.38	1.0E-93	AF231981.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4458	16978	28394	1.73	1.0E-93	AL163284.2	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
5931	18411	31078	1.38	1.0E-93	U79509.1	NT	Homo sapiens chromosome 21 segment HS21C084
5931	18411	31079	1.38	1.0E-93	U79509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
						NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6046	18618	31307	1.15	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6210	18778	31482	12.28	1.0E-93	4557782	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6511	19065	31807	1.05	1.0E-93	7662241	NT	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA
7177	19890	32713	2.09	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7700	20145	33003	6.33	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
8821	21255	34181	1.89	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
9031	21463	34371	1.43	1.0E-93	Y10183.1	NT	H. sapiens mRNA for MEMD protein
9102	21534	34443	1.18	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9856	20947	33846	1.25	1.0E-93	AB040318.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9859	20950	33849	1.13	1.0E-93	AF091395.1	NT	Homo sapiens Tric isoform mRNA, complete cds
9758	22159	36090	5.38	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 8)
9758	22159	35091	5.36	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
11599	24681	30773	2.2	1.0E-93	AJ258262.1	EST_HUMAN	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
12232	24340		1.55	1.0E-93	AJ230125.1	NT	gmo3c12.1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP:1884.4 CE13742;
12330	24369		3.27	1.0E-93	11417858	NT	Homo sapiens GGT1 gene, exon 1
12523	24949		2.11	1.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
10427	22827		0.86	6.0E-94	AL163208.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
3975	16510	28917	2.19	6.0E-94	AF142482.1	NT	Homo sapiens chromosome 21 segment HS21C009
12484	24484		1.81	6.0E-94	11418351	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
5623	18210	30810	3.65	5.0E-94	AB014512.1	NT	Homo sapiens mitogen-activated protein kinase 12 (MAPK12), mRNA
5623	18210	30811	3.65	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
6354	18912	31845	4.38	5.0E-94	AA722434.1	EST_HUMAN	Homo sapiens mRNA for KIAA0612 protein, partial cds
7431	19936	32768	1.55	5.0E-94	AJ015800.1	EST_HUMAN	cg83d05.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:408594 3'
9086	21528	34435	0.92	6.0E-94	BF629115.1	EST_HUMAN	cg83d05.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:1823369 3'
10753	23191	36176	3.59	5.0E-94	11423962	NT	602042163F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180023 5'
10753	23191	36177	3.59	5.0E-94	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
11352	23718	36775	1.8	5.0E-94	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
11352	23718	36776	1.8	5.0E-94	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
11930	24952	30467	7.88	5.0E-94	788398.1	EST_HUMAN	Homo sapiens adenylate kinase 2 (AK2), mRNA
12549	24537		1.28	5.0E-94	9558724	NT	y498b04.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:118239 3'
1815	14338		10.55	4.0E-94	LO5094.1	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160KD subunit (CPSF1), mRNA
							Homo sapiens ribosomal protein L27 mRNA, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2594	16080	27605	2.14	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3671	18211	28616	0.98	4.0E-94	AW197851.1	EST_HUMAN	xn89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3671	18211	28617	0.98	4.0E-94	AW197851.1	EST_HUMAN	xn89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4769	17283	29668	3.45	4.0E-94	AI591312.1	EST_HUMAN	tw11f10.x1 NCI CGAP Bms2 Homo sapiens cDNA clone IMAGE:2269403 3' similar to TR:Q15285 Q15286 PROTEIN TYROSINE PHOSPHATASE;
6813	19354	32130	1.83	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6813	19354	32131	1.83	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7320	19732		0.92	4.0E-94	L27386.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
10889	23320	36319	3.13	4.0E-94	AB004929.1	NT	Homo sapiens gene for Smad 3, exon 8
11204	22858	35829	2.49	4.0E-94	11645762	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
630	13194	25600	1.26	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
747	13302	25726	0.99	3.0E-94	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1732	14259	26744	1.84	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
1732	14259	26745	1.84	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
1757	14284	26767	2.47	3.0E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4205	16730	28119	0.65	3.0E-94	AA484805.1	EST_HUMAN	zw63g08.f1 Soares_total_fetus_NB2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
5950	18526	31210	3.72	3.0E-94	11496288	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6464	18020	31753	1.12	3.0E-94	AB011538.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6704	18337	32108	4.63	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
8374	20788	33687	0.68	3.0E-94	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8778	21210	34113	1.06	3.0E-94	AF152308.1	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
9059	21491	34402	4.88	3.0E-94	AB014578.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
9760	22163	36097	5.08	3.0E-94	AF087842.1	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
10885	23317	36314	4.26	3.0E-94	4757821	NT	Homo sapiens truncated form 1 lacking leucine zipper mRNA, complete cds
11412	23773	36832	3.08	3.0E-94	U28711.1	NT	601176732F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
153	12758	25178	2.42	1.0E-94	BE295714.1	EST_HUMAN	60111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3532569 5'
3051	15605	28014	2.36	1.0E-94	BE293433.1	EST_HUMAN	60111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3532569 5'
3051	16605	28015	2.36	1.0E-94	BE293433.1	EST_HUMAN	60111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3532569 5'
4380	16802	29287	0.94	1.0E-94	9606892	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
4842	17354	29739	3.22	1.0E-94	AI804151.1	EST_HUMAN	CM-BT043-090299-075 BT043 Homo sapiens cDNA
6379	18936	31674	1.04	1.0E-94	AE000289.1	NT	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome
6590	19141	31888	0.88	1.0E-94	AL040518.1	EST_HUMAN	DKFZp434G0314_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G0314 5'

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6589	19150	31899	0.78	1.0E-94	H09270.1	EST_HUMAN	X87102.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:45053 5'
8869	18409	32183	0.69	1.0E-94	AV725992.1	EST_HUMAN	AV725992 HTC Homo sapiens cDNA clone HTCBF06 5'
9517	21980	34606	2.28	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
9889	22282	35232	1.57	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872089 5'
10847	23280	38270	5.68	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist (IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11083	23508	36540	2.35	1.0E-94	A1272244.1	EST_HUMAN	ap22e02.x1 Schiller oligodendrogloma Homo sapiens cDNA clone IMAGE:1056122 3' similar to TR:Q62845
11466	23824	36859	1.99	1.0E-94	11418871	NT	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR. ;
12375	12758	25176	1.28	1.0E-94	BE295714.1	EST_HUMAN	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA
1505	14037	26501	1.41	9.0E-95	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3114	15667	28079	1.04	9.0E-95	7662027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3114	15667	28080	1.04	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5661	18246	30645	1.44	9.0E-95	X82569.1	NT	M.musculus glyt1 gene (exons 1c and 2)
5661	18246	30646	1.44	9.0E-95	X82569.1	NT	M.musculus glyt1 gene (exons 1c and 2)
8814	21248	34152	1.87	9.0E-95	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
4572	17089	29475	1	8.0E-95	A1700988.1	EST_HUMAN	we09e04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340608 3' similar to gb:K00558
4572	17089	29476	1	8.0E-95	A1700988.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
7359	18816	32630	0.98	8.0E-95	11419376	NT	we09e04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340608 3' similar to gb:K00558
7690	20135	32991	1.56	8.0E-95	11426529	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
7690	20135	32992	1.56	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
8774	21208	34110	1.78	8.0E-95	AF032897.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
8988	22078	35001	2.04	8.0E-95	11420844	NT	Homo sapiens potasium channel subunit (HERG-3) mRNA, complete cds
9596	22078	35002	2.04	8.0E-95	11420844	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9930	22332	35280	2.78	8.0E-95	5174644	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9952	22354		3.79	8.0E-95	AB037816.1	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
10202	22603	35567	0.88	8.0E-95	9845523	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10489	22949	35930	6.41	8.0E-95	AF112152.1	NT	Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
11239	23607	36652	4.83	8.0E-95	10884024	NT	Homo sapiens developmental efferies and neural crest EGF-like protein mRNA, complete cds
11415	23776	36834	2.1	8.0E-95	7019572	NT	Homo sapiens HCF-binding transcription factor Zhangfei (ZF), mRNA
11415	23776	36835	2.1	8.0E-95	7019572	NT	Homo sapiens zinedin (ZIN), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12299	24380		17.48	8.0E-95	AA829056.1	EST_HUMAN	zu84b01.a1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.1 L1
289	12886	25305	9.54	7.0E-95	D87875.1	NT	repetitive element;
289	12886	25306	9.54	7.0E-95	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
2349	14852	27371	1.26	7.0E-95	M75973.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
2349	14852	27372	1.26	7.0E-95	M75973.1	NT	Human hepatocyte growth factor gene, exon 8
4388	16910	29295	6.57	7.0E-95	M95708.1	NT	Human hepatocyte growth factor gene, exon 8
4441	16991		1.44	7.0E-95	M95708.1	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
216	12819	25235	0.82	3.0E-95	AV848361	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
5909	18284	30708	1.67	3.0E-95	BF526041.1	EST_HUMAN	AV848361 GLC Homo sapiens cDNA clone GLOBIF01 3'
5943	24586	31203	0.6	3.0E-95	4503354	NT	602071146F1 NCI CGAP Bim84 Homo sapiens cDNA clone IMAGE:4214147 5'
7608	20057	32909	0.42	3.0E-95	AA412321.1	EST_HUMAN	z87d01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7608	20057	32910	0.42	3.0E-95	AA412321.1	EST_HUMAN	z87d01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7841	20281	33142	0.93	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGIE resequences, MAGIE Homo sapiens cDNA
7841	20281	33143	0.93	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGIE resequences, MAGIE Homo sapiens cDNA
9587	22010	34838	1.6	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9587	22010	34839	1.6	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
10662	23102	36083	1.69	3.0E-95	R83190.1	EST_HUMAN	yo87g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194468 5'
1650	14181	26850	1.97	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1650	14181	26851	1.97	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1892	14412	26910	43.75	2.0E-95	4607612	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1895	14415	26914	2	2.0E-95	BE393873.1	EST_HUMAN	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5'
2327	14834	27348	1.56	2.0E-95	8453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2327	14834	27349	1.56	2.0E-95	8453666	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2362	14867	27387	3.15	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2421	14924	27440	0.9	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2521	15021		1.66	2.0E-95	R18245.1	EST_HUMAN	ya49d08.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53393 3'
2776	13514	25957	1.16	2.0E-95	4804374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
3116	15669	28082	7.98	2.0E-95	AF016452.1	NT	Homo sapiens Usuriph-gamma mRNA, complete cds
3652	16094	28510	3.26	2.0E-95	7705800	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3552	16094	28511	3.26	2.0E-95	7705800	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3912	16152	28560	0.82	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3750	16289	28692	0.68	2.0E-95	AI290284.1	EST_HUMAN	qm01c02.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 CE03705;
4363	16905	29289	1.54	2.0E-95	7867186	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
5148	17650	30016	3.04	2.0E-95	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5223	17725	30092	10.92	2.0E-95	AA447831.1	EST_HUMAN	zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:766157 5'
5223	17725	30093	10.92	2.0E-95	AA447831.1	EST_HUMAN	zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:766157 5'
5740	18322	30767	3.72	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51086), mRNA
5740	18322	30768	3.72	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51086), mRNA
5968	18544	31228	1.27	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5968	18644	31229	1.27	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6073	18587	31274	0.84	2.0E-95	11525883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUIK p55 subfamily member 3) (MPP3), mRNA
6455	19011	31745	4.22	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6782	19335	32103	0.82	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6792	19335	32106	0.82	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6923	19462	32240	2.96	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7145	19858	32677	1.35	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9433	21865	34781	1.35	2.0E-95	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10509	22958	35939	4.9	2.0E-95	4767853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A) mRNA
10681	23121	36100	2.58	2.0E-95	7661893	NT	Homo sapiens Ste20-related serine/threonine kinase (KIAA0204), mRNA
11425	23786	36847	4.41	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11425	23786	36848	4.41	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12028	24201	30854	2.04	2.0E-95	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12149	24280		1.25	2.0E-95	11477860	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
12476	24492	30881	6.24	2.0E-95	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
5982	18461	31135	8.04	1.0E-95	AA284651.1	EST_HUMAN	zx23h04.r1 Soares_ovary_tumor_NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F56H2.6;
5982	18461	31136	8.04	1.0E-95	AA284651.1	EST_HUMAN	zx23h04.r1 Soares_ovary_tumor_NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F56H2.6;
8020	20452	33323	4.44	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
8020	20452	33324	4.44	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
8771	21205	34108	1.63	9.0E-98	BE897289.1	EST_HUMAN	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922423 5'
459	15283	25456	0.73	8.0E-96	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
469	16283	26487	0.73	8.0E-08	BE007607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
5773	18354		2.9	8.0E-08	AW836047.1	EST_HUMAN	PMO-LT0019-090300-002-d09 LT0019 Homo sapiens cDNA
11259	23825	36873	1.9	8.0E-08	BE005982.1	EST_HUMAN	RCO-BN0121-280300-032-e08 BN0121 Homo sapiens cDNA
3921	18458	28863	0.93	7.0E-08	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
3285	18834	28232	1.07	6.0E-08	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3458	16002	28421	7.49	6.0E-08	M28873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
5247	17748	30116	1.38	6.0E-08	AW448328.1	EST_HUMAN	UHH-B18-ak-b-02-0-UJ.s1 NCJ CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734394 3'
5247	17748	30117	1.38	6.0E-08	AW448328.1	EST_HUMAN	UHH-B18-ak-b-02-0-UJ.s1 NCJ CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734394 3'
5907	18485	31187	0.68	6.0E-08	11422642	NT	Homo sapiens sialyltransferase 8 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
11289	23664	36709	5.64	6.0E-08	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11289	23664	36710	5.64	6.0E-08	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11340	23704	36758	3.48	6.0E-08	8923539	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11473	23831	36889	3.28	6.0E-08	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11473	23831	36900	3.28	6.0E-08	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
334	12927	25343	41.18	5.0E-06	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
865	13420	25866	4.1	3.0E-08	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
865	13420	25867	4.1	5.0E-08	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2548	16047		5.91	6.0E-08	11416767	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2886	15541	27855	0.76	6.0E-08	6912735	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
4972	17483		2.04	6.0E-08	X60812.1	NT	Homo sapiens DNA for noncatalytic domain type A (7) (partial)
6368	17866	30214	93.54	6.0E-06	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
7014	19550	32336	1.13	5.0E-08	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
7084	19818	32413	0.49	6.0E-08	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
7166	19878	32702	3.99	5.0E-08	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7166	19878	32703	3.99	5.0E-08	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7448	19949	32784	0.94	5.0E-08	AB023177.1	NT	Homo sapiens mRNA for KIAA0950 protein, partial cds
8021	20453	33325	0.72	5.0E-08	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8707	21142	34045	2.05	5.0E-08	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8707	21142	34046	2.05	5.0E-08	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 6
4207	16732		8.83	3.0E-08	H68658.1	EST_HUMAN	y687h12.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5'
432	13006		4.68	2.0E-08	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (meprin-associated) (CSPG4), mRNA
768	13328	25769	1.45	2.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4812	17324	29703	2.63	2.0E-98	BE148074.1	EST_HUMAN	RC3-H10230-040600-110-g02 HT0230 Homo sapiens cDNA
6984	19531	32313	70.31	2.0E-98	BE222594.1	EST_HUMAN	hu48e07.x1 NCL CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173318 3' similar to WP:C38D4.5
7949	20386	33282	0.64	2.0E-98	BF369731.1	EST_HUMAN	CE00918 HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III;
7949	20386	33283	0.64	2.0E-98	BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA
9327	21759		5.26	2.0E-98	AV689461.1	EST_HUMAN	QV4-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA
11709	24009		2.47	2.0E-98	AW249440.1	EST_HUMAN	AV689461 GK Homo sapiens cDNA clone GKCFMD07 6'
690	13253	25870	2.9	1.0E-98	Y18890.1	NT	2818351.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2818351 5'
1763	14290	26772	3.97	1.0E-98	AW955054.1	EST_HUMAN	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1763	14290	26773	3.97	1.0E-98	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
1821	14343	26840	2.92	1.0E-98	4503756	NT	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
1821	14343	26841	2.92	1.0E-98	4503756	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
2168	16268	27206	3.86	1.0E-98	U51472.2	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
7381	18051	30389	1.12	1.0E-98	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7480	18684	32481	0.75	1.0E-98	6912455	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
8787	21221	34126	1.19	1.0E-98	7661803	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8787	21221	34127	1.19	1.0E-98	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
9146	21678	34484	25.68	1.0E-98	11419429	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
9254	21866	34597	2	1.0E-98	AF274863.1	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
10810	23246	36231	2.66	1.0E-98	11428722	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
11695	18004	30326	2.33	1.0E-98	4826863	NT	Homo sapiens A kinase (PRKA) anchor protein 2 (AKAP2), mRNA
11695	18004	30327	2.33	1.0E-98	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3286	15845	28263	0.6	6.0E-97	BF245240.1	EST_HUMAN	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8072	20501		3.67	6.0E-97	BE141848.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 6'
11161	23541	36580	5.14	6.0E-97	X16804.1	NT	IL6-HT0117-011068-004-D07 HT0117 Homo sapiens cDNA
8643	21078	33985	1.72	5.0E-97	AL043314.2	EST_HUMAN	Human mRNA for alpha-actinin
8732	21166	34071	12.21	5.0E-97	AA418028.1	EST_HUMAN	DKFZp434N0323_1 434 (synonym: hss3) Homo sapiens cDNA clone DKFZp434N0323 5'
9816	22219	35155	4.91	5.0E-97	BF154912.1	EST_HUMAN	z07e12.s1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
11300	23665	36711	2.36	5.0E-97	BE148597.1	EST_HUMAN	G1304125 PMS4 MRNA
11300	23665	36712	2.36	5.0E-97	BE148597.1	EST_HUMAN	RC0-BT0812-250900-032-a09 BT0812 Homo sapiens cDNA
963	13516	25980	1.45	4.0E-97	BE004438.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
							MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
							CM0-BN0106-170300-283-a08 BN0106 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6830	18410	31077	0.81	4.0E-97	4557326	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
6143	18711	31412	0.57	4.0E-97	U09002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (hNMR2A) mRNA, complete cds
6143	18711	31413	0.57	4.0E-97	U09002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (hNMR2A) mRNA, complete cds
7218	19828	32844	6.41	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7218	19828	32845	6.41	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7444	19947	32781	1.21	4.0E-97	7710126	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
7500	19704	32503	1.08	4.0E-97	11422155	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8188	24845	32503	0.47	4.0E-97	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
8497	20909	33804	0.45	4.0E-97	10947063	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA
8497	20909	33805	0.45	4.0E-97	10947063	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA
8897	21331	34242	1.54	4.0E-97	11421783	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
9082	21514	34423	2.78	4.0E-97	11423233	NT	Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA
9511	21974	34887	1.25	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9511	21974	34898	1.25	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11184	22838	35807	3.11	4.0E-97	AB042557.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
11369	23731	36760	1.95	4.0E-97	AF219226.1	NT	Homo sapiens neuroendocrine differentiation factor mRNA, complete cds
11900	24126		4.83	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
258	12855	25272	1.08	3.0E-97	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
897	13462	25900	13.11	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
897	13462	25901	13.11	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1470	16311	26469	1.68	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2338	15269	27360	3.55	3.0E-97	U36255.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3129	16882	28098	6.73	3.0E-97	K02212.1	NT	Human alpha-1-antitrypsin gene (S variant), complete cds
3221	16773	28192	0.94	3.0E-97	5174478	NT	Homo sapiens pericentriin (PCNT) mRNA
4832	17344	29727	26.25	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6766	19309	32074	2.77	1.0E-97	BE568486.1	EST_HUMAN	601339520F1 NIH_MGC 63 Homo sapiens cDNA clone IMAGE:3681821 5'
7908	19718	32521	0.61	1.0E-97	6453881	NT	Homo sapiens phosphorylase kinase, gamma 1 (muscle) (PHKG1) mRNA
8876	22779	35219	1.26	1.0E-97	R10887.1	EST_HUMAN	Y38C08.s1 Soares fetal liver spleen 1N1FS Homo sapiens cDNA clone IMAGE:128134 3'
10491	22941	35922	2.28	1.0E-97	11427767	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
10491	22941	35923	2.28	1.0E-97	11427767	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
11219	22871	35845	52.39	1.0E-97	11428272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11219	22871	35846	52.39	1.0E-07	11426272	NT	Homo sapiens ribosomal protein S16 (RPS16), mRNA
924	13478	25925	2.43	9.0E-08	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1309	13844	26284	3.31	9.0E-08	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
4716	17232		14.78	9.0E-08	8400716	NT	Homo sapiens nebulin (NEB), mRNA
5387	17884	30243	1.02	9.0E-08	11419594	NT	Homo sapiens FSH primary response (LRPR1, rat) homolog 1 (FSHPRH1), mRNA
6630	19179		0.78	9.0E-08	AJ250713.1	NT	Homo sapiens GLDN12 gene for claudin-12
7747	20191	33052	0.57	9.0E-08	7681871	NT	Homo sapiens leucyl-tRNA synthetase, mitochondrial (KIAA0028), mRNA
7865	20304	33169	0.61	9.0E-08	11419408	NT	Homo sapiens A kinase (PRKA) anchor protein (yotiao) 8 (AKAP8), mRNA
8678	21014	33914	6.2	9.0E-08	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8578	21014	33915	6.2	9.0E-08	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
9420	21852	34768	3.29	9.0E-08	X08889.1	NT	Human mRNA for amyloid A4(761) protein
8484	21925	34848	1.3	9.0E-08	11321580	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
9545	21960	34883	1.49	9.0E-08	AB037789.1	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9577	22000		1.08	9.0E-08	AF057726.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9597	22077	35003	1.15	9.0E-08	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9597	22077	35004	1.15	9.0E-08	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10784	23222	36205	2.15	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
10784	23222	36206	2.15	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
10849	23282	36272	1.99	9.0E-08	11418982	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), mRNA
11914	13478	25925	2.64	9.0E-08	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
25	12845		1.26	8.0E-08	AJ251158.1	NT	Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1405	13939	26395	1.48	8.0E-08	AB033768.1	NT	Homo sapiens HPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
1581	14112	26578	0.94	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1581	14112	26579	0.94	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1723	14251	26735	2.57	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1723	14251	26736	2.57	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3588	16128	28541	0.94	8.0E-08	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3588	16128	28542	0.94	8.0E-08	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3768	16335	28737	7.73	8.0E-08	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
6390	18947	31683	1.18	5.0E-08	BE858573.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908097 5'
2536	15034	27550	1.52	3.0E-08	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2708	16188		4.04	3.0E-98	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7357	19814	32827	1.79	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7357	19814	32828	1.79	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
9176	21808	34518	3.92	3.0E-98	H46698.1	EST_HUMAN	yo17g09.r1 Scores adult brain N2551B55Y Homo sapiens cDNA clone IMAGE:178240 5'
9959	22358	35309	1.35	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
9959	22358	35307	1.35	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
10368	22768	36726	0.89	3.0E-98	BE900454.1	EST_HUMAN	601673886F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
10731	23169	36152	3.11	3.0E-98	U59309.1	NT	Human fumarate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
12539	24529		3.66	3.0E-98	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
758	13318	25745	0.78	2.0E-98	BE261894.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2003	14519	27030	3.19	2.0E-98	BE294281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3628134 5'
2145	14858	27182	0.86	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2269	14777	27299	2.66	2.0E-98	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
2269	14777	27300	2.66	2.0E-98	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
4316	16939	29228	0.83	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4382	16884	29265	3.95	2.0E-98	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4883	17395	29764	1.04	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4883	17395	29765	1.04	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
5193	17697	30060	4.65	2.0E-98	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI1), mRNA
5193	17697	30061	4.65	2.0E-98	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI1), mRNA
5421	17916	30287	1.35	2.0E-98	4768976	NT	Homo sapiens protein tyrosine kinase 2 beta (PTK2B) mRNA
6632	18219	30620	6.19	2.0E-98	7708512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
7020	19558	32342	1.36	2.0E-98	4805788	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
8154	20577	33453	1.13	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8154	20577	33454	1.13	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
9078	21508	34417	3.86	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
9078	21508	34418	3.86	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
9721	22144	36071	2.16	2.0E-98	X12664.1	NT	H. sapiens arginase gene exon 3 (EC 3.5.3.1)
10312	22712		1.27	2.0E-98	7705868	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
10972	23401	36412	2.16	2.0E-98	U22028.1	NT	Human cytochrome P450 (CYP2A13) gene, complete cds
11368	23730	36789	1.83	2.0E-98	AF273046.1	NT	Homo sapiens CTGL tumor antigen se20-9 mRNA, complete cds
422	12986	25422	40.51	1.0E-98	AJ862007.1	EST_HUMAN	iw36b04.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2281743 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
472	13046	25467	2.86	1.0E-98	AW998611.1	EST_HUMAN	PMO-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA
1774	14289	26786	27.68	1.0E-98	N49818.1	EST_HUMAN	Y2305.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L29 - human ;
5570	18158	30522	4.44	1.0E-98	AA195854.1	EST_HUMAN	zp88c09.1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562 G806562 NEBULIN.;
5834	18414	31083	1.71	1.0E-98	BE390827.1	EST_HUMAN	601284986F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3606692 5'
5834	18414	31084	1.71	1.0E-98	BE390827.1	EST_HUMAN	601284986F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3606692 5'
5940	21772	34676	0.94	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
9340	21772	34677	0.94	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
6103	18872	31387	1.06	9.0E-99	AI905004.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
6103	18872	31388	1.06	9.0E-99	AI905004.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
6348	18804	31638	4.44	9.0E-99	AW988895.1	EST_HUMAN	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
10902	23334	36337	12.81	9.0E-99	AI479829.1	EST_HUMAN	Im69h07.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW_BID_HUMAN P65957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
10902	23334	36338	12.81	9.0E-99	AI479829.1	EST_HUMAN	Im69h07.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW_BID_HUMAN P65957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11167	23547	36587	2.17	9.0E-99	AA134604.1	EST_HUMAN	z190d02.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to TR:G662894 G662894 GPI-ANCHORED PROTEIN P137. ;
9155	21587	34495	1.41	8.0E-99	9835487	NT	Human endogenous retrovirus, complete genome
6120	18689	31387	10.26	7.0E-99	AF035808.1	NT	Homo sapiens oscilin (hLn) gene, exon 5
11356	23719	36779	2.3	7.0E-99	AF001886.1	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
489	13082	25482	0.77	6.0E-99	U10991.1	NT	Human G2 protein mRNA, partial cds
2046	14562	27074	1.36	6.0E-99	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
2046	14562	27075	1.36	6.0E-99	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
3888	18433	28841	1.94	6.0E-99	AW976384.1	EST_HUMAN	EST388473 MAGE resequences, MAGN Homo sapiens cDNA
4801	17316	29683	1.43	6.0E-99	4502660	NT	Homo sapiens GD34 antigen (CD34) mRNA
6954	19491	32271	1.19	6.0E-99	7708138	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
7047	19581	32375	0.83	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
7047	19581	32376	0.83	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8708	21141	34044	1.49	6.0E-99	X69101.1	NT	H.sapiens mRNA for estrogen receptor
9187	21619	34530	2.7	6.0E-99	AB038429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylaseN-sulfotransferase 4, complete cds
9262	21694	34605	6.6	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
9262	21694	34606	6.6	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
10505	22954	35835	3.95	6.0E-99	11526289	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11205	22857	35830	1.9	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
11205	22857	35831	1.9	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
943	13496	26938	1.36	5.0E-99	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
943	13496	26939	1.36	5.0E-99	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
4601	17117	29505	2.01	5.0E-99	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S342 to TORBV12S2 region
11929	24145		2.67	6.0E-99	BE890177.1	EST_HUMAN	601513167F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3914391 5'
8857	21301		4.98	3.0E-99	M95586.1	NT	Human E2AHLA fusion protein (E2AHLF) mRNA, complete cds
1272	13809		12.88	2.0E-99	AW274792.1	EST_HUMAN	xc09e08.x1 NCI_CGAP_JH9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3219	15771	28191	1.13	2.0E-99	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4579	17085	29483	3.22	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
8211	20631	33620	0.55	2.0E-99	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
9141	21573	34480	10.43	2.0E-99	W23507.1	EST_HUMAN	zb49d08.r1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:305635 5' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
10899	23321	36320	4.86	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
329	12922	26340	1.5	1.0E-99	AF114487.1	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
394	12979	25401	1.18	1.0E-99	11528150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1452	13984	26445	1.49	1.0E-99	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1578	14109	26573	0.98	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1578	14109	26574	0.99	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
3047	15601	28011	1.03	1.0E-99	J03171.1	NT	Human Interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4402	16924	28309	2.58	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4402	16924	28310	2.58	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5456	17951	30300	0.68	1.0E-99	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
5456	17951	30301	0.68	1.0E-99	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6021	18595	31282	0.68	1.0E-99	7662349	NT	Homo sapiens cell recognition molecule Casp2 (KJAA0868), mRNA
7194	19905	32734	1.31	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7194	19905	32735	1.31	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7579	24633	32874	0.78	1.0E-99	X98022.1	NT	H sapiens E8-AP gene exon 2
9474	21805		1.27	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC61309), mRNA
9707	22130	35056	1.53	1.0E-99	AW340174.1	EST_HUMAN	hd02h02.x1 Soares NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2808371 3' similar to TR-O02711
10915	23347	36355	4.3	1.0E-99	7427514	NT	Q02711 PRO-POL-DUTPASE POLYPROTEIN ; Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10916	23347	36356	4.3	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11192	23584	36925	3.77	1.0E-99	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11678	23987		4.1	1.0E-99	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1	12623	25010	1.72	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	12623	25010	2.3	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
71	12690	25098	1.84	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
71	12690	25098	1.84	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
89	12706	25121	1	1.0E-100	AW275237.1	EST_HUMAN	x78b11.x1 NCI_CGAP_Brm53 Homo sapiens cDNA clone IMAGE:2824605 3'
173	12777	25191	1.46	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
331	12824	25342	1.19	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
357	12947	25361	2.69	1.0E-100	U05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#836208) Homo sapiens cDNA clone HFBRCR32
454	13029		1.8	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
507	13081		6	1.0E-100	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
527	13099	25511	1.19	1.0E-100	BE180609.1	EST_HUMAN	RC3-HIT0625-040500-022-b09 HT0626 Homo sapiens cDNA
1045	13591	26030	2.89	1.0E-100	7681685	NT	Homo sapiens DKFZP686M0122 protein (DKFZP686M0122), mRNA
1045	13591	26031	2.86	1.0E-100	7681685	NT	Homo sapiens DKFZP686M0122 protein (DKFZP686M0122), mRNA
1569	14101		1.1	1.0E-100	AW207656.1	EST_HUMAN	UI-H-BH1-afk-c-07-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1574	14105	26568	1.54	1.0E-100	AI200857.1	EST_HUMAN	q62f09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA
2151	14664		6.9	1.0E-100	D83349.1	NT	P81061 CYSTATIN1
2337	14843	27359	9.84	1.0E-100	X62468.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2656	15149	27660	1.41	1.0E-100	11418976	NT	H. sapiens mRNA for IFN-gamma (pKC-0)
2978	15533		3.45	1.0E-100	D111078.1	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
4225	16760	28141	2.04	1.0E-100	AF067354.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4253	16778	29162	2.35	1.0E-100	4503792	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
5226	17728	30095	2.99	1.0E-100	5032104	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5226	17728	30096	2.89	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5541	18131	30498	1.64	1.0E-100	BF244218.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
6770	18361	30810	0.98	1.0E-100	AW076983.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5971	18547	31232	1.32	1.0E-100	AU118182.1	EST_HUMAN	901863184F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4080999 5'
6024	18588	31285	2.04	1.0E-100	AF135118.1	NT	901863184F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4080999 5'
							602401.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:X12433
							PROTEIN PHP31-2 (HUMAN);
							AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003049 5'
							Homo sapiens NF-E2-related factor 3 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6124	18893	31390	0.91	1.0E-100	X14690.1	NT	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
6477	19032	31769	0.85	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6477	19032	31770	0.85	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6776	19319		0.41	1.0E-100	5729867	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6846	19387	32162	7.07	1.0E-100	AU140214.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6905	19444	32222	0.58	1.0E-100	AU136800.1	EST_HUMAN	AU136800 PLACE1 Homo sapiens cDNA clone PLACE1005089 5'
7055	19589	32383	1.37	1.0E-100	R10887.1	EST_HUMAN	y38c08.s1 Soares fetal liver spleen TNF α Homo sapiens cDNA clone IMAGE:129134 3'
7151	19864	32884	1.22	1.0E-100	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7237	19849	32667	1.25	1.0E-100	AA498841.1	EST_HUMAN	ee33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897687 5' similar to TR:G487418
7237	19849	32668	1.25	1.0E-100	AA498841.1	EST_HUMAN	ee33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897687 5' similar to TR:G487418
7291	19706	32608	1.27	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
7291	19706	32607	1.27	1.0E-100	BF376478.1	EST_HUMAN	MR1-TN0048-060900-004-b05 TN0048 Homo sapiens cDNA
7299	19803	32615	5.64	1.0E-100	X04571.1	NT	MR1-TN0048-060900-004-b05 TN0048 Homo sapiens cDNA
8268	20685	33577	0.41	1.0E-100	U63139.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
8268	20685	33578	0.41	1.0E-100	U63139.1	NT	Homo sapiens Rad50 (Rad50) mRNA, complete cds
8511	20923	33819	0.47	1.0E-100	AJ250408.1	NT	Homo sapiens Rad50 (Rad50) mRNA, complete cds
9021	21454	34364	2.63	1.0E-100	BF103853.1	EST_HUMAN	Homo sapiens GLI3 gene for GLI3 protein
9048	21480		3.71	1.0E-100	AL163203.2	NT	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3631310 5'
9499	21830	34854	3.09	1.0E-100	AB040918.1	NT	Homo sapiens chromosome 21 segment HS21C003
9560	22123		1.87	1.0E-100	A1972388.1	EST_HUMAN	Homo sapiens mRNA for KIAA1485 protein, partial cds
9842	20933	33830	1.72	1.0E-100	AW988611.1	EST_HUMAN	W37G09.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2489920 3' similar to contains element
9884	22098		0.95	1.0E-100	AU127720.1	EST_HUMAN	MER22 repetitive element ;
9754	22167	35088	2.26	1.0E-100	AB048848.1	NT	PMO-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
9754	22167	35089	2.26	1.0E-100	AB048848.1	NT	AU127720 NT2RP2 Homo sapiens cDNA clone NT2RP2001918 5'
9927	22329	35276	1.66	1.0E-100	AW630487.1	EST_HUMAN	Homo sapiens mRNA for KIAA1828 protein, partial cds
9927	22329	35277	1.66	1.0E-100	AW630487.1	EST_HUMAN	Homo sapiens mRNA for KIAA1828 protein, partial cds
10355	22755	35722	1	1.0E-100	BF347519.1	EST_HUMAN	hh83c11.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969398 5'
10409	22809		1.6	1.0E-100	Y10391.1	NT	hh83c11.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969398 5'
10540	22987	35967	6.52	1.0E-100	BF327292.1	EST_HUMAN	602020554F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156165 5'
11056	23482	36508	10	1.0E-100	X94633.1	NT	Human endogenous retrovirus HERV-K, pol gene
11056	23482	36509	10	1.0E-100	X94633.1	NT	MR0-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
							H. sapiens CD97 gene exon 4
							H. sapiens CD97 gene exon 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11111	23564	36804	4.89	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11111	23564	36605	4.89	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11414	23775		2.27	1.0E-100	AF268285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11463	23821	36884	1.98	1.0E-100	AA115605.1	EST_HUMAN	zK89a03.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:489984 5'
11463	23821	36885	1.96	1.0E-100	AA115605.1	EST_HUMAN	zK89a03.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:489984 5'
11598	23931	37007	8.55	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11733	24825		1.42	1.0E-100	BF446549.1	EST_HUMAN	7q88h03.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to TR:Q21997 Q21997
11919	24139	30971	2.96	1.0E-100	11645732	NT	COSMID R151. [2] TR:Q8UA08 :
12177	24297	30940	1.25	1.0E-100	11418123	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12589	24568	30849	4.25	1.0E-100	11417974	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
80	12698	25111	0.79	1.0E-101	1110714	NT	Homo sapiens transcalabalin II; macrocytic anemia (TCN2), mRNA
80	12698	25112	0.79	1.0E-101	1110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
706	13268	25684	1.91	1.0E-101	AB007815.2	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
724	13285	25710	7.04	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
724	13285	25711	7.04	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
793	13351	25786	1.3	1.0E-101	7657454	NT	Homo sapiens pascadillo (zabratfish) homolog 1, containing BRCT domain (PES1), mRNA
876	13431	25879	1.21	1.0E-101	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylamidimidazole synthetase (GART) mRNA
948	13500	25943	1.19	1.0E-101	Z20658.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
1011	13562	26008	11.89	1.0E-101	BF681218.1	EST_HUMAN	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5'
1078	13624	26063	1.28	1.0E-101	A1221878.1	EST_HUMAN	qg89e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843338 3'
1600	14132	26600	1.23	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1600	14132	26601	1.23	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1738	14265	26751	1.22	1.0E-101	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1738	14265	26752	1.22	1.0E-101	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1896	14416	26815	1.04	1.0E-101	4502996	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1882	14498	27007	1.69	1.0E-101	BE843070.1	EST_HUMAN	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2245	15332	27273	0.94	1.0E-101	5729892	NT	RC3-ST0281-160600-016-h09 ST0281 Homo sapiens cDNA
2545	15044	27561	5.89	1.0E-101	X72983.1	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2700	15180	27703	6.32	1.0E-101	AJ237744.1	NT	H sapiens EWS gene, exon 6
2700	15180	27704	6.32	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2809	15464		13.66	1.0E-101	AJ252312.1	NT	Homo sapiens RIBLIR gene (partial), exon 12 Homo sapiens genomic downstream Rhesus box

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriplor
3159	15712	28133	3.13	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3200	15752		2.47	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3862086 5'
3358	15904	28324	1.98	1.0E-101	AW865556.1	EST_HUMAN	EST377629 MAGI resequences, MAGI Homo sapiens cDNA
3378	15190	27703	2.36	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3378	15190	27704	2.36	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3884	16419	28823	4.08	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5141	17845	30009	1.48	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5141	17845	30010	1.48	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5571	18159	30523	1.36	1.0E-101	AW865139.1	EST_HUMAN	EST377212 MAGI resequences, MAGI Homo sapiens cDNA
6306	18887	31593	5.11	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6306	18887	31594	5.11	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
7055	19599	32395	1.25	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7727	20171		1.34	1.0E-101	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7784	20226	33085	5.33	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7784	20226	33086	5.33	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7978	20412	33281	5.92	1.0E-101	AW008475.1	EST_HUMAN	ww55f12.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
8091	20518		1.96	1.0E-101	BE257384.1	EST_HUMAN	601108217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349901 5'
8270	20687	33580	7.33	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA
8673	21108	34010	3.65	1.0E-101	BF028174.1	EST_HUMAN	601764686F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3986837 5'
8868	21302	34211	1.09	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb.J03143
8868	21302	34212	1.09	1.0E-101	AW630070.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
9347	21779	34686	1.02	1.0E-101	AA038800.1	EST_HUMAN	hh74g10.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb.J03143
9571	21894	34923	1.02	1.0E-101	AB037772.1	NT	INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
9571	21894	34924	1.02	1.0E-101	AB037772.1	NT	Zk29908.11 Soares_pregnant_uterus_Nib-HPU Homo sapiens cDNA clone IMAGE:471988 5' similar to
9685	20855	33558	17.39	1.0E-101	X60069.1	NT	PIR:S54640 S54640 YD9335.03c protein - yeast;
9685	20855	33557	17.39	1.0E-101	X60069.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9674	22021	34951	21.3	1.0E-101	9845492	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9870	22273	35213	8.9	1.0E-101	BE619687.1	EST_HUMAN	Human mRNA for pancreatic gamma-glutamyltransferase
9870	22273	35214	8.9	1.0E-101	BE619687.1	EST_HUMAN	Human mRNA for pancreatic gamma-glutamyltransferase
10309	22709	35675	2.15	1.0E-101	11429127	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
							601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
							601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
							Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10332	22732	36698	1.86	1.0E-101	AI570293.1	EST_HUMAN	to77411.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10332	22732	36699	1.86	1.0E-101	AI570293.1	EST_HUMAN	to77411.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10660	23100	36082	4.82	1.0E-101	S88327.1	NT	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt, segment 8 of 8]
10892	23324	36323	1.73	1.0E-101	AB020626.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
11493	23851	36921	23.8	1.0E-101	AA321316.1	EST_HUMAN	EST23783 Bone marrow Homo sapiens cDNA 5' end similar to defensin 1
12203	24320		4.79	1.0E-101	AW639051.1	EST_HUMAN	QV1-DT0068-240200-085-401 DT0068 Homo sapiens cDNA
41	12681	25053	0.85	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
365	12945	25358	4.88	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
639	13203	25811	0.74	1.0E-102	BE252470.1	EST_HUMAN	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
797	13355	25791	1.83	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1144	13688	26128	2.78	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1301	13836	26284	2.39	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1301	13836	26285	2.39	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1450	13982	26442	128.87	1.0E-102	BE408447.1	EST_HUMAN	601299982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3029801 5'
2204	14714	27238	1.6	1.0E-102	AI124688.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ;
2204	14714	27237	1.6	1.0E-102	AI124688.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ;
2883	15538		0.81	1.0E-102	Y13932.1	NT	Homo sapiens PRKY exon 7
3025	15580	27891	1.43	1.0E-102	7681979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3094	15648	28058	3	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3094	15648	28059	3	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4249	16774	29160	1.77	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4439	16859	29346	2.62	1.0E-102	BE261310.1	EST_HUMAN	601107843F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3343882 5'
5144	17648	30013	5.58	1.0E-102	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
5144	17648	30014	5.58	1.0E-102	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
5274	17776	30141	1.39	1.0E-102	R68488.1	EST_HUMAN	y32c04.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140834 5'
5627	18214	30616	1.88	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
6027	18601		4.41	1.0E-102	AB034951.1	NT	Homo sapiens HSC84 mRNA for heat shock cognate protein 84, complete cds
6068	18640	31335	3.41	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
6068	18640	31336	3.41	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6075	18046	31341	0.63	1.0E-102	11433046	NT	Homo sapiens haet domain and RLD 2 (HERC2), mRNA ar8209.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2161785 3' similar to TR:Q13137 Q13137 NDP52 ;
6818	19188	31921	3.43	1.0E-102	AI459825.1	EST_HUMAN	
7513	19715	32518	0.49	1.0E-102	AW451643.1	EST_HUMAN	U1H-B13-ajl-d-10-0-J1.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736635 3'
7576	20026	32870	0.79	1.0E-102	BE728323.1	EST_HUMAN	601591505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
7607	20056	32808	1.05	1.0E-102	BE368108.1	EST_HUMAN	601277215F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618243 5'
7733	20177	33037	0.85	1.0E-102	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7825	20266	33127	9.23	1.0E-102	AJ238994.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
8155	20578	33455	2.84	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CUAAKD03 5'
8489	20882	33780	0.42	1.0E-102	11420841	NT	Homo sapiens GLL-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA
8507	20919	33815	0.54	1.0E-102	10947053	NT	Homo sapiens ankryrin 2, neuronal (ANK2), transcript variant 2, mRNA
8795	21228	34136	4.26	1.0E-102	BE763031.1	EST_HUMAN	QV3-NT0025-210600-236-108 NT0028 Homo sapiens cDNA
9566	21989	34915	1.82	1.0E-102	T70393.1	EST_HUMAN	yf13d07.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:67021 5'
9568	21989	34918	1.82	1.0E-102	T70393.1	EST_HUMAN	yf13d07.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:67021 5'
9828	22043	34975	3.51	1.0E-102	AU124829.1	EST_HUMAN	AU124829 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'
10354	22754	35720	2.76	1.0E-102	AI805037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
10354	22754	35721	2.76	1.0E-102	AI805037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
10393	22793	35784	2.19	1.0E-102	AA970786.1	EST_HUMAN	on57n04.st Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1660823 3' similar to SW:CAV2_HUMAN P51636 CAVEOLIN-2, [1];
10850	23283	36273	3.59	1.0E-102	BE897488.1	EST_HUMAN	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924166 5'
10855	23288	36279	4.62	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
10855	23288	36280	4.62	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
10870	23303	36297	1.89	1.0E-102	AA490201.1	EST_HUMAN	aa44h06.r1 Soares_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:323835 5'
11169	23539	36577	2.83	1.0E-102	BF369243.1	EST_HUMAN	RC6-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA
11432	23793	36855	2.87	1.0E-102	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A6) and (CDM) paralogous genes, complete cds
11491	23849	36918	3.8	1.0E-102	U57053.1	NT	Human unconventional myosin-ID (MYO1F) gene, partial cds
11602	23936		2.81	1.0E-102	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
12191	24311	30911	6.03	1.0E-102	AW300862.1	EST_HUMAN	x07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'
12243	24346	30823	1.35	1.0E-102	11419169	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA
12527	24524		3.43	1.0E-102	J05235.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
72	12691	25100	1.49	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
72	12691	25101	1.49	1.0E-103	BE908158.1	EST_HUMAN	80160405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
103	12720	25133	8.41	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
214	12817	25233	0.87	1.0E-103	5453763	NT	Homo sapiens nuclear protein (KKE/D repeat) (NOP56) mRNA
1008	13557	25989	0.9	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1276	13812	26266	12.32	1.0E-103	BE877541.1	EST_HUMAN	801486388F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3887878 5'
1613	14144	26614	1.74	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1920	14438	26940	0.89	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteoinductive protein 2) (BMP8) mRNA
1920	14439	26941	0.89	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteoinductive protein 2) (BMP8) mRNA
2199	14710	27232	1.15	1.0E-103	AU134891.1	EST_HUMAN	AU134891 PLACE1 Homo sapiens cDNA clone PLACE1000885 6'
2349	14854	27374	4.34	1.0E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2518	15018	27532	1.05	1.0E-103	BF528378.1	EST_HUMAN	602041882F1 NCI_CGAP_Brr67 Homo sapiens cDNA clone IMAGE:4179429 5'
2518	15018	27533	1.05	1.0E-103	BF528379.1	EST_HUMAN	602041882F1 NCI_CGAP_Brr67 Homo sapiens cDNA clone IMAGE:4179429 5'
2550	15049	27584	2.08	1.0E-103	N32770.1	EST_HUMAN	yw81d08.s1 Soares placenta_8kb8weeks_2NbhP8to9W Homo sapiens cDNA clone IMAGE:259599 3'
3029	15584	28323	2.96	1.0E-103	BE744722.1	EST_HUMAN	601673113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834316 5'
3357	15903	28323	4.7	1.0E-103	AW298246.1	EST_HUMAN	UI-H-BW0-ajh-h-11-UJ.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733165 3'
3417	15961	28372	1.13	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3756	16205		5.2	1.0E-103	AF023881.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3796	16333	28735	0.96	1.0E-103	AA485663.1	EST_HUMAN	ab10d12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element:
3840	16377	28778	1.22	1.0E-103	11430876	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
4017	16550	28947	3.68	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cat109+10-Bto Homo sapiens cDNA clone b4HB3MA-Cat109+10-Bto-7 3'
6232	18787	31508	1.05	1.0E-103	BF569527.1	EST_HUMAN	602186023F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4310573 5'
6240	18804	31516	2.06	1.0E-103	AF179995.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6591	19142	31889	0.55	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6591	19142	31889	0.55	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6803	19345	32116	0.84	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6803	19345	32117	0.84	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6848	19389	32164	0.8	1.0E-103	10947051	NT	Homo sapiens ankryrin 2, neuronal (ANK2), transcript variant 1, mRNA
6948	24819	32285	1	1.0E-103	AA781442.1	EST_HUMAN	aj28e03.s1 Soares testis_NHT Homo sapiens cDNA clone 1381452 3'
6993	19530	32312	0.98	1.0E-103	AF053480.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
7093	19828	32423	1.59	1.0E-103	AI590071.1	EST_HUMAN	tm68b06.x1 NCI_CGAP_Brr26 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7093	19826	32424	1.59	1.0E-103	AI590071.1	EST_HUMAN	tm58605.x1 NCL CGAP Bm26 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;
7244	18018	30432	1.81	1.0E-103		5032282 NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS164, DXS206, DXS230, DXS239, DXS268, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7244	18018	30433	1.81	1.0E-103		6032282 NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS164, DXS206, DXS230, DXS239, DXS268, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7394	18054	30392	1.05	1.0E-103		11431100 NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7482	19964	32798	1.28	1.0E-103	AJ289880.1	NT	Homo sapiens KIA0851 gene (partial), X13 gene and LZTFL1 gene
7675	20121	32976	1.4	1.0E-103	AW965778.1	EST_HUMAN	EST1377849 IMAGE resequences, MAGI Homo sapiens cDNA
7800	20242	33099	3.99	1.0E-103	BE749158.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3888545 5'
8331	20746	33641	4.64	1.0E-103	AI590071.1	EST_HUMAN	tm58605.x1 NCL CGAP Bm26 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;
8331	20746	33642	4.64	1.0E-103	AI590071.1	EST_HUMAN	tm58605.x1 NCL CGAP Bm26 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;
9083	21515	34424	1.09	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
9083	21515	34425	1.09	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
9138	21570	34477	1.2	1.0E-103	BF109244.1	EST_HUMAN	7160603.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3625864 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;
9415	21847	34761	3.58	1.0E-103	6005921 NT	NT	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA
9415	21847	34762	3.58	1.0E-103	6005921 NT	NT	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA
9438	21870	34788	0.8	1.0E-103	AA581086.1	EST_HUMAN	nd13602.s1 NCL CGAP_OV1 Homo sapiens cDNA clone IMAGE:600162 3' similar to gb1L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
10082	22483	35440	1.95	1.0E-103	Z37876.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
10116	22517	35482	2.38	1.0E-103	AW663678.1	EST_HUMAN	EST1375749 IMAGE resequences, MAGH Homo sapiens cDNA
10204	22605	35570	11.32	1.0E-103	AIB78956.1	EST_HUMAN	au51904.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518328 5' similar to TR:O15046 O15046 KIA00338 ;
10438	22890	35868	21.36	1.0E-103	BE549708.1	EST_HUMAN	7b41f03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb:M68043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
10617	22965	35944	5.63	1.0E-103	A1792759.1	EST_HUMAN	cd02006.y5 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1622283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
10814	23057	36045	4.38	1.0E-103	11424081 NT	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
10814	23057	36046	4.38	1.0E-103	11424081 NT	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10622	23064	36050	2.45	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
10622	23064	36051	2.45	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
10683	23103	36084	2.47	1.0E-103	X87831.2	NT	Homo sapiens mRNA for partial OCT/plestin-A2 protein
10683	23103	36085	2.47	1.0E-103	X87831.2	NT	Homo sapiens mRNA for partial OCT/plestin-A2 protein
10777	23215		1.66	1.0E-103	BE971418.1	EST_HUMAN	7e50f08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3286927 3' similar to gb.J05272 INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1 (HUMAN);
11005	23433	36451	6.32	1.0E-103	BE88278.1	EST_HUMAN	601506347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908147 5'
11131	23583	36624	2.89	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
11195	22847	35820	17.08	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11405	23765		2.28	1.0E-103	AB024759.1	NT	Homo sapiens TSA305 gene, exon 18
11597	23832		2.63	1.0E-103	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11629	23956		1.83	1.0E-103	11528291	NT	Homo sapiens hypothetical protein FLJ20464 (FLJ20464), mRNA
11839	24091	30991	3.49	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-9, complete cds
245	12846	25260	2.73	1.0E-104	AL037549.3	EST_HUMAN	DKFZ5684H1072_r1 564 (synonym: hfb2) Homo sapiens cDNA clone DKFZ5684H1072 5'
245	12846	25261	2.73	1.0E-104	AL037549.3	EST_HUMAN	DKFZ5684H1072_r1 564 (synonym: hfb2) Homo sapiens cDNA clone DKFZ5684H1072 5'
1853	14376	26867	1.24	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2099	14813	27132	8.9	1.0E-104	AA132875.1	EST_HUMAN	z022c06.s1 Stralagene cdon (#837204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb.Z14116_mai CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2109	14822	27144	3.09	1.0E-104	BE744628.1	EST_HUMAN	601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3826438 5'
2264	14772	27262	1.52	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2264	14772	27263	1.52	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2336	14842	27368	8.31	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2410	14914	27431	4.28	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2410	14914	27432	4.26	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2824	15380	27794	10.39	1.0E-104	M34871.1	NT	Human lymphocytic antigen CD59/MEIM43 mRNA, complete cds
2870	15426		2.17	1.0E-104	Y11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3225	15777	28195	1.07	1.0E-104	AU133928.1	EST_HUMAN	AU133928 OVARC1 Homo sapiens cDNA clone OVARC1000836 5'
3369	15915		2.02	1.0E-104	AA310438.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3595	16136	28549	0.62	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3595	16136	28550	0.62	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3568	16491	28900	1	1.0E-104	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4399	16921	29306	8.31	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4650	17168	29545	243.68	1.0E-104	AF231020.1	NT	Homo sapiens chromosome 21 unknown mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4850	17168	29548	243.68	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
6238	18802	31512	1.34	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6238	18802	31513	1.34	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6288	18850	31571	1.07	1.0E-104	AB017332.1	NT	Homo sapiens alk3 mRNA for Aurora/Plp1-related kinase 3, complete cds
6812	19353	32128	8.67	1.0E-104	A1768797.1	EST_HUMAN	KIAA0132 PROTEIN ; contains element LTR7 repetitive element ;
6812	19353	32129	8.67	1.0E-104	A1768797.1	EST_HUMAN	W03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145
7012	19548	32334	0.69	1.0E-104	7706512	NT	KIAA0132 PROTEIN ; contains element LTR7 repetitive element ;
7191	19802	32729	2.91	1.0E-104	BE314182.1	EST_HUMAN	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
7191	19802	32730	2.91	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7873	20119	32874	2.21	1.0E-104	11425572	NT	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
9087	21499	34403	0.93	1.0E-104	BF509244.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9452	21893	34803	2.65	1.0E-104	BF448230.1	EST_HUMAN	U1-H-814-aw-b-09-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086176 3'
9538	21953		1.3	1.0E-104	774219.1	EST_HUMAN	ncd16g11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3369948 3'
9561	21984	34909	5.41	1.0E-104	AF091395.1	NT	y68302.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22440 5'
9561	21984	34910	5.41	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9847	20838	33838	4.78	1.0E-104	BF352841.1	EST_HUMAN	Homo sapiens Trio isoform mRNA, complete cds
9847	20838	33837	4.78	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9867	22270	35210	0.97	1.0E-104	AW103848.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9867	22270	35211	0.97	1.0E-104	AW103848.1	EST_HUMAN	x676d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
10110	22511	35475	2.48	1.0E-104	BE701713.1	EST_HUMAN	Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
10110	22511	35476	2.48	1.0E-104	BE701713.1	EST_HUMAN	x676d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
10304	22704	35689	1.49	1.0E-104	AV728070.1	EST_HUMAN	601681503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10333	22733	35700	5.02	1.0E-104	AU130785.1	EST_HUMAN	601681503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10405	22805	35782	4.95	1.0E-104	U66535.1	NT	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
10411	22811		0.87	1.0E-104	11427757	NT	AU130785 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
11067	23493	36519	4.38	1.0E-104	BE720191.1	EST_HUMAN	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
11067	23493	36520	4.38	1.0E-104	BE720191.1	EST_HUMAN	Homo sapiens KIAA0648 gene product (KIAA0648), mRNA
11082	23518	36552	10.44	1.0E-104	BF684288.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
12481	24494		2.33	1.0E-104	BE3393892.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
							G02141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
							G01312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3668678 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
292	15254	25309	4.6	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
442	12620	25007	11.4	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
611	13179	25582	6.42	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
611	13179	25583	6.42	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1797	14322	26818	1.56	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1879	14401	26895	1.38	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2095	14609	27128	2.83	1.0E-105	AA318369.1	EST_HUMAN	EST20609 Spleen 1 Homo sapiens cDNA 5' end similar to autoimmunity antigen Ku, p70/p80 subunit
2674	15167		4.56	1.0E-105	AA584808.1	EST_HUMAN	no10d05.st NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
2881	15416	27837	1.19	1.0E-105	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2881	15416	27838	1.19	1.0E-105	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2964	15519		3.22	1.0E-105	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3324	15871	28292	0.85	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3324	15871	28293	0.85	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3843	16183		0.84	1.0E-105	11425532	NT	Homo sapiens dermatopontin (DPT), mRNA
4114	16844	29029	7.26	1.0E-105	AW861888.1	EST_HUMAN	EST373761 IMAGE sequences, MAGG Homo sapiens cDNA
4796	17310	29688	0.83	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4796	17310	29689	0.83	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
5020	17530		8.59	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5254	17765	30124	1.38	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0798 protein, partial cds
5327	17826	30185	2.69	1.0E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0868 protein, complete cds
5343	17842	30200	0.89	1.0E-105	AW868016.1	EST_HUMAN	EST378088 IMAGE sequences, MAGI Homo sapiens cDNA
5418	17765	30124	1.8	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0798 protein, partial cds
5583	18171	30535	0.94	1.0E-105	AF016704.1	NT	Homo sapiens E8-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5653	18239		1.05	1.0E-105	11420134	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7312	19724	32525	1.53	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7312	19724	32526	1.53	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7399	18068	30358	3.14	1.0E-105	11419193	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7399	18068	30359	3.14	1.0E-105	11419193	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7451	19954	32788	0.73	1.0E-105	AW861634.1	EST_HUMAN	EST363689 IMAGE sequences, MAGB Homo sapiens cDNA
7741	20185	33047	0.62	1.0E-105	BE902816.1	EST_HUMAN	60167720F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3660019 5'
8614	20826	33822	0.41	1.0E-105	L07627.1	NT	Homo sapiens protein-tyrosine phosphatase mRNA, complete cds
8532	20967	33869	1.1	1.0E-105	X12556.1	NT	Human mRNA for dbi proto-oncogene
8651	21086	33994	7.11	1.0E-105	TD5087.1	EST_HUMAN	EST02875 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HIFBCR32

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8931	21365	34277	1.37	1.0E-105	AW007194.1	EST_HUMAN	ws50c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2500628 3' similar to
9378	21810	34723	3.07	1.0E-105	AW016879.1	EST_HUMAN	SW:ACSA_PENCH_P38333 ACETYL-COENZYME A SYNTHETASE:
9478	21809	34830	0.9	1.0E-105	AW882372.1	EST_HUMAN	UI-H-B10p-ab1-b-12-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9479	21809	34831	0.9	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-009 OT0062 Homo sapiens cDNA
10708	23147	36131	7.2	1.0E-105	AF254822.1	NT	QV2-OT0062-140300-083-009 OT0062 Homo sapiens cDNA
11336	23700	36764	3.17	1.0E-105	AW027554.1	EST_HUMAN	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11409	23770	36829	3.5	1.0E-105	BF430921.1	EST_HUMAN	wf7407.x1 Soares_thymus_NHFT11 Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892
11514	23872	36982	1.93	1.0E-105	AF218896.1	NT	P87892 PROTEASE:
11517	23875	36953	3.05	1.0E-105	AB004924.1	NT	7d18c10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574291 3' similar to TR:P97680 P97680
11517	23875	36956	3.05	1.0E-105	AB004924.1	NT	RIN1.1
155	12760		1.54	1.0E-106	AW503208.1	EST_HUMAN	Homo sapiens attractin precursor (ATRIN) gene, exon 8
211	12814	25231	1.52	1.0E-106	AI565095.1	EST_HUMAN	Homo sapiens gene for Smad 3, exon 2 and 3
560	13132	25543	2.3	1.0E-106	AW866596.1	EST_HUMAN	Homo sapiens gene for Smad 3, exon 2 and 3
624	13190	25595	0.84	1.0E-106	J00146.1	NT	UI-HF-BNO-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
625	13190	25595	1.19	1.0E-106	J00146.1	NT	IQ78c01.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2216008 3'
1549	14081	26542	2.66	1.0E-106	AF145712.1	NT	EST377629 MAGI resequences, MAGI Homo sapiens cDNA
1698	14226	26708	4.17	1.0E-106	U48724.1	NT	Human dihydrofolate reductase pseudogene (psh-hd1)
1779	14304	26782	3.81	1.0E-106	AA527446.1	EST_HUMAN	Human dihydrofolate reductase pseudogene (psh-hd1)
1779	14304	26783	3.81	1.0E-106	AA527446.1	EST_HUMAN	Homo sapiens soluble neuropilin-1 mRNA, complete cds
2042	14568	27069	0.99	1.0E-106	BE144286.1	EST_HUMAN	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
2211	14721	27243	5	1.0E-106	4504184	NT	ng41c05.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element
2412	14916	27434	3.42	1.0E-106	AF003528.1	NT	LTR3 repetitive element:
2527	15028	27542	4.64	1.0E-106	U64675.2	NT	ng41c05.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element
2528	15028	27644	5.49	1.0E-106	BE260201.1	EST_HUMAN	LTR3 repetitive element:
2716	15208	27723	7.46	1.0E-106	AI276528.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2783	13994	26468	2.12	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2783	13994	26469	2.12	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2829	15385	27797	1.33	1.0E-106	BE384296.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2895	15449	27873	5.98	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
2895	15449	27874	5.98	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
3137	15690	28107	2.54	1.0E-106	8922865	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3137	15690	28108	2.54	1.0E-106	8922865	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3351	15897	28318	0.6	1.0E-106	AB009681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
4051	16583	28972	9.36	1.0E-106	AW974650.1	EST_HUMAN	EST1386875 MAGE resequences, MAGN Homo sapiens cDNA
4051	16583	28973	9.36	1.0E-106	AW974650.1	EST_HUMAN	EST1386875 MAGE resequences, MAGN Homo sapiens cDNA
4069	16600	28980	1.07	1.0E-106	5728728	NT	Homo sapiens APIB-like 1 (APIB1), mRNA
4641	17157	29536	1.25	1.0E-106	BE144288.1	EST_HUMAN	MFO-HT0165-140200-008-010 HT0165 Homo sapiens cDNA
5625	18212	30813	3.15	1.0E-106	AA781155.1	EST_HUMAN	q24b09.s1 Soares_testis_NHTT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN PHPS1-2 (HUMAN);
6141	18709	31409	1.02	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6141	18709	31410	1.02	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6197	18763	31466	0.84	1.0E-106	AA434169.1	EST_HUMAN	zw28d12.s1 Soares ovary tumor NIGROT Homo sapiens cDNA clone IMAGE:770615 3'
6298	18858	31579	0.59	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6298	18858	31580	0.59	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6410	18967	31703	7.52	1.0E-106	BF676574.1	EST_HUMAN	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295067 5'
6524	19077	31818	0.83	1.0E-106	BE897112.1	EST_HUMAN	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6734	19077	31818	0.76	1.0E-106	BE897112.1	EST_HUMAN	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6758	19301	32068	15.52	1.0E-106	11545913	NT	Homo sapiens xylotransferase II (XT2), mRNA
6758	19301	32067	15.52	1.0E-106	11545913	NT	Homo sapiens xylotransferase II (XT2), mRNA
7844	20284	33146	6.12	1.0E-106	AA683779.1	EST_HUMAN	ae72e07.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:069732 3' similar to gb:X66873
7906	20345	33211	5.18	1.0E-106	11428617	NT	KINESIN HEAVY CHAIN (HUMAN);
8008	20441	33309	1.19	1.0E-106	BE292722.1	EST_HUMAN	Homo sapiens XPMC2 protein (LOC57109), mRNA
8138	20561	33437	10.25	1.0E-106	11425503	NT	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2986345 5'
8138	20561	33438	10.25	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
8386	20810	33709	0.55	1.0E-106	AW163047.1	EST_HUMAN	eu91105.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783649 5' similar to TR:O76834
8422	20836	33732	0.51	1.0E-106	AU116850.1	EST_HUMAN	O76834 CULLIN-4A;
8622	21057	33864	3.72	1.0E-106	BE741408.1	EST_HUMAN	AU116850 HEMBA1 Homo sapiens cDNA clone HEMBA1000129 5'
8622	21057	33865	3.72	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3848463 5'
8758	21192	34094	5.16	1.0E-106	AI523086.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3848463 5'
							ar68a07.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233
							CALGRANULIN B (HUMAN);

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9140	21572	34778	2.99	1.0E-106	A1654123.1	EST_HUMAN	ly2a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICAB_HUMAN
9437	21869	34784	2.73	1.0E-106	AA825307.1	EST_HUMAN	Q05084.89 KD ISLET CELL AUTOANTIGEN ;
9437	21869	34785	2.73	1.0E-106	AA825307.1	EST_HUMAN	cc87e08.st NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1354790 3'
							cc87e08.st NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1354790 3'
9540	21955	34878	1.11	1.0E-106	A1750447.1	EST_HUMAN	cn03a04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn03a04 random
9639	22054	34985	1.72	1.0E-106	A179569.1	EST_HUMAN	hm4102.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160689 3' similar to contains MSR1.13
9639	22054	34986	1.72	1.0E-106	A179569.1	EST_HUMAN	TAR1 PTR5 repetitive element ;
10034	22436	35383	1.12	1.0E-106	BE39234.1	EST_HUMAN	hm4102.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160689 3' similar to contains MSR1.13
10102	22503	35466	1.43	1.0E-106	BF027310.1	EST_HUMAN	TAR1 PTR5 repetitive element ;
10102	22503	35467	1.43	1.0E-106	BF027310.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10206	22607	35573	6.61	1.0E-106	AA604417.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10206	22607	35574	6.61	1.0E-106	AA604417.1	EST_HUMAN	np57b10.st NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
10418	22818	35780	3.3	1.0E-106	AL163202.2	NT	np57b10.st NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
10677	23117	36093	4.24	1.0E-106	BF032755.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
10677	23117	36094	4.24	1.0E-106	BF032755.1	EST_HUMAN	601433461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
10845	23278	36268	1.91	1.0E-106	J05200.1	NT	601433461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
10845	23278	36269	1.91	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11163	23543	36582	3.97	1.0E-106	BE257385.1	EST_HUMAN	Human ryanodine receptor mRNA, complete cds
11675	24732		4.84	1.0E-106	AW410406.1	EST_HUMAN	601109219F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349897 5'
11911	24135	30968	2.68	1.0E-106	BE894488.1	EST_HUMAN	fr05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861644 5'
11911	24135	30969	2.68	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12146	24277		6.62	1.0E-106	BE695905.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
248	12847		3.2	1.0E-107	AJ271735.1	NT	RC1-CT0249-080800-024-d05 CT0249 Homo sapiens cDNA
278	12876		1.57	1.0E-107	X60459.1	NT	Homo sapiens Xa pseudautosomal region; segment 1/2
649	13213	25623	2.08	1.0E-107	AF165103.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
836	13303	25831	1.41	1.0E-107	X60459.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
909	13463	25911	1.94	1.0E-107	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
							Human IFNAR gene for Interferon alpha/beta receptor
993	13545	25988	18.44	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1311	13846	26287	1.03	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1588	14120	26587	3.04	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1743	14270	26755	6.15	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3
1814	14337	26831	1.01	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1814	14337	26832	1.01	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2114	14627	27150	0.89	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD28) gene, exon 20
2255	14763	27284	1.5	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
2255	14763	27285	1.5	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
2440	14942	27460	3.03	1.0E-107	BE732480.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2440	14942	27461	3.03	1.0E-107	BE732480.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2965	15520	27840	5.26	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
2965	15520	27841	5.26	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
3082	16816	28025	4.74	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3636	16373	28773	5.04	1.0E-107	AF020871.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
5892	18471	31151	0.64	1.0E-107	AW669038.1	EST_HUMAN	EST381116 IMAGE resequences, MAGK Homo sapiens cDNA
6163	18721	31425	2	1.0E-107	BE867469.1	EST_HUMAN	801442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848494 5'
7193	19904	32733	0.43	1.0E-107	6005708	NT	Homo sapiens A Kinase (PRKA) anchor protein 10 (AKAP10), mRNA
7331	19743	32548	0.62	1.0E-107	11431469	NT	Homo sapiens general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD) (GTF3C1), mRNA
7331	19743	32547	0.62	1.0E-107	11431468	NT	Homo sapiens general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD) (GTF3C1), mRNA
7836	20276	33138	1.47	1.0E-107	AW503913.1	EST_HUMAN	U1HF-BN0-af-c-08-q-U1.1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078310 5'
7836	20276	33139	1.47	1.0E-107	AW503913.1	EST_HUMAN	U1HF-BN0-af-c-08-q-U1.1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078310 5'
8037	20459	33343	1.44	1.0E-107	AI765078.1	EST_HUMAN	wh56h04.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'
8281	20698	33589	0.52	1.0E-107	AJ404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9) gene
8281	20698	33590	0.52	1.0E-107	AJ404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9) gene
8365	20790	33680	0.64	1.0E-107	AW410961.1	EST_HUMAN	ff09d11.x2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2984524 5'
9610	22090	35019	1.08	1.0E-107	AU122489.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002433 5'
10446	22897	35874	2.61	1.0E-107	BE168728.1	EST_HUMAN	QV1-HT0516-140300-107-c10 HT0516 Homo sapiens cDNA
10726	23164	36148	2.08	1.0E-107	L49141.1	NT	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
10740	23178	36162	3.79	1.0E-107	BF656511.1	EST_HUMAN	602123933F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4281039 5'
10827	23263	36248	1.66	1.0E-107	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
10827	23263	36249	1.66	1.0E-107	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11087	23512	36545	6.35	1.0E-107	BE540580.1	EST_HUMAN	601066681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11145	22835	35805	5.73	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11145	22835	35806	5.73	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11748	24882		7.08	1.0E-107	AA001415.1	EST_HUMAN	z645601.s1 Scores relina N2b44-IR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b7 THR repetitive element;
12604	24577	30836	1.25	1.0E-107	BE798189.1	EST_HUMAN	601682652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937188 5'
979	13532	25975	1.47	1.0E-108	BE296042.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
1298	13833	26281	5.09	1.0E-108	Y18000.1	NT	Homo sapiens NF2 gene
2002	14518	27029	1.2	1.0E-108	BF026728.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3984939 5'
2225	14735	27265	7.35	1.0E-108	AI686040.1	EST_HUMAN	U81610.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2225	14735	27266	7.35	1.0E-108	AI686040.1	EST_HUMAN	U81610.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2328	14835	27350	11.35	1.0E-108	BE206694.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863899 3' similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
3322	15869	28288	0.76	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3322	15869	28289	0.76	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4174	16701	29090	1.26	1.0E-108	AW684438.1	EST_HUMAN	h12a11.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE P55194 SH3-BINDING PROTEIN 3BP-1.;
4562	17079	29484	2.47	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4562	17079	29485	2.47	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4861	17373	29751	2.89	1.0E-108	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4893	17503	29879	0.9	1.0E-108	AW504769.1	EST_HUMAN	U1-HF-BN0-ahr-e-04-UJ1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080168 5'
5035	17645	28916	2.73	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5285	17786	30152	9.71	1.0E-108	8055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIIT), mRNA
5309	17809	30174	0.62	1.0E-108	5031624	NT	Homo sapiens GCAAT-box-binding transcription factor (CBF2) mRNA
5739	18321	30756	1.27	1.0E-108	AW384094.1	EST_HUMAN	RCO-HT0372-241199-031-403 HT0372 Homo sapiens cDNA
5789	18370	30833	2.81	1.0E-108	BE869018.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5789	18370	30834	2.81	1.0E-108	BE869018.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
6224	18780		0.77	1.0E-108	AF012623.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6305	18868	31562	0.71	1.0E-108	BF334851.1	EST_HUMAN	PMA-CT0403-240700-001-e10 CT0403 Homo sapiens cDNA
6452	19008	31741	7.24	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6452	19008	31742	7.24	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6585	19136	31883	1.37	1.0E-108	AJ133260.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6691	18666	31592	1.1	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6977	19514	32294	0.83	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6977	19514	32295	0.83	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7599	20048	32898	5.61	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA
7924	20381	33228	3.51	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS6) mRNA
7977	20413	33282	1.33	1.0E-108	BE252607.1	EST_HUMAN	601113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354084 5'
8011	20443	33312	1.6	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181037 5'
8011	20443	33313	1.6	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181037 5'
8400	20814	333712	0.46	1.0E-108	BE535227.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
8680	21115		1.98	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8713	21148	34051	1.78	1.0E-108	AW408694.1	EST_HUMAN	U1-HF-BM0-ads-e-12-O-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8713	21148	34052	1.78	1.0E-108	AW408694.1	EST_HUMAN	U1-HF-BM0-ads-e-12-O-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
10460	20814	33712	2.28	1.0E-108	BE535227.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
10609	18013	30445	4.89	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Gdgi-associated microtubule-binding protein (GMAP-210)
11041	23468	36491	3.3	1.0E-108	AV966185.1	EST_HUMAN	EST378258 IMAGE resequencing, MAGI Homo sapiens cDNA
11088	23513	36546	2.36	1.0E-108	AV708790.1	EST_HUMAN	AV708760 ADC Homo sapiens cDNA clone ADCAEE03 5'
11088	23513	36547	2.36	1.0E-108	AV708790.1	EST_HUMAN	AV708760 ADC Homo sapiens cDNA clone ADCAEE03 5'
11128	23580		2.05	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11157	14735	27255	5.32	1.0E-108	A1686040.1	EST_HUMAN	181610.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
11157	14735	27256	5.32	1.0E-108	A1686040.1	EST_HUMAN	181610.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
11513	23871	36950	1.68	1.0E-108	7019572	NT	Homo sapiens zinedin (ZIN), mRNA
11513	23871	36951	1.68	1.0E-108	7019572	NT	Homo sapiens zinedin (ZIN), mRNA
11925	24142	30972	4.01	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
12351	24411		8.4	1.0E-108	BF346356.1	EST_HUMAN	602018571F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154297 5'
44	12664	25056	1.16	1.0E-109	AW803116.1	EST_HUMAN	IL2-UJ0077-260400-078-D08 UM0077 Homo sapiens cDNA
67	12666	25095	2.26	1.0E-109	D89974.1	NT	Human mRNA for KIAA0220 gene, partial cds
228	12828	25242	1.06	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
236	12837	25248	2.22	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
484	13058	25474	2.58	1.0E-109	4507712	NT	Homo sapiens tetrapeptide repeat domain 2 (TTC2) mRNA
615	13183	25587	13.82	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
815	13183	25588	13.82	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0909 protein, partial cds
1233	13772	26219	9.95	1.0E-109	M28599.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1234	13772	26219	5.28	1.0E-109	M28599.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1565	14097	26569	0.88	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2856636 5'
1565	14097	26569	0.88	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2856636 5'
1844	14386	26860	7.24	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2150	14683	27187	6.27	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2168	14688	27191	1.54	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2553	15092	27568	4.61	1.0E-109	A022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ;
2553	15092	27568	4.61	1.0E-109	A022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ;
2554	15093	27570	1.76	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCY1A) mRNA
3019	15574	27985	2.23	1.0E-109	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3366	15912	28333	1.51	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-710 NN0009 Homo sapiens cDNA
3366	15912	28334	1.51	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-710 NN0009 Homo sapiens cDNA
3498	16041	28462	12.37	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3547	16089	28506	9.29	1.0E-109	M37928.1	NT	Homo sapiens adenosine triphosphatase deaminase 1 (AMPD1) gene, exons 8-10
3547	16089	28507	3.29	1.0E-109	M37928.1	NT	Homo sapiens adenosine triphosphatase deaminase 1 (AMPD1) gene, exons 8-10
3849	16386		1.45	1.0E-109	BE145144.1	EST_HUMAN	MRO-HT0208-110400-108-a04 HT0208 Homo sapiens cDNA
4166	16693	29080	3.78	1.0E-109	AI655417.1	EST_HUMAN	1698e06.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8
4428	16949	29339	2.33	1.0E-109	4504206	NT	CE16100 ;
4840	17166	29535	1.21	1.0E-109	7682083	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCY1A) mRNA
4998	17509	29883	1.14	1.0E-109	RI15400.1	EST_HUMAN	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5168	17870	30033	0.6	1.0E-109	BE283673.1	EST_HUMAN	y448a06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53057 5'
5168	17870	30034	0.6	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2856636 5'
5439	17934	30286	5.46	1.0E-109	11429810	NT	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2856636 5'
5496	18087	30382	0.71	1.0E-109	AU137282.1	EST_HUMAN	Homo sapiens inositol polyphosphate-4-phosphatase, type 1, 107KD (INPP4A), mRNA
5510	18101	30344	1.24	1.0E-109	BF673718.1	EST_HUMAN	AU137282 PLACE1 Homo sapiens cDNA clone PLACE1008159 5'
5566	18164	30516	3.13	1.0E-109	5174622	NT	602138446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5'
5874	18453		1.4	1.0E-109	BE179356.1	EST_HUMAN	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
6226	24603	31497	1.03	1.0E-109	BF376688.1	EST_HUMAN	RC1-HT0815-200400-022-404 HT0815 Homo sapiens cDNA
							CM1-UT0038-060900-389-h07 UT0038 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6289	18453		1.6	1.0E-109	BE176956.1	EST_HUMAN	RC1-HT0615-200400-022-004 HT0615 Homo sapiens cDNA
6681	19229	31978	0.59	1.0E-109	M23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
6681	19229	31979	0.59	1.0E-109	M23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
6943	19481	32260	0.71	1.0E-109	A1221385.1	EST_HUMAN	qg88h08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1842111 3'
7150	19663	32662	0.53	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7150	19663	32663	0.53	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7368	18038	30422	0.43	1.0E-109	BE074888.1	EST_HUMAN	RC5-BT0580-170300-021-F08 BT0580 Homo sapiens cDNA
7689	20134	32980	0.72	1.0E-109	AB046911.1	NT	Homo sapiens mRNA for KIAA1691 protein, partial cds
7951	20388	33255	0.42	1.0E-109	AE000297.1	NT	Escherichia coli K-12 MG1655 section 187 of 400 of the complete genome
8081	20509	33388	3.6	1.0E-109	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8083	20511	33390	5.21	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8083	20511	33391	5.21	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8334	20749	33846	0.63	1.0E-109	BE263297.1	EST_HUMAN	601145017F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160229 5'
8757	21191	34093	1.41	1.0E-109	AL049784.1	NT	Novel human gene mapping to chromosome 13
8840	21274	34164	1.31	1.0E-109	AW749130.1	EST_HUMAN	PMO-BT0340-091289-002-e05 BT0340 Homo sapiens cDNA
9109	21541		2	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
9161	21593	34500	7.12	1.0E-109	BE787640.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9161	21593	34501	7.12	1.0E-109	BE787640.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9503	21934	34858	1.55	1.0E-109	H84860.1	EST_HUMAN	ys80g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP:A53491
9583	22006	34933	1.44	1.0E-109	BE397068.1	EST_HUMAN	A53491 BUMETANIDE-SENSITIVE NA-K-Cl COTRANSPORTER - SPINNY;
9583	22006	34934	1.44	1.0E-109	BE397068.1	EST_HUMAN	601289780F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9682	22094	35023	1.41	1.0E-109	F06804.1	EST_HUMAN	601289780F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
10558	23005	35991	3.64	1.0E-109	BE540909.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
10558	23005	35992	3.64	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
10590	23035	36018	25.99	1.0E-109	BF664831.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
11021	23448	36497	2.04	1.0E-109	AW962574.1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246341 5'
11127	23579	36621	1.95	1.0E-109	4502838	NT	EST374847 MAGE resequences, MAGE Homo sapiens cDNA
						NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
11162	23542	36591	4.24	1.0E-109	W16510.1	EST_HUMAN	zb08b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to
11532	23890	36973	8.17	1.0E-109	AB007632.1	NT	PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat;
11823	14669	27191	1.68	1.0E-109	Y17123.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
12058	14669	27191	1.69	1.0E-109	Y17123.1	NT	Homo sapiens SNF6/INI1 gene, exon 6
12183	24303	30943	4.07	1.0E-109	AB011399.1	NT	Homo sapiens SNF6/INI1 gene, exon 6
						NT	Homo sapiens gene for AF-6, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3	12824	25011	0.77	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
39	12859	25050	7.14	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
39	12859	25051	7.14	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
113	12824	25011	0.81	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
308	12903	25323	3.81	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
545	13117	25526	1.23	1.0E-110	U84550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1211	13752	26187	3.42	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALORL) mRNA
1312	13847	26298	1.07	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1984	14500		1.41	1.0E-110	BF508896.1	EST_HUMAN	U1-H314-aos-b-05-Q-J1.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2788	15353		1.17	1.0E-110	4503098	NT	Homo sapiens chondroin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3049	15803		1.28	1.0E-110	U78027.1	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3151	15704	28123	8.21	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3151	15704	28124	8.21	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4065	16598	28997	3.57	1.0E-110	BE018558.1	EST_HUMAN	bb82a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR:O60312 O60312 KIAA0568 PROTEIN ;
4678	17195	29571	1.9	1.0E-110	AJ017213.1	EST_HUMAN	ou32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627863 3' similar to
4688	17214	29594	2.97	1.0E-110	AU117812.1	EST_HUMAN	SW-N121_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
5069	17379		1.99	1.0E-110	7892441	NT	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5546	18136	30493	2.53	1.0E-110	BE298408.1	EST_HUMAN	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
6000	18374	31260	0.8	1.0E-110	BE621069.1	EST_HUMAN	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
6019	18593	31279	8.55	1.0E-110	11419323	NT	601493677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895785 5'
6019	18593	31280	8.55	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
7092	24923	32422	6.73	1.0E-110	M55112.1	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
7463	19865	32799	0.42	1.0E-110	BE251496.1	EST_HUMAN	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
7541	19891	32829	0.87	1.0E-110	U08888.1	NT	601109388F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350277 5'
7541	19891	32830	0.87	1.0E-110	U08888.1	NT	Human G32 gene, exon 2
						NT	Human G32 gene, exon 2
7788	20230	33091	0.75	1.0E-110	AI560289.1	EST_HUMAN	Int2d08.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN
7907	20346	33212	10.14	1.0E-110	AV714276.1	EST_HUMAN	P50549 ETS TRANSLOCATION VARIANT 1 ;
7907	20346	33213	10.14	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7940	20377	33244	2.96	1.0E-110	AB020875.1	NT	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
8088	20514	33393	1.07	1.0E-110	AU137923.1	EST_HUMAN	Homo sapiens mRNA for KIAA0868 protein, partial cds
						EST_HUMAN	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007511 5'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8510	20922	33818	0.48	1.0E-110	9861251	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant C, mRNA
9750	22153	35084	3.08	1.0E-110	AW838394.1	EST_HUMAN	QV2-LT0053-020400-119-e04 LT0053 Homo sapiens cDNA
10257	22658	36620	3.41	1.0E-110	11432732	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
10529	22976	36957	4.77	1.0E-110	Y12337.1	NT	H. sapiens mRNA for myotonic dystrophy protein kinase like protein
10747	23185	38170	5.18	1.0E-110	BE794357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
10747	23185	38171	5.18	1.0E-110	BE794357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11192	22844	35817	2.71	1.0E-110	AA446529.1	EST_HUMAN	zw67g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781288 5' similar to TR:G1145816
11631	23958		4.47	1.0E-110	BE897218.1	EST_HUMAN	G1145816 FKBP4;
11764	24042		9.03	1.0E-110	AW082258.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
12016	24194		2.18	1.0E-110	AB011399.1	NT	ILO-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA
12074	24228		1.38	1.0E-110	A1127761.1	EST_HUMAN	Homo sapiens gene for AF-6, complete cds
12168	24895		4.87	1.0E-110	BF364546.1	EST_HUMAN	gc31c12.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1711222 3'
12480	14500		1.44	1.0E-110	BF608898.1	EST_HUMAN	PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA
179	12782		12.45	1.0E-111	U43701.1	NT	UHH-BL4-acc-b-05-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
202	12805	25222	0.92	1.0E-111	4758807	NT	Human ribosomal protein L23a mRNA, complete cds
755	13315		2.68	1.0E-111	BF035327.1	EST_HUMAN	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
764	13324	25754	5.83	1.0E-111	8393092	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
951	13503	25948	3.06	1.0E-111	M25142.1	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
2147	14660	27183	1.15	1.0E-111	AF036128.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
4187	16714	28103	1.28	1.0E-111	7661569	NT	Homo sapiens collagen type IX alpha 1 chain (COL9A1) gene, exons 29, 30, 31, and 32
4352	16874	28258	5.91	1.0E-111	K02268.1	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
5739	18318	30752	0.64	1.0E-111	AA151017.1	EST_HUMAN	Human enkephalin B (enbB) gene, exon 4 and 3' flank and complete cds
5736	18318	30753	0.64	1.0E-111	AA151017.1	EST_HUMAN	z47b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5899	18477	31158	1.25	1.0E-111	BE867609.1	EST_HUMAN	z47b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
6022	18596	31283	0.53	1.0E-111	U19869.1	NT	601443580F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847655 5'
6336	18894	31628	1.91	1.0E-111	A1344670.1	EST_HUMAN	Human two-handed zinc finger protein ZEB mRNA, partial cds
7049	19583	32378	1.11	1.0E-111	AL040762.1	EST_HUMAN	qp09g12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29893 RAS-RELATED PROTEIN RAL-A (HUMAN);
7198	19807	32737	1.29	1.0E-111	AW294848.1	EST_HUMAN	DKFZp434C1815_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1815 5'
7643	20090	32842	0.53	1.0E-111	AW698165.1	EST_HUMAN	UHH-BWO-all-d-03-Q-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729525 3'
							RC2-BN0033-160200-013-b05 BN0033 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7932	20369	33234	2.95	1.0E-111	BF369228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
8036	20488	33342	0.87	1.0E-111	9981253	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant A, mRNA
8044	20476	33350	0.83	1.0E-111	A1761228.1	EST_HUMAN	wf88401.x1 NCL CGAP Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813
8142	20565	33442	0.7	1.0E-111	U80017.1	NT	CYTOSCHROME P450 IIIA5 (HUMAN); Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
8347	20762	33659	0.91	1.0E-111	AA133914.1	EST_HUMAN	zr62c12.1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:662774 5' similar to gb:X03740
8699	21134	34037	0.89	1.0E-111	AA278868.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8699	21134	34038	0.89	1.0E-111	AA278868.1	EST_HUMAN	z579g03.1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
8808	21242	34149	3.74	1.0E-111	U66533.1	NT	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.;
9121	21553	34457	0.92	1.0E-111	11420516	NT	z579g03.1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
9220	21652	34612	13.9	1.0E-111	BF214902.1	EST_HUMAN	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.;
9268	21700	34613	14.23	1.0E-111	X17033.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
9268	21700	34613	14.23	1.0E-111	X17033.1	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
9389	21831	34745	3.6	1.0E-111	AF091395.1	NT	Human mRNA for integrin alpha-2 subunit
10150	22551	35518	1.58	1.0E-111	AA604160.1	EST_HUMAN	Human mRNA for integrin alpha-2 subunit
10163	22564	35594	1.4	1.0E-111	D10083.1	NT	Homo sapiens Tiro isoform mRNA, complete cds
10226	22627	35594	5.82	1.0E-111	AA131248.1	EST_HUMAN	aa58g02.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826170 3' similar to gb:U09235
10539	22886	35966	2.14	1.0E-111	AW256487.1	EST_HUMAN	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10719	23157	36245	1.67	1.0E-111	AW374340.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
10824	23260	36245	3.72	1.0E-111	U68159.1	NT	z579g03.1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826170 3' similar to gb:U09235
11238	23606	36651	1.88	1.0E-111	AI751071.1	EST_HUMAN	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
11687	23924	37003	4.42	1.0E-111	11417901	NT	cn07a11.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn07a11 random
12162	24268	38935	1.43	1.0E-111	AV708482.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12293	24676	30771	2.24	1.0E-111	W22562.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCAO508 5'
12444	18016	30447	1.33	1.0E-111	AB035358.1	NT	72C9 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
827	13191	25596	0.98	1.0E-112	4601854	NT	Homo sapiens mRNA for neuraxin I-alpha protein, complete cds
629	13183	25598	5.13	1.0E-112	U29103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
							Human steroidogenic acute regulatory protein (STAR) gene, exon 5

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
629	13193	25599	5.13	1.0E-112	U29103.1	NT	Human staradagenhe acute regulatory protein (SAR) gene, exon 5
651	13216	25625	2.37	1.0E-112	BF609039.1	EST_HUMAN	UHH-BI4-act-g-04-Q-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
651	13216	25626	2.37	1.0E-112	BF609039.1	EST_HUMAN	UHH-BI4-act-g-04-Q-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1028	13579	26020	2.76	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS1) gene, complete cds
1088	13634	26072	0.97	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1682	14211	26689	2.54	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1682	14211	26680	2.54	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1795	14320	26813	1.03	1.0E-112	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
2416	14919	27436	7.62	1.0E-112	BE668859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846859 5'
3040	15595		0.78	1.0E-112	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3204	15756	28174	2.18	1.0E-112	BE083082.1	EST_HUMAN	RC2-BT0842-030400-021-c08 BT0842 Homo sapiens cDNA
3204	15756	28175	2.18	1.0E-112	BE083082.1	EST_HUMAN	RC2-BT0842-030400-021-c08 BT0842 Homo sapiens cDNA
3336	15883	28304	0.76	1.0E-112	A1826511.1	EST_HUMAN	wk45b12.x1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb:M81660_m1
3683	16428	28834	0.81	1.0E-112	BE076073.1	EST_HUMAN	SEMNIOGELIN 1 PROTEIN PRECURSOR (HUMAN);
4844	17160	29539	0.63	1.0E-112	4504118	NT	MR2-BT0580-090300-113-f09 BT0580 Homo sapiens cDNA
4806	17319	29697	6.45	1.0E-112	AB037832.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4806	17319	29698	5.45	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5936	18514	31200	47.31	1.0E-112	N46046.1	EST_HUMAN	yy35d07.r1 Scores melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273229 5'
6384	18941	31678	1.32	1.0E-112	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6458	18914	31747	0.73	1.0E-112	AW502437.1	EST_HUMAN	UHHF-BR0p-aj-s-g-08-Q-U1.r1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3075658 5'
6458	18914	31748	0.73	1.0E-112	AW502437.1	EST_HUMAN	UHHF-BR0p-aj-s-g-08-Q-U1.r1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3075658 5'
6571	18122	31884	1.86	1.0E-112	BE741666.1	EST_HUMAN	601594717F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948657 5'
6804	19346	32118	0.57	1.0E-112	BF672815.1	EST_HUMAN	602152649F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283420 5'
6999	19335	32318	0.7	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508508 5'
6999	19335	32319	0.7	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508508 5'
7238	19848	32666	1.3	1.0E-112	BF674235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7696	20045	32895	0.68	1.0E-112	AL043289.1	EST_HUMAN	DKFZp434M0523_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M0523 5'
7803	20245	33104	1.67	1.0E-112	11418777	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7803	20245	33105	1.67	1.0E-112	11418777	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8770	21204	34107	1.16	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002779 5'
8313	21745	34662	2.79	1.0E-112	BE667635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8313	21745	34653	2.79	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
8965	22367	35316	2.58	1.0E-112	BF111413.1	EST_HUMAN	733007.X1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to TR:Q8VW35 Q9VW35 CG8743 PROTEIN.
10862	23009	35986	63.74	1.0E-112	AW863327.1	EST_HUMAN	MF3-SN0009-100400-108-b12 SN0009 Homo sapiens cDNA
10727	23165	36149	2.51	1.0E-112	AJ249900.1	NT	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
10882	23315	36312	2.64	1.0E-112	BE280479.1	EST_HUMAN	601156323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
10938	23370	36379	2.75	1.0E-112	AI782603.1	EST_HUMAN	q124c08.y5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869802 5' similar to TR:Q84362 Q84362 FUSED TOES ;
10938	23370	36380	2.75	1.0E-112	AI782603.1	EST_HUMAN	q124c08.y5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869802 5' similar to TR:Q84362 Q84362 FUSED TOES ;
10958	23387	36397	6.01	1.0E-112	AW377670.1	EST_HUMAN	PMO-CT0237-141089-001-r02 CT0237 Homo sapiens cDNA
11510	23668	36945	1.9	1.0E-112	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
763	13323	25752	7.42	1.0E-113	AI365586.1	EST_HUMAN	ac95f01.X1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1963625 3'
763	13323	25753	7.42	1.0E-113	AI365586.1	EST_HUMAN	ac95f01.X1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1963625 3'
969	13519	25963	3.47	1.0E-113	M11985.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1564	14098	26558	3.86	1.0E-113	AI365586.1	EST_HUMAN	ac95f01.X1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1963625 3'
1890	16265	26908	0.93	1.0E-113	AF240775.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2352	14857	27377	1.37	1.0E-113	AJ006976.1	NT	Homo sapiens PLP gene
3091	15945	28056	2.58	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5494	24715	30788	2.74	1.0E-113	BE780858.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5753	18335	30788	6.25	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
6102	18871	31365	0.49	1.0E-113	BE789172.1	EST_HUMAN	601476286F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879408 5'
6102	18871	31366	0.49	1.0E-113	BE789172.1	EST_HUMAN	601476286F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879408 5'
6219	18785	31491	4.43	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
6249	18813	31528	1	1.0E-113	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6378	18934	31672	2.99	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetylglucosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
6470	19025	31761	0.61	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6470	19025	31762	0.61	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6844	18192	31943	0.77	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6844	18192	31944	0.77	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7785	20227	33087	0.57	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508382 5'
7785	20227	33088	0.57	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508382 5'
8210	20830	33519	0.49	1.0E-113	AW658960.1	EST_HUMAN	EST1371030 MAGE resequences, MAGE Homo sapiens cDNA
9405	21837	34760	3.35	1.0E-113	BE382842.1	EST_HUMAN	601287709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9405	21837	34761	3.35	1.0E-113	BE382842.1	EST_HUMAN	601287709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
8915	22317	35293	1.3	1.0E-113	11428367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
10429	22829	35799	0.87	1.0E-113	AW600517.1	EST_HUMAN	UHF-BN0-akb-10-0-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077922 5'
10908	23341	36347	7.93	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327 KIAA0594 PROTEIN;
10909	23341	36348	7.93	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327 KIAA0594 PROTEIN;
11031	23468	36478	2.68	1.0E-113	BE282968.1	EST_HUMAN	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2883366 5'
11254	23620	36667	2.03	1.0E-113	AA580720.1	EST_HUMAN	nc80b03.r1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:797068 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1;
11254	23620	36668	2.03	1.0E-113	AA580720.1	EST_HUMAN	nc80b03.r1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:797068 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1;
60	12880	25083	1	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	12880	25084	1	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	12880	25085	1	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
664	13229	25641	19.98	1.0E-114	T70551.1	EST_HUMAN	jd15c01.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element
1097	13842	26082	2.19	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1346	13880	26335	4.67	1.0E-114	7657528	NT	Homo sapiens fibroid tumor deletion region protein 1 (RTDR1), mRNA
1671	14202	26676	5.07	1.0E-114	6678073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2008	14622	27035	0.98	1.0E-114	BE171894.1	EST_HUMAN	MRC-HT0559-250200-002-407 HT0559 Homo sapiens cDNA
2762	12866	25059	584.94	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2762	12868	25060	584.94	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3092	15646	28057	2.54	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3131	15894	28100	0.95	1.0E-114	BF206374.1	EST_HUMAN	601689832F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
4029	16562	28956	2.21	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4232	16757	29144	1.05	1.0E-114	AA574056.1	EST_HUMAN	nk1d02.r1 NCL CGAP_Co2 Homo sapiens cDNA clone IMAGE:1013187 3' similar to gb:X65857_cds1 OLFATORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
4413	16894	29325	0.86	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5341	17840	30199	0.93	1.0E-114	AW294203.1	EST_HUMAN	UI-H-BI2-abc-d-01-Q-JL.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2728424 3'
5349	17848	30205	2.34	1.0E-114	AF004849.1	NT	Homo sapiens PKY protein kinase mRNA, complete cds
5656	18242	30639	1.57	1.0E-114	4506980	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5656	18242	30640	1.57	1.0E-114	4506980	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5882	18441	31116	1.17	1.0E-114	9257201	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
6546	18098	31840	0.53	1.0E-114	Z26298.1	NT	Homo sapiens cleithrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA
7416	18085	30379	0.77	1.0E-114	4759163	NT	H.sapiens isoform 1 gene for L-type calcium channel, exon 20
7510	19713		0.7	1.0E-114	AB041533.1	NT	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (tesican) (SPOCK) mRNA
7688	20133	32888	1.12	1.0E-114	AU134187.1	EST_HUMAN	Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds
7688	20133	32889	1.12	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARG1001444 5'
7739	20163	33044	9.04	1.0E-114	Y18000.1	NT	AU134187 OVARC1 Homo sapiens cDNA clone OVARG1001444 5'
7739	20163	33045	9.04	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
8554	20989	33887	2.14	1.0E-114	4557600	NT	Homo sapiens NF2 gene
8751	21185	34086	1.74	1.0E-114	A1363139.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8751	21185	34087	1.74	1.0E-114	A1363139.1	EST_HUMAN	qy68d08.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8136	21688	34475	2.78	1.0E-114	U63041.1	NT	qy68d08.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8188	21620	34531	7.41	1.0E-114	AB011133.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
8188	21620	34532	7.41	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
8462	21893	34814	1.79	1.0E-114	BF109832.1	EST_HUMAN	Homo sapiens mRNA for KIAA0561 protein, partial cds
8631	22046		4.23	1.0E-114	AW327455.1	EST_HUMAN	7169g12.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526847 3' similar to TR:Q9UHN6 Q9UHN6 TRANSMEMBRANE PROTEIN 2.:
8668	20956	33858	2.86	1.0E-114	AF077754.1	NT	dq03f05.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9729	22151		1.41	1.0E-114	M13536.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
10143	22544	35513	1.06	1.0E-114	BE870004.1	EST_HUMAN	Human ceruloplasmin mRNA
10156	22557	35525	1.18	1.0E-114	AL163227.2	NT	601449752F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863600 5'
10400	22800	35776	0.94	1.0E-114	BE171984.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
							MRO-HT0559-250200-002-007 HT0559 Homo sapiens cDNA
10569	23016		12.39	1.0E-114	BE302666.1	EST_HUMAN	bat3g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse L1Rap3 protein mRNA from a repetitive element, complete (MOUSE).
10965	23394	36405	10.35	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
10965	23394	36406	10.35	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11302	23687	36714	10.76	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11302	23687	36715	10.76	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11454	23813	36873	2.24	1.0E-114	BF574757.1	EST_HUMAN	602134549F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289558 5'
11454	23813	36874	2.24	1.0E-114	BF574757.1	EST_HUMAN	602134549F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289558 5'
11511	23869	36946	3.04	1.0E-114	BE391856.1	EST_HUMAN	601286813F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613514 5'
11511	23869	36947	3.04	1.0E-114	BE391856.1	EST_HUMAN	601286813F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613514 5'
12050	24935		5.55	1.0E-114	11418041	NT	Homo sapiens TNF-Inducible protein CG12-1 (CG12-1), mRNA
12344	24407	30888	4.1	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12344	24407	30889	4.1	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
23	12843	25032	3.85	1.0E-115	4788111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
134	12740	25159	1.6	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
138	12744		5.58	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
306	12801	26320	2.9	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-158-b08 UM0094 Homo sapiens cDNA
554	13126	25535	1.45	1.0E-115	A1339206.1	EST_HUMAN	q108101.x1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536
554	13126	25538	1.45	1.0E-115	A1339206.1	EST_HUMAN	q108101.x1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536
809	13367	25803	0.77	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
809	13367	25804	0.77	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
811	13368	25806	131.74	1.0E-115	4503784	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1), mRNA
1580	14111	26576	0.95	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1580	14111	26577	0.95	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
2806	15363		1.11	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-158-b08 UM0094 Homo sapiens cDNA
3078	15630	28037	2.25	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3078	15630	28038	2.25	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3448	15992	28411	2.17	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4054	16366	28976	4.72	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4283	16808	29182	0.68	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4425	16946	29336	2.94	1.0E-115	6812659	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4465	16985	29368	4.49	1.0E-115	4768278	NT	Homo sapiens EphA4 (EPHA4) mRNA
4721	17237	29617	3.03	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4721	17237	29618	3.03	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4974	17485	29862	3.97	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
4974	17485	29863	3.97	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6362	17860	30218	2.61	1.0E-115	4504658	NT	Homo sapiens Interleukin 1 receptor, type I (IL1R1) mRNA
6601	18189	30554	2.24	1.0E-115	AW070335.1	EST_HUMAN	EST382418 IMAGE resequences, MAGK Homo sapiens cDNA
6680	18265	30668	1.05	1.0E-115	BF665387.1	EST_HUMAN	602119346F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278738 5'
5805	18385	31048	1.76	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5805	18385	31047	1.76	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5981	18537	31222	0.91	1.0E-115	A028799.1	EST_HUMAN	au64g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
5981	18537	31223	0.91	1.0E-115	A028799.1	EST_HUMAN	au64g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
6594	19135	31881	0.53	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6594	19135	31882	0.53	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6732	19278	32040	14.7	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63436), mRNA
6879	19419	32183	1.82	1.0E-115	7681853	NT	Homo sapiens KIAA0084 gene product: Helicase (KIAA0054), mRNA
6879	19419	32184	1.82	1.0E-115	7681853	NT	Homo sapiens KIAA0054 gene product: Helicase (KIAA0054), mRNA
7344	19766	32561	0.49	1.0E-115	T86774.1	EST_HUMAN	Y08608.11 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:115095 5' similar to SP:POG_YEAST P18801 DNA POLYMERASE GAMMA;
7732	20176	33035	1.39	1.0E-115	A076598.1	EST_HUMAN	cc31a06.x1 Soares fetal, fetus, Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7732	20176	33036	1.39	1.0E-115	A076598.1	EST_HUMAN	cc31a06.x1 Soares fetal, fetus, Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7888	20327	33193	8.12	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0958 protein, partial cds
8745	21179	34082	10.9	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8745	21179	34083	10.9	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
9223	21655	34665	2.26	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
10033	22435	35381	2.13	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10033	22435	35382	2.13	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10387	22787	35766	1	1.0E-115	A0221878.1	EST_HUMAN	qg99a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10387	22787	35767	1	1.0E-115	A0221878.1	EST_HUMAN	qg99a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10503	22982	35933	4.53	1.0E-115	AW671544.1	EST_HUMAN	xx32068.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANFA P10463 CALYPTOSINE;
11027	23454	36474	2.34	1.0E-115	BE045890.1	EST_HUMAN	h054c10.x1 NCL CGAP_Pen3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378 PRP4 PROTEIN KINASE HOMOLOG;
11027	23454	36475	2.34	1.0E-115	BE045890.1	EST_HUMAN	h054c10.x1 NCL CGAP_Pen3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378 PRP4 PROTEIN KINASE HOMOLOG;
11152	23533	36571	2.51	1.0E-115	4502528	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11811	23942		1.47	1.0E-115	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
589	13159	26563	2.08	1.0E-116	BE275502.1	EST_HUMAN	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2888876 5'
823	13381	25818	1.48	1.0E-116	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
882	13437		0.85	1.0E-116	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1940	14459	26962	1.79	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
1940	14459	26963	1.79	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
2202	14712	27234	0.84	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2236	14745		3.08	1.0E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo olfr17-01 (OR17-01) pseudogene, complete cds
2354	14859	27378	3.31	1.0E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2690	15273	27693	9.78	1.0E-116	BE889268.1	EST_HUMAN	601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3133	15686	28101	3.61	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3133	15686	28102	3.61	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4400	16922	29307	2.28	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4913	17424	29786	1.51	1.0E-116	AI907096.1	EST_HUMAN	PM-BT135-070499-016 BT135 Homo sapiens cDNA
5165	17689	30031	16.21	1.0E-116	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
5165	17689	30032	16.21	1.0E-116	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
5469	17684	30312	11.95	1.0E-116	AI221878.1	EST_HUMAN	gg99e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
5530	18120	30476	0.8	1.0E-116	AI302062.1	EST_HUMAN	qn18d04.x1 NCJ_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898695 3' similar to contains element
							MER25 repetitive element ;
6279	18841	31559	2.54	1.0E-116	W42822.1	EST_HUMAN	zc24d07.r1 Soares_senescent_fibroblasts_Nb4SF Homo sapiens cDNA clone IMAGE:323245 5' similar to
5528	19080	31820	2.07	1.0E-116	AB046859.1	NT	SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
5528	19080	31821	2.07	1.0E-116	AB046859.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6601	19152	31900	1.05	1.0E-116	BE408097.1	EST_HUMAN	Homo sapiens mRNA for KIAA1636 protein, partial cds
6733	19279	32041	6.1	1.0E-116	BF677910.1	EST_HUMAN	601302281F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638784 5'
6850	19391	32165	0.76	1.0E-116	5729867	NT	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6850	19391	32166	0.76	1.0E-116	5729867	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6864	19404		1.68	1.0E-116	BE158133.1	EST_HUMAN	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7364	19911	32623	1.48	1.0E-116	C02944.1	EST_HUMAN	MR2-HT0379-210200-102-b04 HT0379 Homo sapiens cDNA
7648	20094	32948	11.06	1.0E-116	AV716314.1	EST_HUMAN	C02944 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC0567
8907	21341	34258	1.61	1.0E-116	AA354256.1	EST_HUMAN	AV716314 DCB Homo sapiens cDNA clone DCBCCG06 5'
							EST92685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8907	21341	34257	1.61	1.0E-116	AA354256.1	EST_HUMAN	EST62895 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2.
9300	21732	34639	1.48	1.0E-116	BE565507.1	EST_HUMAN	601338268F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680880 5'
9408	21840	34754	2.5	1.0E-116	A1216352.1	EST_HUMAN	q106c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to gp-X63741_mai FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
9815	22218	35154	1.56	1.0E-116	11418646	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA
10224	22825	35592	1.16	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase 1 (XT-1) gene
10224	22825	35593	1.15	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase 1 (XT-1) gene
10271	22872	35635	0.88	1.0E-116	BE158913.1	EST_HUMAN	QV4-HT0401-281299-083-c08 HT0401 Homo sapiens cDNA
10912	23344	36352	2.76	1.0E-116	A1387140.1	EST_HUMAN	q41604.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1835102 3' similar to WP:B0495.7
12332	24401		1.52	1.0E-116	11525293	NT	CE017665
12394	24812		1.8	1.0E-116	AL134889.1	EST_HUMAN	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
575	13146	25553	1.35	1.0E-117	4826636	NT	DKFZ762L1110_r1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp762L1110 5'
1104	13301	26090	1.02	1.0E-117	AF124393.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1298	13786	26242	0.83	1.0E-117	AF264750.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1744	14271	26756	0.89	1.0E-117	AF123320.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1807	14330	26823	1.37	1.0E-117	M19816.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
2117	14630	27153	1.17	1.0E-117	AW957699.1	EST_HUMAN	Human apolipoprotein B-100 (apoB) gene, exon 10
2540	15038	27554	1.98	1.0E-117	M693488.1	NT	EST389769 IMAGE resequences, IMAGE Homo sapiens cDNA
3230	15782	28200	1.97	1.0E-117	AA978114.1	EST_HUMAN	Human alpha-5 collagen type IV gene, exon 6
4004	16538	28937	16.92	1.0E-117	AA316723.1	EST_HUMAN	op32c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1678648 3'
4366	16888	29269	2.62	1.0E-117	8659564	NT	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4616	17132	29517	0.98	1.0E-117	AL042120.1	EST_HUMAN	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4775	17289	29673	0.98	1.0E-117	X89870.1	NT	DKFZp434C1120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1120 5'
4776	17289	29674	0.98	1.0E-117	X89870.1	NT	H. sapiens mRNA for TPCR16 protein
4868	17380	29757	11.23	1.0E-117	AF134304.2	NT	H. sapiens mRNA for TPCR16 protein
4868	17380	29758	11.23	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4928	17439	29816	7.01	1.0E-117	U58109.1	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4928	17439	29816	7.01	1.0E-117	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
5021	17531	29803	4.98	1.0E-117	AB020675.1	NT	Mus musculus nebulin mRNA, partial cds
5452	17947	30298	0.88	1.0E-117	6912461	NT	Homo sapiens mRNA for KIAA0868 protein, complete cds
5602	18190	30555	4.07	1.0E-117	BE730508.1	EST_HUMAN	Homo sapiens atrophin-1 interacting protein 1; actin receptor interacting protein 1 (KIAA0705), mRNA

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7371	18041	30426	0.67	1.0E-117	AA323348.1	EST_HUMAN	EST28111 Cerebellum II Homo sapiens cDNA 5' end similar to similar to zinc finger domain
7935	20372	33238	6.1	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7935	20372	33239	6.1	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
8061	20492	33369	3.63	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
8061	20492	33370	3.63	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
9550	21984	34887	1.39	1.0E-117	D16524.1	NT	Human gene for very low density lipoprotein receptor, exon 11
9888	22291	35231	2.16	1.0E-117	BE739922.1	EST_HUMAN	601569317F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843748 5'
10412	22812	35787	1.01	1.0E-117	11420222	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
10639	23080	36084	3.19	1.0E-117	D83778.1	NT	Human mRNA for KIAA0191 gene, partial cds
10799	23236	36219	16.74	1.0E-117	W80605.1	EST_HUMAN	z883b11.r1 Soares_fetal Heart_NbHH19W Homo sapiens cDNA clone IMAGE:347229 5' similar to
10814	23260	36233	3.44	1.0E-117	11424836	NT	gbM14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
10814	23260	36234	3.44	1.0E-117	11424835	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11044	23470	36484	2.87	1.0E-117	AB011541.1	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11044	23470	36485	2.87	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11148	23529		71.28	1.0E-117	BE269856.1	EST_HUMAN	601186203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544288 5'
11342	23706	36780	6.82	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11342	23706	36781	6.82	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11496	23854	36926	1.95	1.0E-117	AA584764.1	EST_HUMAN	nc04c12.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099702 3'
11496	23854	36927	1.95	1.0E-117	AA584764.1	EST_HUMAN	nc04c12.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099702 3'
11860	24804		1.66	1.0E-117	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
73	12692	25102	3.25	1.0E-118	AF161500.1	NT	(UBE2D3) genes, complete cds
98	12715	25128	2.68	1.0E-118	AL045854.1	EST_HUMAN	Homo sapiens HSPC151 mRNA, complete cds
535	13107	25518	6.84	1.0E-118	7657016	NT	DKFZ4341056_r1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZ4341056 5'
837	15297	25634	1.59	1.0E-118	5174880	NT	Homo sapiens hypothetical protein (D1328E19.C1.1), mRNA
2141	14654	27176	2.73	1.0E-118	BE389705.1	EST_HUMAN	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2141	14654	27177	2.73	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2141	14654	27178	2.73	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2224	14734		3.87	1.0E-118	AW951729.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2697	15188	27700	9.57	1.0E-118	U07000.1	NT	EST363789 MAGE resequences, MAGEB Homo sapiens cDNA
2697	15188	27701	9.57	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3095	15619		4.92	1.0E-118	Y13932.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3162	15705	28125	5.94	1.0E-118	A1347694.1	EST_HUMAN	Homo sapiens PRKY exon 7
							qp0105.x1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1916769 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3162	15705	28126	5.94	1.0E-118	AL347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1918769 3'
4104	16034	28021	20.15	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
4757	17271	29654	11.57	1.0E-118	11425793	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
5676	18264	30664	2.21	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5679	18264	30665	2.21	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5898	18476	31156	0.85	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5898	18476	31157	0.85	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5986	18562	31247	0.63	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5986	18562	31248	0.63	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
6051	18623	31313	1.04	1.0E-118	M55109.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
6150	18718	31421	0.84	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6150	18718	31422	0.84	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6241	18805	31517	1.52	1.0E-118	11420764	NT	Homo sapiens transient receptor potential channel 6 (TRPC6), mRNA
7081	19595	32389	1.51	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7081	19595	32390	1.51	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7336	19886	32821	1.15	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O0127 5'
7336	19886	32822	1.15	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O0127 5'
8125	20549	33426	5.42	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
8141	20564	33441	0.72	1.0E-118	L40590.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds
8508	20918	33814	0.85	1.0E-118	BF685272.1	EST_HUMAN	602141620F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302749 5'
8911	21046	33951	2.25	1.0E-118	BE761223.1	EST_HUMAN	601469159F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247 5'
8919	21353	34268	7.8	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-030200-097-h03 BT0263 Homo sapiens cDNA
8919	21353	34269	7.8	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-030200-097-h03 BT0263 Homo sapiens cDNA
8923	21357	34271	1.18	1.0E-118	AA443024.1	EST_HUMAN	z098d07.t1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8923	21357	34272	1.18	1.0E-118	AA443024.1	EST_HUMAN	z098d07.t1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:811789 5'
9151	21583	34488	1.9	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9151	21583	34489	1.9	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9368	21798	34706	5.01	1.0E-118	BE263134.1	EST_HUMAN	Homo sapiens hypothetical protein (DJ328E19.O1.1), mRNA
9761	22164	35098	1.43	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.O1.1), mRNA
10263	22664	35626	0.98	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10263	22664	35627	0.98	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10269	22690	35654	1.37	1.0E-118	BF195407.1	EST_HUMAN	7n17e09.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3664785 3' similar to SW:ZP3A_HUMAN
11009	23436	36453	3.2	1.0E-118	BF685214.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR;
							602141529F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302798 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11038	23465	38486	1.72	1.0E-118	11055968	NT	Homo sapiens protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum protein (ERPROT213-21), mRNA
11047	23473	38499	11.1	1.0E-118	AA315007.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) H1 Homo sapiens cDNA 5' and similar to dynein, light chain 1, cytoplasmic
11310	23674	36724	4.12	1.0E-118	BE008676.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11310	23674	36725	4.12	1.0E-118	BE008676.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11313	23677	36728	3.47	1.0E-118	BF093687.1	EST_HUMAN	QV0-UM00091-120900-385-b12 UM0091 Homo sapiens cDNA
11313	23677	36729	3.47	1.0E-118	BF093687.1	EST_HUMAN	QV0-UM00091-120900-385-b12 UM0091 Homo sapiens cDNA
11479	23837	36905	1.63	1.0E-118	BE218235.1	EST_HUMAN	h36a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175474 3' similar to TR:Q922H4
11541	23898	36981	2.82	1.0E-118	D87682.1	NT	Q922H4 G PROTEIN-COUPLED RECEPTOR LGR4.;
778	13337	25772	2.46	1.0E-119	AF170492.1	NT	Human mRNA for KIAA0241 gene, partial cds
1062	16300	26047	0.85	1.0E-119	7705607	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1884	14405	26900	2.9	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
2419	14922	27439	4.98	1.0E-119	AA912739.1	EST_HUMAN	0141c12.81 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1626038 3' similar to gb:M94055.
3199	18751		1.22	1.0E-119	AA918760.1	EST_HUMAN	SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT (HUMAN);
3968	18501	28909	0.84	1.0E-119	4604116	NT	0110505.s1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WPE04F6.2
5591	18179	30544	4.35	1.0E-119	AU133399.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5604	18192	30557	12.93	1.0E-119	M89914.1	NT	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001897 5'
5810	18188	30564	3.6	1.0E-119	BE636121.1	EST_HUMAN	Human neurofibromin (NF1) gene, complete cds
5690	18276	30686	1.51	1.0E-119	AV693731.1	EST_HUMAN	RC1-NN0079-250800-018-g08 NN0073 Homo sapiens cDNA
5857	18436	31110	1.03	1.0E-119	AL134903.1	EST_HUMAN	AV693731 GKG Homo sapiens cDNA clone GKGCDH803 5'
5857	18436	31111	1.03	1.0E-119	AL134903.1	EST_HUMAN	DKFZp762M0710_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6440	18996	31727	7.29	1.0E-119	AI150703.1	EST_HUMAN	DKFZp762M0710_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6608	19159	31807	0.66	1.0E-119	AF315683.1	NT	qB77c09.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone DKFZp762M0710 5'
6608	19159	31808	0.66	1.0E-119	AF315683.1	NT	SW:K1CJ_MOUSE_P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
6661	19209	31957	1.19	1.0E-119	AX787832.1	EST_HUMAN	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6805	19347	32119	2.59	1.0E-119	X06292.1	NT	tm23110.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'
6817	19358	32136	4.06	1.0E-119	AW974193.1	EST_HUMAN	Human c-fos/fps proto-oncogene
7890	20328	33195	1.28	1.0E-119	BE796814.1	EST_HUMAN	EST186298 IMAGE reassurances, MAGM Homo sapiens cDNA
							601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8103	20529	33408	0.49	1.0E-119	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
9113	21545	34449	1.1	1.0E-119	BE615150.1	EST_HUMAN	601280564F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622528 5'
9974	22376	35328	0.93	1.0E-119	11038843	NT	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA
10209	22810	35975	2.27	1.0E-119	AA488124.1	EST_HUMAN	es32105.1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
10379	22779	35747	1.08	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10835	23270	36257	3.37	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10835	23270	36258	3.37	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10975	23404		24.2	1.0E-119	BF568571.1	EST_HUMAN	60218072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
11917	24880		2.8	1.0E-119	AW847618.1	EST_HUMAN	RC3-CT0212-240999-011-403 CT0212 Homo sapiens cDNA
260	12850	25288	3.08	1.0E-120	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
315	12910	25329	0.93	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1066	13612	26053	3.5	1.0E-120	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1066	13612	26054	3.5	1.0E-120	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1456	13988	28450	2.35	1.0E-120	N44873.1	EST_HUMAN	y40g12.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:273768 5'
1618	14149	26820	3.62	1.0E-120	AF187706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1782	14307	26797	2.47	1.0E-120	4557250	NT	Homo sapiens dishegryn and metalloprotease domain 10 (ADAM10) mRNA
2029	14544	27058	2.56	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
2029	14544	27059	2.56	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
2434	14937	27452	10.12	1.0E-120	4755124	NT	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA
3272	12910	25329	1.14	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4379	16901	29285	1.6	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4379	16901	29286	1.6	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4706	17222	28605	2.41	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4706	17222	28606	2.41	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
6011	18585	31271	16.29	1.0E-120	BF568222.1	EST_HUMAN	602183904F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6011	18585	31272	16.29	1.0E-120	BF568222.1	EST_HUMAN	602183904F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6821	19170	31923	0.44	1.0E-120	6912583	NT	Homo sapiens PTAIRE protein kinase 1 (PTFK1), mRNA
6783	19326	32083	0.42	1.0E-120	M28428.1	NT	Human P-glycoprotein (MDR1) gene, exons 6 and 7
6783	19326	32084	0.42	1.0E-120	M28428.1	NT	Human P-glycoprotein (MDR1) gene, exons 6 and 7
8089	20516	33395	1.59	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
8492	20904	33798	0.46	1.0E-120	AB023177.1	NT	Homo sapiens mRNA for KIAA0860 protein, partial cds
8587	20992	33889	1.53	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8587	20992	33890	1.53	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8876	21310	34223	3.11	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCI CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4183393 5'
8938	21370	34283	2	1.0E-120	AB007894.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8938	21370	34284	2	1.0E-120	AB007894.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8966	21399	34311	1.55	1.0E-120	AB007834.1	NT	Homo sapiens mRNA for KIAA0495 protein, partial cds
9893	22105	35032	5.02	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3825544 5'
9893	22105	35033	5.02	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3825544 5'
9893	22266	35205	4.2	1.0E-120	BF306541.1	EST_HUMAN	601888956F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
9873	22276	35217	2.47	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
9893	22296	35227	0.86	1.0E-120	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10096	22497	35458	3.18	1.0E-120	AB028000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
10866	23299	36293	1.74	1.0E-120	BE741519.1	EST_HUMAN	601604805F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948769 5'
10805	23337	36343	17.26	1.0E-120	BE296387.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532016 5'
11103	23566	36596	2.46	1.0E-120	BE867679.1	EST_HUMAN	601443155F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11103	23566	36597	2.46	1.0E-120	BE867679.1	EST_HUMAN	601443155F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
76	12694	25106	1	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
393	12978	25400	1.52	1.0E-121	AU134063.1	EST_HUMAN	AU134063 PLAGE1 Homo sapiens cDNA clone PLAGE1000899 5'
744	16291	25729	1.65	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1812	14431	26929	0.98	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
1912	14431	26930	0.98	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2922	15477	27900	0.64	1.0E-121	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
3043	15597	28008	3.96	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3043	15597	28009	3.96	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3519	16062	28484	1.2	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3519	16062	28485	1.2	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3677	16217	28625	9.29	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
3722	16262	28687	0.64	1.0E-121	AB04151.1	EST_HUMAN	GM-BT043-090298-075 BT043 Homo sapiens cDNA
4353	16875	29259	1.18	1.0E-121	A283294.1	EST_HUMAN	q57b01 x1 NCI CGAP_Part1 Homo sapiens cDNA clone IMAGE:2005417 3'
5072	17582	29948	3.44	1.0E-121	X91837.1	NT	H. sapiens EOE-1 gene (exon 17)
5519	18109	30363	0.80	1.0E-121	BE222250.1	EST_HUMAN	hu09108.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166119 3'
5826	18406	31072	0.56	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6981	19518	32300	0.46	1.0E-121	M91463.1	NT	Human glucose transporter (GLUT4) gene, complete cds
7293	19798		1.09	1.0E-121	A1271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7378	18048	30385	0.81	1.0E-121	AW898088.1	EST_HUMAN	RC3-NN0068-270400-011-402 NN0068 Homo sapiens cDNA
7378	18048	30386	0.81	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0068-270400-011-402 NN0068 Homo sapiens cDNA
8283	20700	33591	0.5	1.0E-121	11429714	NT	Homo sapiens U5 snRNP-specific protein (220 kD), ortholog of S. cerevisiae Prp8p (PRP8), mRNA
8283	20700	33592	0.5	1.0E-121	11429714	NT	Homo sapiens U5 snRNP-specific protein (220 kD), ortholog of S. cerevisiae Prp8p (PRP8), mRNA
8589	21024	33925	1.43	1.0E-121	11438217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
8593	21028	33829	2.35	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8593	21028	33930	2.35	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8836	22338	35286	1.09	1.0E-121	AW683868.1	EST_HUMAN	la0505.y1 Human Pancreatic islets Homo sapiens cDNA 5' similar to TR:Q75457 O76457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA;
8836	22338	35287	1.09	1.0E-121	AW683858.1	EST_HUMAN	la0505.y1 Human Pancreatic islets Homo sapiens cDNA 5' similar to TR:Q75457 O76457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA;
10560	23007	35994	3.33	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
10749	23187	36173	8.75	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
10776	23214	36197	4.42	1.0E-121	N58824.1	EST_HUMAN	W74601.s1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248448 3'
11097	23521	36558	2.53	1.0E-121	AU118320.1	EST_HUMAN	AU118320 HEMBA1 Homo sapiens cDNA clone HEMBA1005536 5'
281	12878	25294	1.81	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
350	12940	25354	2.2	1.0E-122	AF114488.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
372	12860	25379	1.76	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
905	13459	25808	3.22	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN), complete cds
1262	13790	26236	11.95	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1691	14220	26700	2.81	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1710	14238	26723	2.73	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1710	14238	26724	2.73	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1790	14315	26809	4.06	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3868358 5'
2394	14898	27416	7.08	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2394	14898	27417	7.08	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
4804	17415	29787	4.27	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5088	17598		1.19	1.0E-122	AW604846.1	EST_HUMAN	U1-HF-BN0-ail-a-03-0-U1.F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078948 5'
5437	17932	30285	0.91	1.0E-122	5174688	NT	Homo sapiens eex comb on midleg like 2 (SCML2) mRNA
5828	18408	31076	1.32	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7137	18408	31075	6.56	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7660	20106	32958	0.54	1.0E-122	AA888871.1	EST_HUMAN	ak49h06.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1409339 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8448	20862	33763	0.48	1.0E-122	AA224259.1	EST_HUMAN	z15a03.11 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:663436 5' similar to TR:G940370 G940370 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE;
8448	20862	33764	0.48	1.0E-122	AA224259.1	EST_HUMAN	z15a03.11 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:663436 5' similar to TR:G940370 G940370 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE;
9360	21792	34701	1.52	1.0E-122	11424216	NT	Homo sapiens lateral giant larva (Drosophila) homolog 2 (LGL2), mRNA
9588	21991	34919	0.83	1.0E-122	A1359618.1	EST_HUMAN	qy2h07.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.;
9588	21991	34920	0.83	1.0E-122	A1359618.1	EST_HUMAN	qy2h07.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.;
10768	23206	36188	2.01	1.0E-122	AW965834.1	EST_HUMAN	EST367604 MAGE resequences, MAGD Homo sapiens cDNA
11138	23589	36830	3.25	1.0E-122	AB024068.1	NT	Homo sapiens gene for B120, exon 10
11501	23859	36934	1.94	1.0E-122	BE002805.1	EST_HUMAN	QV4-BN0090-300300-158-h01 BN0080 Homo sapiens cDNA
11501	23859	36935	1.94	1.0E-122	BE002805.1	EST_HUMAN	QV4-BN0090-300300-158-h01 BN0080 Homo sapiens cDNA
11651	23972		6.9	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
12608	13780	26236	2.43	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
194	12797	25212	0.94	1.0E-123	U31519.1	NT	Human phosphoenolpyruvate carboxylase (PCK1) gene, promoter region and partial cds
790	13348	25782	1.47	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4163670 5'
790	13348	25783	1.47	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4163670 5'
1039	13587	26027	6.28	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1048	13594	26034	2.42	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1271	13807	26257	4.79	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1271	13807	26258	4.79	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1484	14016	26482	15.1	1.0E-123	AJ388841.1	NT	Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02
2021	14537	27049	1.52	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2021	14537	27050	1.52	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2021	14537	27051	1.52	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2209	14719		2.63	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC61209), mRNA
3210	15762	28181	0.69	1.0E-123	6912817	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutamyl cyclase) (QPCT), mRNA
5264	17765	30134	0.58	1.0E-123	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and EGF-binding protein gene, complete cds
5704	18288	30713	1.5	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (ORALBP) gene, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5704	18288	30714	1.5	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (RALBP) gene, complete cds
5848	18426	31096	1.72	1.0E-123	BE769746.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
6814	19355	32132	2.05	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7424	19929	32760	1.02	1.0E-123	H53198.1	EST_HUMAN	Y84a03.r1 Soares fetal liver spleen 'NFLS' Homo sapiens cDNA clone IMAGE:202444 5' similar to SP-YAK1_YEAST P14680 PROTEIN KINASE YAK1 ;
7437	19941	32776	1.45	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7638	20085	32939	0.61	1.0E-123	U55258.1	NT	Human hBRAVOINr-CAM precursor (hBRAVOINr-CAM) gene, complete cds
7882	20321	33189	0.98	1.0E-123	11525833	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HSST2), mRNA
8173	20595	33479	1.43	1.0E-123	11439439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
8182	20804	33491	1.86	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
8190	20612	33489	0.63	1.0E-123	11437202	NT	Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA
8370	20785	33684	0.59	1.0E-123	N35841.1	EST_HUMAN	Y88d11.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611
8370	20785	33685	0.59	1.0E-123	N35841.1	EST_HUMAN	S49611 protein kinase Pkpa - Phycomyces blakesleearius ;
9024	21457		0.94	1.0E-123	AW371924.1	EST_HUMAN	Y88d11.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611
9598	22078	35005	1.56	1.0E-123	AB007923.1	NT	S49611 protein kinase Pkpa - Phycomyces blakesleearius ;
							RC4-BT0311-251189-012-a07 BT0311 Homo sapiens cDNA
							Homo sapiens mRNA for KIAA0454 protein, partial cds
9894	22108	35034	36.87	1.0E-123	U09823.1	NT	Onyctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
11354	20595	33479	2.48	1.0E-123	11439439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
11442	23802	36860	5.83	1.0E-123	BF677292.1	EST_HUMAN	60208679F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
11442	23802	36861	5.83	1.0E-123	BF677292.1	EST_HUMAN	60208679F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
282	12879	25295	1.17	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
282	12879	25296	1.17	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
288	12885		2.36	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
503	13077	25494	2.74	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
711	13272	25691	2.68	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
711	13272	25692	2.68	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG [RETROVIRAL ELEMENT] ;
779	13336	25773	2.98	1.0E-124	AF155654.1	NT	z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
831	13388	25827	1.51	1.0E-124	4507500	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG [RETROVIRAL ELEMENT] ;
927	13481	25927	3.6	1.0E-124	77054449	NT	Human putative ribosomal protein S1 mRNA
1378	13913	26368	9.43	1.0E-124	AF274892.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
							Homo sapiens hypothetical protein (HSPC068), mRNA
							Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1378	13913	26369	8.43	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1791	14318	26810	2.2	1.0E-124	AJ131712.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (noH81 gene)
1988	14502	27011	2.14	1.0E-124	BE79524.1	EST_HUMAN	007491719F1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3893894 5'
3468	16010	28431	0.71	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3480	16010	28432	0.71	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3908	16443	28849	0.95	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4060	16621	29010	1.27	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4795	17309	29887	0.71	1.0E-124	BE220437.1	EST_HUMAN	h936c07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176788 3'
4797	17311	29890	1.68	1.0E-124	AB024068.1	NT	Homo sapiens gene for B120, exon 11
5016	17625		1.26	1.0E-124	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5230	17732	30101	0.8	1.0E-124	AW963390.1	EST_HUMAN	EST375463 IMAGE resequences, MAGH Homo sapiens cDNA
5549	18139	30498	13.4	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5941	18519	31202	0.96	1.0E-124	4508786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
6177	18745	31446	0.69	1.0E-124	BF696135.1	EST_HUMAN	002124644F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:4281636 5'
6483	19038	31778	0.82	1.0E-124	AV711263.1	EST_HUMAN	AV711263 Cu Homo sapiens cDNA clone CUAADF07 5'
6772	19315	32082	0.83	1.0E-124	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7433	19937	32770	3.08	1.0E-124	Y11717.1	NT	M.musculus mRNA for hoxa3 gene
7577	20027	32871	0.97	1.0E-124	BE271295.1	EST_HUMAN	000943771F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:2866585 5'
7577	20027	32872	0.97	1.0E-124	BE271295.1	EST_HUMAN	000943771F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:2866585 5'
8097	20498	33377	0.82	1.0E-124	AA630331.1	EST_HUMAN	ac08h05.s1 Stratagene Helix cell s3 837216 Homo sapiens cDNA clone IMAGE:855697 3'
8441	20855	33756	0.42	1.0E-124	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
8441	20855	33757	0.42	1.0E-124	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
8819	21253	34159	9.87	1.0E-124	4508654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8976	21408	34322	1.48	1.0E-124	AW612106.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:085162
8976	21408	34323	1.48	1.0E-124	AW612106.1	EST_HUMAN	085162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE ;
9688	22100	35028	4.5	1.0E-124	AV645633.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2853240 3' similar to TR:085162
9688	22100	35029	4.5	1.0E-124	AV645633.1	EST_HUMAN	085162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE ;
9688	22100	35029	4.5	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9771	22174	35106	8.43	1.0E-124	AJ767133.1	EST_HUMAN	AV646633 GLC Homo sapiens cDNA clone GLCACE04 3'
9771	22174	35107	8.43	1.0E-124	AJ767133.1	EST_HUMAN	w93102.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
9946	22348	35288	1.51	1.0E-124	AW503755.1	EST_HUMAN	w93102.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
10828	23284	36250	1.87	1.0E-124	U94778.1	NT	UJ-HF-BNO-ek2-b-04-0-UJ1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3078946 5'
10828	23284	36250	1.87	1.0E-124	U94778.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11094	23518	36664	6.68	1.0E-124	AW66663.1	EST_HUMAN	h05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980908 3'
11226	22878	35854	4.26	1.0E-124	A1446455.1	EST_HUMAN	i19e03.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31682 O31662 YKRS PROTEIN.;
11226	22878	35855	4.28	1.0E-124	A1446455.1	EST_HUMAN	i19e03.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31682 O31662 YKRS PROTEIN.;
11731	13272	25691	4.3	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG [RETROVIRAL ELEMENT];
11731	13272	25692	4.3	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG [RETROVIRAL ELEMENT];
12198	24315	30914	1.4	1.0E-124	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12486	24826	30591	1.81	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12486	24826	30592	1.81	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
333	12928		7.08	1.0E-125	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
443	12821	25008	6.24	1.0E-125	BE743922.1	EST_HUMAN	601377981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
663	13228	25639	16.54	1.0E-125	A110656.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
663	13228	25640	16.54	1.0E-125	A110656.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
748	13308	25733	1.87	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
883	13438	25896	2.32	1.0E-125	AA042813.1	EST_HUMAN	z633c07.s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857.cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
1025	13576	26017	1.24	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS210010
1181	13723	26102	1.53	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1672	15317	26677	2.27	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1787	14312	26806	5.36	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1787	14312	26806	5.36	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2411	14915	27433	3.74	1.0E-125	AA042813.1	EST_HUMAN	z633c07.s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857.cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2520	15020	27635	2.58	1.0E-125	4504698	NT	Homo sapiens inhibitor, alpha (INH-A) mRNA
2520	15020	27636	2.58	1.0E-125	4504698	NT	Homo sapiens inhibitor, alpha (INH-A) mRNA
2525	15024	27540	17.07	1.0E-125	A1732968.1	EST_HUMAN	ch64d02.x5 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1471778 3'
3864	16400	28805	1.01	1.0E-125	AA042813.1	EST_HUMAN	z633c07.s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857.cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4586	17102	29492	2.71	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4586	17102	29493	2.71	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4660	17176	29556	0.88	1.0E-125	BE315412.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140786 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6037	18611	31289	0.58	1.0E-125	BF683645.1	EST_HUMAN	602139874F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4300770 5'
6161	18728	31433	1.64	1.0E-125	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
6182	18749	31449	1.22	1.0E-125	BE175169.1	EST_HUMAN	QV2-HT0577-010500-165-B08 HT0577 Homo sapiens cDNA
6229	18784	31502	3.46	1.0E-125	BE892680.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6278	18838	31554	0.82	1.0E-125	AI679904.1	EST_HUMAN	U07C07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2286108 3' similar to WP:C45G9.2
6606	19157	31805	0.7	1.0E-125	BE736055.1	EST_HUMAN	601305670F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640097 5'
6934	19473	32251	5.54	1.0E-125	BE562528.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
6934	19473	32252	5.54	1.0E-125	BE562528.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7483	19697	32494	4.53	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
7483	19697	32495	4.53	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
8039	20471	33345	0.95	1.0E-125	BE278823.1	EST_HUMAN	601169076F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5'
8310	20725	33618	0.42	1.0E-125	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8408	20820	33717	0.48	1.0E-125	BE515100.1	EST_HUMAN	601236183F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608084 5'
8934	21466	34376	1.16	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9034	21466	34376	1.16	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9421	21853	34767	11.64	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
9421	21853	34768	11.64	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
9608	22086	35014	1.13	1.0E-125	AI565998.1	EST_HUMAN	U02B03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089
10473	22923	35903	3.99	1.0E-125	AF043458.1	NT	HYPOTHETICAL PROTEIN;
10554	23001	35985	1.85	1.0E-125	AW131202.1	EST_HUMAN	Homo sapiens HREL gene, exon 5
10554	23001	35985	1.85	1.0E-125	AW131202.1	EST_HUMAN	Xf59f02.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284
10554	23001	35985	1.85	1.0E-125	AW131202.1	EST_HUMAN	LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];
10630	23072	36058	1.68	1.0E-125	11425570	NT	Xf59f02.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284
10800	23313	36311	36.18	1.0E-125	AL040655.1	EST_HUMAN	LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];
10813	23345	36353	2.94	1.0E-125	AB014567.1	NT	Homo sapiens ryanodine receptor 1 (skeletal) (RYR1), mRNA
11059	23485	36511	2.48	1.0E-125	7668505	NT	DKFZp434N2414.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N2414.6
11064	23480	36516	10.99	1.0E-125	AF026029.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11155	23536	36574	2.01	1.0E-125	AW812899.1	EST_HUMAN	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11257	23623	36670	4.48	1.0E-125	BE074267.1	EST_HUMAN	RC3-ST0188-260200-018-c11 ST0188 Homo sapiens cDNA
							QV3-BT0569-020200-076-g09 BT0569 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11257	23623	38871	4.48	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0568-020200-075-g09 BT0568 Homo sapiens cDNA
796	13354	25790	4.27	1.0E-126	4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
799	13357	25793	1.45	1.0E-126	M81936.1	NT	Human laminin B1 chain gene, exon 20
842	13495	25937	4.28	1.0E-126	X68735.1	NT	H. sapiens gene for alpha1-antichymotrypsin, exon 3
2239	14748	27268	2.23	1.0E-126	8923058	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2239	14748	27269	2.23	1.0E-126	8923058	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2522	15022	27537	3.32	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3033	15888	27999	8.17	1.0E-126	AA160709.1	EST_HUMAN	zo72c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3033	15888	28000	8.17	1.0E-126	AA160709.1	EST_HUMAN	zo72c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3034	15589	28001	0.76	1.0E-126	BF510408.1	EST_HUMAN	U1H-B14-acc-b-05-0-U1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084608 3'
3034	15589	28002	0.76	1.0E-126	BF510408.1	EST_HUMAN	U1H-B14-acc-b-05-0-U1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084608 3'
3627	16167	28576	0.97	1.0E-126	X63941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3656	16195	28602	2.64	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4839	17351	29734	1.2	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4839	17351	29735	1.2	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4891	17403	29774	2.63	1.0E-126	N34078.1	EST_HUMAN	yx78c06.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:267850 5'
5973	18549	31234	0.72	1.0E-126	T66998.1	EST_HUMAN	yx62b12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66527 3'
6553	19105	31849	4.11	1.0E-126	AA460075.1	EST_HUMAN	zx66e03.r1 Soares_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:798444 5' similar to
6915	19165	31816	3.79	1.0E-126	AB040958.1	NT	TR:G1145880 G1145880 TITIN ;
6915	19169	31917	3.79	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
8004	20437	33304	1.08	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8004	20437	33305	1.06	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8243	20860	33550	0.6	1.0E-126	AU136463.1	EST_HUMAN	AU136463 PLACE1 Homo sapiens cDNA clone PLACE1004325 5'
8309	20724	33617	0.61	1.0E-126	AI808483.1	EST_HUMAN	wf08f01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350009 3' similar to
8625	21060	33968	2.57	1.0E-126	X16809.1	NT	SW:MPP2_HUMAN Q14168 MAGUK P65 SUBFAMILY MEMBER 2 ;
							Human mRNA for ankryrin (variant 2.1)
8764	21188	34100	1.09	1.0E-126	AA483668.1	EST_HUMAN	ne74b12.s1 NCI CGAP Ew1 Homo sapiens cDNA clone IMAGE:909983 similar to SW:TSg6_HUMAN
10575	23022	36007	1.74	1.0E-126	M93186.1	NT	P98068 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR ;
10840	23081	36085	2.18	1.0E-126	BF683175.1	EST_HUMAN	Human macrophage mannose receptor (MRC1) gene, exon 5
11270	23638	36087	0.48	1.0E-126	BE261660.1	EST_HUMAN	602139138F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298240 5'
11458	23817	36378	3.62	1.0E-126	AF077820.1	NT	601149-04F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3602129 5'
							Homo sapiens LDL receptor member LR3 mRNA, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12235	18012	30444	3.04	1.0E-126	BE743922.1	EST_HUMAN	601577981.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
176	12780	25185	5.06	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
176	12780	25188	5.06	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	12780	25195	3.17	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	12780	25188	3.17	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
287	12884	25303	3.23	1.0E-127	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
287	12884	26304	3.23	1.0E-127	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
804	13468	25907	0.86	1.0E-127	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
839	13492	25938	1.72	1.0E-127	U72821.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1698	14218	26688	1.03	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
1990	14508	27014	3.19	1.0E-127	5803055	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
1990	14508	27015	3.19	1.0E-127	5803055	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2105	14619	27139	17.75	1.0E-127	4506820	NT	Homo sapiens ribosomal protein L28 (RPL28) mRNA
2237	14748	27288	2.71	1.0E-127	AF245505.1	NT	Homo sapiens adiccan mRNA, complete cds
2637	15035	27551	7.84	1.0E-127	X12881.1	NT	Human mRNA for cytokeratin 18
2551	15050	27565	3.97	1.0E-127	AA450131.1	EST_HUMAN	zx42a02.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
2551	15050	27568	3.97	1.0E-127	AA450131.1	EST_HUMAN	zx42a02.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
							au80e08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR-Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22 repetitive element ;
3819	16356	28756	0.67	1.0E-127	AW161287.1	EST_HUMAN	Homo sapiens delayed rectifier potassium channel subunit 1aK mRNA, complete cds
4133	16681	29048	0.74	1.0E-127	AF135188.1	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4270	16795	29177	23.96	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4270	16795	29178	23.96	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4633	17051	29434	0.83	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 reductase metabolizing protein P450RA1-2 mRNA, complete cds
4643	17169	29538	6.43	1.0E-127	45069394	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4677	17193		2.55	1.0E-127	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
4715	17231	29614	1.63	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
							zad1a10.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291258 5' similar to SW:P1P6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 ;
5977	18553	31238	2.26	1.0E-127	W03547.1	EST_HUMAN	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
6012	18598	31273	0.83	1.0E-127	4826863	NT	Homo sapiens NOS2 gene, exon 6
6086	18656	31350	4.93	1.0E-127	X85764.1	NT	Homo sapiens NOS2 gene, exon 6

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6476	19031	31766	2.41	1.0E-127	XB4060.1	NT	H.sapiens TCF11 gene, exon 3-6
6849	18187	31848	5.93	1.0E-127	4504778	NT	Homo sapiens Integrin, beta 8 (ITGB8) mRNA
7024	19560	32347	1.1	1.0E-127	11421595	NT	Homo sapiens Immunoglobulin superfamily, member 3 (IGSF3), mRNA
7494	19698	32498	0.76	1.0E-127	4826977	NT	Homo sapiens reelin (RELN) mRNA
8346	20761	33667	1.38	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
8346	20761	33668	1.38	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
8363	20778	33678	0.66	1.0E-127	BF071355.1	EST_HUMAN	602151232F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4292575 5'
8368	20781	33681	0.67	1.0E-127	AW896292.1	EST_HUMAN	QV3-BN0046-150300-121-h11 BN0046 Homo sapiens cDNA
9791	22184	35131	4.45	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9791	22184	35132	4.45	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
8948	22350	35298	0.93	1.0E-127	AI298832.1	EST_HUMAN	gm94h08.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896449 3'
10269	22870	35633	1.65	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
10936	23368	36376	8.05	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H. sapiens) (LOC63184), mRNA
10936	23368	36377	8.05	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H. sapiens) (LOC63184), mRNA
11376	23738	36796	4.3	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3919917 5'
11376	23738	36797	4.3	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3919917 5'
11965	12780	25195	2.88	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
11965	12780	25198	2.88	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12184	24304	30944	2.2	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-9, complete cds
477	13051	25469	1.84	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3618822 5'
1183	13725	26164	1.34	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1183	13725	26165	1.34	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1995	14511	27019	19.31	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
1995	14511	27020	19.31	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2115	14828	27151	24.89	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3372	15918	28336	1.33	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4708	17224	28608	6.34	1.0E-128	11426673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5809	18369	31050	0.68	1.0E-128	X69539.1	NT	H.sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6757	19300	32095	1.29	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7340	19762	32566	6.71	1.0E-128	BF224345.1	EST_HUMAN	7q86b10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
7812	20351	33219	0.5	1.0E-128	BE614105.1	EST_HUMAN	601603846F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3905794 5'
8260	20877	33567	0.64	1.0E-128	BF529831.1	EST_HUMAN	602042322F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179888 5'

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8260	20877	33568	0.64	1.0E-128	BF528931.1	EST_HUMAN	602042322F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4179988 5'
8260	20877	33569	0.64	1.0E-128	BF528931.1	EST_HUMAN	602042322F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4179988 5'
8367	20782	33682	0.66	1.0E-128	11546923	NT	Homo sapiens putative ABC transporter (WHITE2), mRNA
10494	22944	35925	2.74	1.0E-128	11426284	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
10504	22953	35934	3.79	1.0E-128	AA926989.1	EST_HUMAN	am88108.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
10579	23026	36010	2.24	1.0E-128	AL252060.1	NT	Homo sapiens mRNA for TRABID protein (TRABID gene)
10634	23075	36060	2.28	1.0E-128	BE394475.1	EST_HUMAN	601277826F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818760 5'
10748	23186	36172	2.64	1.0E-128	BE887594.1	EST_HUMAN	601811912F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913371 5'
11827	24080		6.3	1.0E-128	AW955290.1	EST_HUMAN	EST367360 MAGE resequencing, MAGC Homo sapiens cDNA
128	13004	25432	1.56	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
430	13004	25432	1.27	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1716	14244	26727	2.6	1.0E-128	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1720	14248	26731	1.32	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1720	14248	26732	1.32	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1818	14340	26835	2.48	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
2737	15227	27738	2.35	1.0E-128	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
2737	15227	27739	2.35	1.0E-128	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
3089	15843	28061	1.34	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3089	15843	28062	1.34	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3089	15843	28063	1.34	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4180	16707	28097	2.2	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4297	16922	28206	1.99	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
4297	16922	28207	1.99	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
6399	18958	31690	4.95	1.0E-129	AJ006345.1	NT	Cardiomyopathy associated gene 5
6876	19416	32190	0.75	1.0E-129	BE888934.1	EST_HUMAN	Homo sapiens KVLQT1 gene
7324	19736	32539	0.59	1.0E-129	BE869933.1	EST_HUMAN	601513861F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3916350 5'
7324	19736	32540	0.59	1.0E-129	BE869933.1	EST_HUMAN	601449740F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853688 5'
7567	20017	32861	3.62	1.0E-129	AJ006345.1	NT	601449740F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3853688 5'
7634	20081	32934	7.86	1.0E-129	11420850	NT	Homo sapiens KVLQT1 gene
							Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63684), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8035	20467	33340	0.87	1.0E-128	AF041058.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8036	20467	33341	0.87	1.0E-128	AF041058.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8864	21288		3.82	1.0E-129	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
10099	22500	35482	1.28	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10098	22500	35483	1.28	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10984	23423	36440	4.08	1.0E-128	AA625528.1	EST_HUMAN	af7207.r1 Soares_NhHMPu_ST Homo sapiens cDNA clone IMAGE:1047589 5'
11068	20081	32834	19.88	1.0E-128	11420850	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63684), mRNA
11814	24071		3.26	1.0E-129	H83155.1	EST_HUMAN	Y49c05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:189112 5' similar to
12227	24336		1.67	1.0E-128	AL120739.1	EST_HUMAN	SP-B48150 B48150 HP-25-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS-ASIAN ;
79	12697	25110	0.94	1.0E-130	7705630	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
1201	13742	26188	1.57	1.0E-130	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1666	14197	26871	20.44	1.0E-130	BE275192.1	EST_HUMAN	601121895F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346368 5'
1666	14197	26872	20.44	1.0E-130	BE275192.1	EST_HUMAN	601121895F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346368 5'
1927	14446		1.53	1.0E-130	X04082.1	NT	Human gene for cathepsin (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2729	15219		4.84	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2833	15389	27801	1.39	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
2833	15389	27802	1.39	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3568	16110	28525	1.25	1.0E-130	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3768	15389	27801	6.69	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3768	15389	27802	6.69	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3949	16484	28893	1.82	1.0E-130	AW503580.1	EST_HUMAN	UHF-BNO-ky-g-08-D-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4087	16618	29006	0.89	1.0E-130	M9710.1	NT	Human T-cell receptor (V alpha 22.1, J alpha RPL4285-variant, C alpha 1) mRNA
4574	17091	29478	9.57	1.0E-130	AW843993.1	EST_HUMAN	CNA-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA
6234	17736	30106	1.35	1.0E-130	AW363299.1	EST_HUMAN	RCO-CT0318-201189-031-e11 CT0318 Homo sapiens cDNA
5234	17736	30107	1.35	1.0E-130	AW363299.1	EST_HUMAN	RCO-CT0318-201189-031-e11 CT0318 Homo sapiens cDNA
7106	19839	32434	0.66	1.0E-130	X57826.1	NT	Human germline immunoglobulin lambda light chain pseudogene (Vil.1)
7212	19824	32638	0.97	1.0E-130	AW843875.1	EST_HUMAN	CNA-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
7212	19824	32639	0.97	1.0E-130	AW843875.1	EST_HUMAN	CNA-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
7228	19840	32687	0.73	1.0E-130	11425446	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7704	20149	33006	2.02	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7820	20261	33121	0.62	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7820	20261	33122	0.62	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9229	21681	34570	2.8	1.0E-130	AW88242.1	EST_HUMAN	EST368312 IMAGE resequences, MAGD Homo sapiens cDNA
9487	21918	34842	1.77	1.0E-130	AB037758.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
11043	23469	36492	2.38	1.0E-130	8923197	NT	Homo sapiens hypothetical protein FLJ20208 (FLJ20208), mRNA
11043	23469	36493	2.38	1.0E-130	8923197	NT	Homo sapiens hypothetical protein FLJ20208 (FLJ20208), mRNA
11428	23789	36850	2.94	1.0E-130	4504142	NT	Homo sapiens glutamate receptor, metabotropic 8 (GRM5) mRNA
4	12825	25012	2.31	0.0E+00	AA228126.1	EST_HUMAN	z58c04.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:687590 5' similar to TR:G222811
4	12825	25013	2.31	0.0E+00	AA228126.1	EST_HUMAN	z58c04.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:687590 5' similar to TR:G222811
7	12827	25018	1.61	0.0E+00	4885136	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;
15	12835	25022	1.57	0.0E+00	8923349	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
15	12835	25023	1.57	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
22	12842	25030	4.2	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
22	12842	25031	4.2	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
28	12848	25038	6.57	0.0E+00	AF141349.1	NT	Homo sapiens DCRR1 mRNA, partial cds
36	12856	25046	1.29	0.0E+00	5802997	NT	Homo sapiens beta-tubulin mRNA, complete cds
38	12868	25049	0.88	0.0E+00	M88600.1	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
42	12862	25054	3.29	0.0E+00	8857825	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
59	12879	25081	9.18	0.0E+00	Y17151.2	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
59	12879	25082	9.18	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	12881	25086	1.38	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	12881	25087	1.38	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
62	12882	25088	13.98	0.0E+00	L16558.1	NT	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
64	12884	25091	11.54	0.0E+00	AW069834.1	EST_HUMAN	Human ribosomal protein L7 (RPL7) mRNA, complete cds
64	12884	25092	11.54	0.0E+00	AW069834.1	EST_HUMAN	cr48c07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBIMSC cr48c07 3'
68	12887	25096	5.51	0.0E+00	M60878.1	EST_HUMAN	cr48c07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBIMSC cr48c07 3'
70	12889		5.62	0.0E+00	M60878.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
78	12606	25108	5.32	0.0E+00	4758977	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
78	12606	25109	5.32	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
81	12608	25108	2.25	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
81	12608	25109	2.25	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
84	12701	25115	0.82	0.0E+00	4501850	NT	Homo sapiens anilofide binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
85	12702		15.17	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
94	12711	25124	44.65	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
97	12714	25127	28.51	0.0E+00	U89277.1	NT	Human polyomavirus 1 homolog (HPH1) mRNA, partial cds
104	12721	25134	3.22	0.0E+00	AI114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
105	12722	25135	1.41	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
111	12726	25139	0.83	0.0E+00	X81213.1	NT	H. sapiens next1 gene (exon 2)
120	12732	25145	0.86	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q89551 Q89551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
121	12732	25145	1.28	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q89551 Q89551
122	16253	25146	1.84	0.0E+00	N36040.1	EST_HUMAN	MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
122	16253	25147	1.84	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270017 5'
125	12735	25152	2.11	0.0E+00	4505458	NT	yy01h09.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270017 5'
135	12741	25160	4.28	0.0E+00	4505938	NT	Homo sapiens neuroligin 2 (NRP2) mRNA
135	12741	25161	4.28	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
143	12992	25166	1.15	0.0E+00	4503680	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
145	12748	25168	1.05	0.0E+00	T56945.1	EST_HUMAN	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
145	12749	25169	1.05	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
157	12782		14.16	0.0E+00	4504444	NT	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
161	12786	25182	1.87	0.0E+00	BF036881.1	EST_HUMAN	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
163	12788		42.85	0.0E+00	4504444	NT	G01460375F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863803 5'
168	12771	25185	0.92	0.0E+00	AF111183.2	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
168	12773	25186	0.87	0.0E+00	BE289973.1	EST_HUMAN	Homo sapiens epsilon palmitoyl transferase, subunit II gene, complete cds, and unknown genes
169	12773	25186	0.7	0.0E+00	BE289973.1	EST_HUMAN	G01174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528864 5'
170	12774	25187	2.84	0.0E+00	W79973.1	EST_HUMAN	G01174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528864 5'
171	12776	25188	0.59	0.0E+00	BE162832.1	EST_HUMAN	zid82b05.r1 Soares_fetal_heard_NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
171	12775	25189	0.59	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
172	12776	25190	1.27	0.0E+00	AF244088.1	NT	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
176	12779	25193	16.54	0.0E+00	AL163202.2	NT	Homo sapiens zinc finger protein mRNA, complete cds
175	12779	25194	16.54	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
185	12787	25201	5.09	0.0E+00	BE018970.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
185	12787	25202	5.09	0.0E+00	BE018970.1	EST_HUMAN	b524e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631 ;
							b524e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
190	12762	25205	2.93	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
190	12762	25206	2.93	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	12763	25207	2.53	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	12763	25208	2.53	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
200	12803	25220	103.51	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
205	12808	25225	4.27	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set14-3 mRNA, complete cds
205	12808	25226	4.27	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set14-3 mRNA, complete cds
207	12810	25228	4.22	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
207	12810	25229	4.22	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
217	15278	25236	14.31	0.0E+00	AI587308.1	EST_HUMAN	lq04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN1 (HUMAN);
217	15278	25237	14.31	0.0E+00	AI587308.1	EST_HUMAN	lq04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN1 (HUMAN);
219	12821	25239	1.95	0.0E+00	AF195958.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
222	12824		18.76	0.0E+00	4506832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
223	12825		8.83	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
229	12831	25244	2.38	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
230	12831	25244	2.08	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
231	12832	25245	2.68	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA
238	12840	25249	0.67	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
238	12840	25250	0.67	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
238	12840	25251	0.67	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
239	12840	25249	0.65	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
239	12840	25250	0.65	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
239	12840	25251	0.65	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
247	12848	25262	4.46	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0768 protein, partial cds
247	12848	25263	4.46	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0768 protein, partial cds
251	12851	25268	5.49	0.0E+00	6453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
263	12853		5.16	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
260	12858	25275	3.28	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
262	12860	25278	2.01	0.0E+00	X69772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
270	12868		9.68	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
283	12880	25297	1.24	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
283	12880	25298	1.24	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
285	12882	25300	2.17	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC61250), mRNA
296	12892		1.4	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
297	12893	25313	2.25	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
297	12893	25314	2.25	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
298	12894		1	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181198-020-B03 CT003.1 Homo sapiens cDNA
307	12902	25321	7.98	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
307	12902	25322	7.66	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
318	12913	25332	5.38	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
318	12914	25333	3.87	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
320	15281		9.69	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
321	12915	25334	0.63	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
322	12916		2.89	0.0E+00	AA480002.1	EST_HUMAN	zv18c06.r1 Soares NIHMPu, S1 Homo sapiens cDNA clone IMAGE:753994 5'
323	12917	25335	18.21	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
324	12917	25335	20.52	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
328	12921	25339	1.58	0.0E+00	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
341	12933	25348	1.12	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
341	12933	25349	1.12	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
342	12934	25350	5.45	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
343	12934	25350	2.15	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
358	12948	25362	8.22	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL4) mRNA
369	12949	25363	2.07	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
362	12952	25367	8.78	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
365	12955	25372	1.56	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds
370	12959	25376	2.06	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
370	12959	25377	2.06	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
371	15282	25378	2.71	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
373	12961	25380	0.91	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
376	12964	25384	1.58	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GBPA), mRNA
377	12965	25385	1.54	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
378	12965	25385	1.43	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
380	12967	25387	0.95	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
391	12976	25398	3.09	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
402	13018	25442	8.24	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
403	13019	25443	1.03	0.0E+00	AJ363014.1	EST_HUMAN	qy81h05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:354199
408	12984	25405	1.6	0.0E+00	AW764180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LYASE (HUMAN);
411	12988	25408	2.28	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
412	12987	25409	2.88	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
412	12987	25410	2.86	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
413	12988	25411	1.84	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
414	12988	25412	1.73	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
414	12989	25413	1.73	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
415	12990	25414	1.38	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
416	12991	25415	3.02	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
417	12992	25416	1.58	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
418	12993	25417	1.42	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
418	12993	25418	1.42	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
419	12993	25417	1.58	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
419	12993	25418	1.58	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
423	12997		48.38	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
437	12615	25002	1.32	0.0E+00	R17785.1	EST_HUMAN	yg08a02.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31652 5'
445	13020	25444	1.05	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
446	13021		8.07	0.0E+00	4506728	NT	phosphoribosylamimidazole synthetase (GART) mRNA
447	13022	25445	3.69	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
448	13023	25446	8.58	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
448	13023	25447	8.58	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
449	13024	25448	4.28	0.0E+00	AF183507.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
461	13035		0.78	0.0E+00	AL163201.2	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
463	13037	25461	4.21	0.0E+00	4567879	NT	Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
488	13042		0.8	0.0E+00	AA324282.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' and
489	13043		1.04	0.0E+00	BE254447.1	EST_HUMAN	601111520F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3352348 5'
485	13059	25476	3.5	0.0E+00	4504632	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
485	13059	25476	3.5	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
491	13064	25484	5.55	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
491	13064	25485	5.55	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
501	13075	25491	3.25	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
502	13076	25492	6.81	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
502	13076	25493	6.81	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
511	13084	25498	4.94	0.0E+00	AB030355.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
513	13088	25500	1.82	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
521	13094	25506	2.32	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616766 5'
522	15285	25507	1.26	0.0E+00	AW936825.1	EST_HUMAN	PMO-DT0066-130400-002-c08 DT0065 Homo sapiens cDNA
525	13097	25509	1.13	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
526	13098	25510	1.07	0.0E+00	8823955	NT	Homo sapiens PCS28 protein (PCS28), mRNA
530	13102		0.76	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
537	13109	25520	6.87	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
544	16286	25524	1.89	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
549	13121	25530	1.77	0.0E+00	BF028005.1	EST_HUMAN	601784859F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996908 5'
555	13127	25537	1.28	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
568	13130	25540	8.8	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
559	13131	25541	4.21	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
559	13131	25542	4.21	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
565	13136		5.28	0.0E+00	AF003528.1	NT	UI-H-B11-ecb-h-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
573	13144	25552	1.44	0.0E+00	AW135324.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
583	13154		4.68	0.0E+00	D10083.1	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
603	13172	25577	1.42	0.0E+00	5174742	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
616	13184		7.27	0.0E+00	J04066.1	NT	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
619	13187	25591	2.11	0.0E+00	BF104898.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
621	13189	25593	0.7	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
621	13189	25594	0.7	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
622	13189	25593	0.88	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
622	13189	25694	0.88	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
623	13189	25693	1.08	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
623	13189	25694	1.08	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
628	13182	25697	0.83	0.0E+00	4501864	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
633	13187	25693	1.39	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
633	13187	25694	1.38	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
641	13206	25612	3.17	0.0E+00	AF14973.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
643	13207	25616	0.81	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1388 protein, partial cds
645	13209	25618	0.85	0.0E+00	8808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
648	13210	25617	1.71	0.0E+00	8808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
648	13210	25618	1.71	0.0E+00	8808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
647	13211	25619	0.85	0.0E+00	8808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
647	13211	25620	0.85	0.0E+00	8808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
654	13219	25630	1.41	0.0E+00	AA399486.1	EST_HUMAN	z60c07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728732 5'
658	13223	25634	5.83	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
662	13227	25637	24.68	0.0E+00	W79811.1	EST_HUMAN	zh51b04.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415587 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
662	13227	25638	24.88	0.0E+00	W79811.1	EST_HUMAN	zh51b04.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415587 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
665	13230		4.4	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
672	13237	25650	2.98	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
674	13239	25653	1.3	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
677	13242	25657	1.43	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
681	13246	25680	1.19	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
681	13246	25681	1.16	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
687	13251	25666	4.84	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
687	13251	25687	4.84	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
693	15289		1.26	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
702	13264	25681	9.4	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosome) protein 1 (HMG1) mRNA
707	13289	25685	3.74	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
717	13278	25700	3.48	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
729	13290	25714	53.12	0.0E+00	AA614537.1	EST_HUMAN	np49d01.e1 NCJ CGAP_B1.1 Homo sapiens cDNA clone IMAGE:1128633 3' similar to gb:X67352
733	13294	25718	12.8	0.0E+00	M60676.1	NT	INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN); Human von Willebrand factor gene, exons 23 through 34

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
733	13284	25719	12.8	0.0E+00	M60876.1	NT	Human von Willebrand factor gene, exons 23 through 34
743	13304	25728	1.88	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
749	13309	25734	4.85	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
749	13309	25735	4.85	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
751	13311	25738	11.82	0.0E+00	11845800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
757	13317	25746	2.35	0.0E+00	BE241577.1	EST_HUMAN	TCAAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP0779
777	13336	25770	3.05	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
777	13336	25771	3.05	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
780	13339	25774	8.37	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
780	13339	25775	8.37	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
783	13342	25776	1	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
784	13343	25777	1.33	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
786	15293	25779	1.34	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
787	13346	25780	2.28	0.0E+00	BE869735.1	EST_HUMAN	601446847F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3849803 5'
791	13348	25784	4.17	0.0E+00	R48915.1	EST_HUMAN	y58908.1 Spores breast 2NbhBst Homo sapiens cDNA clone IMAGE:154046 5'
792	13350	25785	3.22	0.0E+00	5032088	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
801	13359	25784	1.81	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
804	13363	25798	2.98	0.0E+00	7681965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
815	13373	25810	1.15	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
815	13373	25811	1.15	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
820	13378	25815	2.83	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
824	13382	25819	4.46	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
824	13382	25820	4.46	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
829	13386	25826	10.33	0.0E+00	5174478	NT	Homo sapiens pericentriin (PCNT) mRNA
830	13387		8.7	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
847	13404	25847	1.73	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
848	13405	25848	3.66	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	13407	25850	3.21	0.0E+00	4557868	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
856	13412	25856	1.5	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
856	13412	25857	1.5	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
867	13413	25858	0.85	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
862	13418	25863	1.55	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GBPA), mRNA
866	13421	25868	2.9	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
868	13421	25869	2.9	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
873	13428		1.83	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC6A3) gene, complete cds
877	13432	25880	5.39	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
877	13432	25881	5.39	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
878	13433	25882	10.17	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
879	13434	25883	4.21	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
880	13435	25884	5.55	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
884	13439	25887	1.34	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
884	13439	25888	1.34	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
885	13440	25889	2.51	0.0E+00	AA533272.1	EST_HUMAN	U66d07.e1 NCI CGAP_P10 Homo sapiens cDNA clone IMAGE:997453
885	13440	25890	2.51	0.0E+00	AA533272.1	EST_HUMAN	U66d07.e1 NCI CGAP_P10 Homo sapiens cDNA clone IMAGE:997453
886	13441		6.56	0.0E+00	BF677694.1	EST_HUMAN	60208578F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:424915 5'
890	13445	25891	1.47	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
890	13445	25892	1.47	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	13446	25893	3.31	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	13446	25894	3.31	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
914	13488	25917	1.08	0.0E+00	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
921	13475	25922	2.12	0.0E+00	BE089592.1	EST_HUMAN	QVO-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
921	13475	25923	2.12	0.0E+00	BE089592.1	EST_HUMAN	QVO-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
931	13485	25932	2.83	0.0E+00	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
941	13494		13.1	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
944	13494		8.4	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
945	13497	25940	3.38	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antitrypsin precursor, mRNA, partial cds
948	13498	25941	2.28	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds
948	13501	25944	0.96	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
949	13501	25945	0.96	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
950	13502	25946	1.38	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
950	13502	25947	1.38	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
975	13526	25970	2.8	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
976	13529	25971	9.71	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
977	13530	25972	1.53	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
978	13531	25973	2.26	0.0E+00	4507430	NT	Homo sapiens thymidic embryonic factor (TEF), mRNA
978	13531	25974	2.26	0.0E+00	4507430	NT	Homo sapiens thymidic embryonic factor (TEF), mRNA
986	15298	25981	2.66	0.0E+00	AI001948.1	EST_HUMAN	os98e03.s1 NCI CGAP_GC3 Homo sapiens cDNA clone IMAGE:1013404 3'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
989	13298	25982	2.69	0.0E+00	AI001948.1	EST_HUMAN	os88e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1813404 3'
988	13540	25984	9.3	0.0E+00	7657266	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
989	13550	25984	3.44	0.0E+00	AB030568.1	NT	Homo sapiens mRNA for PSP24, complete cds
1008	13559	26001	1.81	0.0E+00	BF386974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1008	13559	26002	1.81	0.0E+00	BF386974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1008	13559	26003	1.81	0.0E+00	BF386974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1010	13561	26006	3.12	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1010	13561	26007	3.12	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1018	13570	26014	1.68	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
1031	13581	26022	1.21	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1032	13582	26023	8.88	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1033	13582	26023	8.27	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1039	13585		4.93	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1037	13585		9.13	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1040	13588	26028	1.67	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1041	13588	26028	4.07	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1042	13588	26028	2.76	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1043	13589	26028	2.2	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1046	13592	26032	2.52	0.0E+00	7681685	NT	Homo sapiens DKFZP686M0122 protein (DKFZP686M0122), mRNA
1050	13596	26036	1.69	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1051	13597		2.03	0.0E+00	AA458880.1	EST_HUMAN	sa86g07.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PR58_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8 ;
1054	13600	26040	1.55	0.0E+00	N43182.1	EST_HUMAN	EST51124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1054	13600	26041	1.55	0.0E+00	N43182.1	EST_HUMAN	EST51124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1055	13601	26042	1.41	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1056	13601	26043	1.41	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1058	13604	26059	4.67	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ111198 (FLJ11198), mRNA
1073	13619	26074	2.26	0.0E+00	4758563	NT	Homo sapiens heat shock 70kD protein 95 (hsc70) (HSPA95) mRNA
1091	13638	26074	1.98	0.0E+00	4828672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1081	13638	26075	1.98	0.0E+00	4828672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1085	13640	26079	3.19	0.0E+00	8922624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1095	13640	26080	3.19	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20685 (FLJ20685), mRNA
1098	13641	26081	19.5	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1098	13643		0.99	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1100	13645	26085	3.13	0.0E+00	5174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1109	13653	26096	2.94	0.0E+00	4768117	NT	Homo sapiens Death associated protein 3 (DAP3), mRNA
1123	13657	26108	1.97	0.0E+00	BE006208.1	EST_HUMAN	MRO-BN0115-200300-003-H08 BN0115 Homo sapiens cDNA
1146	13690	26130	5.14	0.0E+00	7708134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1146	13690	26131	5.14	0.0E+00	7708134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1159	13702	26141	1.28	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1159	13702	26142	1.28	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1160	13703	26143	9.97	0.0E+00	4508712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1162	13705	26145	1.03	0.0E+00	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1165	13708	26148	4.01	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2M, complete cds
1167	13710	26149	11.5	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2M, complete cds
1168	13711	26150	3.42	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1168	13711	26151	3.42	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1172	13714	26154	1.31	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1173	13716	26155	0.76	0.0E+00	X95828.1	NT	H.sapiens ART4 gene
1173	13715	26156	0.76	0.0E+00	X95826.1	NT	H.sapiens ART4 gene
1174	13716	26157	0.71	0.0E+00	AI147650.1	EST_HUMAN	q22d10.Xt Soares_pregnant_uterus_Nib-PU Homo sapiens cDNA clone IMAGE:16970113
1178	13718	26159	1.82	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
1185	13727	26168	0.98	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1185	13727	26169	0.88	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1186	13728	26170	1.22	0.0E+00	986844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1199	13740	26183	1.63	0.0E+00	7305078	NT	Homo sapiens glutamate decarboxylase 1 (brain, 87kD) (GAD1), transcript variant GAD25, mRNA
1199	13740	26184	1.63	0.0E+00	7305078	NT	Homo sapiens glutamate decarboxylase 1 (brain, 87kD) (GAD1), transcript variant GAD25, mRNA
1202	13743	26187	1.42	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1209	13750	26196	5.55	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1240	13778		1.06	0.0E+00	7657338	NT	Homo sapiens mitf (E. coli) homolog 3 (MLH3), mRNA
1255	13793	26239	1.01	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1259	13797	26243	1.76	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1259	13797	26244	1.76	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1260	13798	26245	2.24	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1261	15304	26246	1.24	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1279	13815	26289	5.51	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1280	13816	26270	1.71	0.0E+00	4503088	NT	Homo sapiens chondrin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1280	13825	26276	0.64	0.0E+00	4505740	NT	Homo sapiens pifoldin 4 (PFND4) mRNA
1289	13834		1.7	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1307	13842	26291	61.9	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1314	13848	26300	3.11	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
1320	13855	26304	1.84	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1320	13855	26305	1.84	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1332	13868	26318	4.24	0.0E+00	5174748	NT	Homo sapiens Wolfgram syndrome (WFS) mRNA
1332	13868	26319	4.24	0.0E+00	5174748	NT	Homo sapiens Wolfgram syndrome (WFS) mRNA
1332	13868	26320	4.24	0.0E+00	5174748	NT	Homo sapiens Wolfgram syndrome (WFS) mRNA
1333	13869		3.15	0.0E+00	AF096156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1343	15306	26332	1.27	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1343	15308	26333	1.27	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1348	13883	26338	1.12	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1349	13884	26339	1.48	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1351	13886	26340	0.8	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1352	13887	26341	1.37	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1354	13889	26343	4.82	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1355	13890	26344	1.5	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1356	13891	26345	6.48	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1357	13892	26346	5.58	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1357	13892	26347	5.58	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1369	13903	26360	1.19	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1440	13972	26429	1	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cylid gene
1448	13980	26440	1.03	0.0E+00	AI208756.1	EST_HUMAN	qg38b06.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:TZTA1.5 CE14213;
1449	13981	26441	6.18	0.0E+00	6042206	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1457	13989	26451	1.12	0.0E+00	4505846	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1457	13989	26452	1.12	0.0E+00	4505846	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1459	13991	26455	1.62	0.0E+00	7706565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1459	13991	26456	1.62	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1461	13993	26457	7.47	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1488	14001	28468	5.12	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-6glucosyltransferase (alpha1-6fucT) gene, exon 7
1482	14014	28470	0.91	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1482	14014	28480	0.81	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1490	14022	28485	4.87	0.0E+00	AL132989.1	NT	Novel human gene on chromosome 20
1482	14024	28486	1.11	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1498	14028	28491	1.62	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1489	14031	28494	4.92	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1501	14033	28498	1.18	0.0E+00	7681965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1501	14033	28487	1.18	0.0E+00	7681965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1508	14038	28502	4.21	0.0E+00	M80876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1508	14038	28503	4.21	0.0E+00	M80876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1539	14070	28530	2.23	0.0E+00	7708434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51896), mRNA
1550	14082	28543	1.14	0.0E+00	AA481172.1	EST_HUMAN	as34ac3.r1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:816116 5'
1554	14086	28545	16.18	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1554	14086	28548	16.18	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1556	14088	28549	0.95	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1556	14088	28550	0.95	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1557	14089	28551	1.13	0.0E+00	D10894.1	NT	Bovine mRNA for neurocalcin
1559	14091		1.71	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1560	14092	28554	1.08	0.0E+00	M16768.1	NT	Human T-cell receptor gamma chain VJCH1-CII region mRNA, complete cds
1561	14093	28555	4.62	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1561	14093	28556	4.62	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1562	14094	28557	3.44	0.0E+00	7682405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1563	14095		8.16	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1568	14100	28563	8.04	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
1571	14103	28565	1.08	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1571	14103	28568	1.08	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1572	15314		13.83	0.0E+00	4508654	NT	Homo sapiens ribosomal protein L6 (RPL6) mRNA
1573	14104	28567	12.87	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1583	14116	28581	15.4	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1590	14122		1.13	0.0E+00	D00333.1	NT	human c-yes-2 gene
1597	14129	28595	3.08	0.0E+00	Z83738.1	NT	H. sapiens HH2B/e gene
1598	14130	28596	1.9	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA

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1598	14130	26597	1.9	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1599	14131	26598	8.48	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCB0F02 5'
1600	14131	26599	8.48	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCB0F02 5'
1602	15315	26602	1.8	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1605	14136	26603	1.04	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1607	14138	26606	4.06	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1607	14138	26607	4.06	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1609	14140	26608	42.7	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1609	14140	26609	42.7	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1611	14142	26611	1.18	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1624	14155	26625	3.74	0.0E+00	H26973.1	EST_HUMAN	yo76c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1631	14163	26634	1.53	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1631	14163	26635	1.53	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1646	14177	26646	0.92	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-elw-c-04-0-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1684	14195	26668	0.92	0.0E+00	BE144384.1	EST_HUMAN	MR0-HT0168-191199-004-b11 HT0168 Homo sapiens cDNA
1684	14195	26668	0.92	0.0E+00	BE144384.1	EST_HUMAN	MR0-HT0168-191199-004-b11 HT0168 Homo sapiens cDNA
1688	14189	26673	0.97	0.0E+00	AI788104.1	EST_HUMAN	wg81b07.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to
1689	14200	26674	3	0.0E+00	AF057177.1	NT	TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN. ;
1673	14203	26678	1.18	0.0E+00	M29580.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1673	14203	26679	1.18	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1675	14205	26681	10.8	0.0E+00	4557887	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1676	14206	26682	1.83	0.0E+00	7657065	NT	Homo sapiens keratin 18 (KRT18) mRNA
1679	14209	26685	0.94	0.0E+00	BE222374.1	EST_HUMAN	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1679	14209	26686	0.94	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168281 3' similar to TR:O95147 O95147
1681	14210	26689	1.16	0.0E+00	4557670	NT	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1683	14212	26691	2.89	0.0E+00	H30132.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1683	14212	26692	2.89	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbhBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1685	14214	26694	3.06	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (HUMAN);
1685	14214	26695	3.06	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (HUMAN);
1685	14214	26695	3.06	0.0E+00	Z80780.1	NT	yo59e08.r1 Soares breast 3NbhBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1685	14214	26695	3.06	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
1685	14214	26695	3.06	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1688	14217		9.14	0.0E+00	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1696	14224	26708	4.64	0.0E+00	8923841	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1699	14227	26709	0.91	0.0E+00	6463855	NT	Homo sapiens parietal cell material 1 (PCM1), mRNA
1702	14230	26713	1.33	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1702	14230	26714	1.33	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1705	14233	26718	0.93	0.0E+00	4828973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1), mRNA
1711	14239	26725	9.69	0.0E+00	AB028542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1713	14241		1.59	0.0E+00	S94400.1	NT	TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]
1721	14249	26733	1.19	0.0E+00	4557538	NT	Homo sapiens solute carrier family 28 (sulfate transporter), member 2 (SLC28A2), mRNA
1727	15319	26739	0.93	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
1737	14284	26750	2.09	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1766	15320		32.45	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1769	14294	26778	1.95	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300), mRNA
1769	14294	26779	1.95	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300), mRNA
1770	14296	26782	1.87	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1772	15321	26784	3.87	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP), mRNA
1773	14298	26785	0.98	0.0E+00	AA113030.1	EST HUMAN	z165c09.s1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:563066 3'
1783	14308	26788	17.08	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
1786	14310	26801	8.43	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1786	14311	26802	10.84	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), mRNA
1786	14311	26803	10.84	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), mRNA
1786	14311	26804	10.84	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), mRNA
1800	14324	26818	1.03	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1800	14324	26820	1.03	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1809	14332	26825	4.97	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1809	14332	26826	4.97	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1816	14339	26833	1.76	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1816	14339	26834	1.76	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1819	14341	26836	2.77	0.0E+00	4826793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1819	14341	26837	2.77	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1820	14342	26838	4.12	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1820	14342	26839	4.12	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1824	14346	26844	1.72	0.0E+00	AW207280.1	EST_HUMAN	U1H-B11-efn-f-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1824	14346	26845	1.72	0.0E+00	AW207280.1	EST_HUMAN	U1H-B11-efn-f-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1845	14367	26861	1.89	0.0E+00	BE277465.1	EST_HUMAN	501179184F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1845	14367	26862	1.89	0.0E+00	BE277465.1	EST_HUMAN	501179184F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1874	14398	26889	1.05	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1874	14398	26890	1.05	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1876	14398	26891	2.26	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1878	14398	26892	2.26	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1882	14404		1.25	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1883	15324	26898	16.65	0.0E+00	M99478.1	NT	Human transglutaminase mRNA, complete cds
1883	15324	26899	16.65	0.0E+00	M99478.1	NT	Human transglutaminase mRNA, complete cds
1888	14409	26906	1.81	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1888	14409	26907	1.81	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1891	14411	26908	1.38	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1893	14413		3.73	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1898	14418		3.93	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1899	15325	26916	4.47	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1914	14433	26932	0.88	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1914	14433	26933	0.88	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1915	14434	26934	7.48	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1915	14434	26936	7.48	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1925	14444	26947	2.33	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
1825	14444	26948	2.33	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
1930	14449	26949	2.77	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1930	14449	26950	2.77	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1932	14451	26951	2.43	0.0E+00	AW193024.1	EST_HUMAN	x69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879913 3'
1932	14451	26952	2.43	0.0E+00	AW193024.1	EST_HUMAN	x69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879913 3'
1933	14452	26953	6.14	0.0E+00	8912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1933	14452	26954	6.14	0.0E+00	8912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1935	14454	26956	2.33	0.0E+00	7682095	NT	Homo sapiens KIAA0408 gene product (KIAA0408), mRNA
1936	14455	26957	1.04	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0377 protein, complete cds
1943	14462	26966	6.1	0.0E+00	AB040949.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
1957	14475	26981	1.68	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1957	14475	26982	1.68	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1983	14499	27008	6.95	0.0E+00	BE743215.1	EST_HUMAN	601673896F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3833198 5'
1983	14499	27009	6.95	0.0E+00	BE743215.1	EST_HUMAN	601673896F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3833198 5'
1985	14501	27010	6.18	0.0E+00	AU140831	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
1987	14503	27012	1.11	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
1987	14503	27013	1.11	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
1989	14505		3.22	0.0E+00	7657468	NT	Homo sapiens similar to rat Integral membrane glycoprotein POM121 (POM121L1), mRNA
1991	14507		1.07	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
1992	14508	27016	1.07	0.0E+00	Z42398.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02
1994	14510		1.2	0.0E+00	A1244247.1	EST_HUMAN	q980708.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:198871 3' similar to contains Alu repetitive element;
1998	14514	27024	3.99	0.0E+00	BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2000	14518	27028	1.5	0.0E+00	BF315325.1	EST_HUMAN	601802604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2000	14516	27027	1.5	0.0E+00	BF315325.1	EST_HUMAN	601802604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2005	14521	27033	3.31	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-310 CT0413 Homo sapiens cDNA
2005	14521	27034	3.31	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-310 CT0413 Homo sapiens cDNA
2011	14527	27041	1.57	0.0E+00	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2011	14527	27042	1.57	0.0E+00	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2016	14532	27046	2.04	0.0E+00	4768489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2034	14550		12.42	0.0E+00	BE767864.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2035	14551		1.11	0.0E+00	AF018993.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 6 and complete cds
2037	14553	27064	3.31	0.0E+00	BF027562.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2038	14554	27065	1.24	0.0E+00	BE072624.1	EST_HUMAN	PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2039	14555	27066	7.22	0.0E+00	4503766	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
2041	14557	27068	4.31	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2043	14559	27070	2.48	0.0E+00	AI904840.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2043	14559	27071	2.48	0.0E+00	AI904840.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2066	14600		0.89	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2093	14607	27125	0.9	0.0E+00	D87685.1	NT	Human mRNA for KIAA0244 gene, partial cds
2094	14608	27126	30.97	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBMBDE08 6'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2094	14608	27127	30.97	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CENBDE08 5'
2096	14610	27128	9.71	0.0E+00	AA831691.1	EST_HUMAN	cc32e01.s1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1667896 3'
2100	14614	27133	67.91	0.0E+00	BF344434.1	EST_HUMAN	602014828F1 NCI CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4150734 5'
2101	14615	27134	34.41	0.0E+00	BE748899.1	EST_HUMAN	601672186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2104	14618	27137	4.46	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2104	14618	27138	4.46	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2108	15329	27143	3.62	0.0E+00	BF313617.1	EST_HUMAN	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5'
2111	14624	27146	9.85	0.0E+00	BE018750.1	EST_HUMAN	bb84e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170
2113	14628	27149	1.53	0.0E+00	AA042813.1	EST_HUMAN	z463c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFATORY RECEPTOR-LIKE PROTEIN HGMPD7E (HUMAN);
2113	14628	27149	1.53	0.0E+00	AA042813.1	EST_HUMAN	z463c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFATORY RECEPTOR-LIKE PROTEIN HGMPD7E (HUMAN);
2120	14633	27156	1.15	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2120	14633	27157	1.15	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2121	14634	27158	1.47	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2121	14634	27159	1.47	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2126	14639		1.03	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2127	14640	27164	6.17	0.0E+00	AA282281.1	EST_HUMAN	z12b10.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2134	14647	27170	1.53	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
2135	14648		1.05	0.0E+00	M20903.1	NT	Human apolipoprotein C-I pseudogene, complete cds
2149	14662	27186	4.92	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2158	14671	27194	6.59	0.0E+00	BE896281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2161	14674	27197	1.67	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2161	14674	27198	1.67	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2163	14675	27200	1.09	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2194	14709	27224	5.07	0.0E+00	BF344759.1	EST_HUMAN	602014009F1 NCI CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4149770 5'
2194	14705	27225	6.07	0.0E+00	BF344759.1	EST_HUMAN	602014009F1 NCI CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4149770 5'
2195	14706	27226	2.4	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2195	14706	27227	2.4	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2198	14707	27228	3.37	0.0E+00	A076404.1	EST_HUMAN	cc09c07.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2198	14709	27230	1.47	0.0E+00	AA429001.1	EST_HUMAN	z178a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2198	14709	27231	1.47	0.0E+00	AA429001.1	EST_HUMAN	z178a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2200	14711	27233	1.47	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4157339 5'

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2201	14092	26554	5.31	0.0E+00	M16708.1	NT	Human T-cell receptor gamma chain VJCL-CI-CII region mRNA, complete cds
2206	14716	27239	2.61	0.0E+00	L02840.1	NT	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2207	14717	27240	1.17	0.0E+00	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2213	14723	27245	6.33	0.0E+00	BE676095.1	EST_HUMAN	722a02.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296370 3' similar to TR:094939 C94939 KIAA0857 PROTEIN ;
2216	14726	27247	9.13	0.0E+00	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PHKA2) gene, exon 32
2217	14727	27248	1.62	0.0E+00	A182542.1	EST_HUMAN	1567a08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'
2218	14728	27249	1.63	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2223	14733	27253	1.66	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2223	14733	27254	1.66	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2232	14741	27261	6.22	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2232	14741	27262	5.22	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2233	14742		3.87	0.0E+00	4557521	NT	Homo sapiens deiodinase, iodothyronine, type I (DIO1) mRNA
2234	14743	27263	1.23	0.0E+00	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
2234	14743	27264	1.23	0.0E+00	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
2244	14753	27272	2.63	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2246	14756	27276	1.69	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2249	14757		13.3	0.0E+00	BE794026.1	EST_HUMAN	601586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2250	14758	27277	1.49	0.0E+00	AW867076.1	EST_HUMAN	MR1-SN0033-120400-002-a04 SN0033 Homo sapiens cDNA
2251	14759	27278	6	0.0E+00	7682017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2252	14760	27279	2.58	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2262	14760	27280	2.56	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2263	14761		5.97	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2254	14762	27281	6.26	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2254	14762	27282	6.26	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2254	14762	27283	6.25	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2273	14781		1.75	0.0E+00	BE814424.1	EST_HUMAN	MR0-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA
2314	14821	27339	1.6	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2316	14823		2.25	0.0E+00	A1042035.1	EST_HUMAN	oa60102.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:008662 O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE ;
2317	14824	27340	1.12	0.0E+00	8923820	NT	Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA
2321	14828		3.6	0.0E+00	BE895605.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2325	14832	27348	11	0.0E+00	BE937632.1	EST_HUMAN	MR1-TN0021-280800-001-h06 TN0021 Homo sapiens cDNA
2331	14838		1.42	0.0E+00	AB005622.1	EST_HUMAN	AB005622 Hela cDNA (T.Norma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2335	14841	27367	5.09	0.0E+00	6005002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2340	14845	27361	3.53	0.0E+00	D85608.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2340	14845	27362	3.53	0.0E+00	D85608.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2347	14853	27378	3.39	0.0E+00	AF108276.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (LIT1c) gene, exon 6
2356	14861	27382	1.99	0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2359	14864	27384	9.93	0.0E+00	BE831003.1	EST_HUMAN	CMO-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2369	14864	27385	9.93	0.0E+00	BE831003.1	EST_HUMAN	CMO-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2363	14868	27388	6.02	0.0E+00	BE569144.1	EST_HUMAN	602184668T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2376	14880	27399	3.6	0.0E+00	AW466922.1	EST_HUMAN	h604104.X1 NCI CGAP K1d12 Homo sapiens cDNA clone IMAGE:2872759 3'
2379	14884	27402	2.97	0.0E+00	AW501010.1	EST_HUMAN	U1HF-BP0p-als-c-07-0-U1r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2380	14894		8.14	0.0E+00	A1287878.1	EST_HUMAN	q23706.x1 NCI CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
2398	14902	27421	8.68	0.0E+00	5453965	NT	MIR repetitive element
2398	14902	27422	8.68	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2413	14917		2.26	0.0E+00	AW813853.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2416	14920	27437	24.94	0.0E+00	BE705542.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2417	14411	26909	5.17	0.0E+00	7657038	NT	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2418	14921	27438	1.88	0.0E+00	BF509482.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2422	14925	27441	1.59	0.0E+00	Z32684.2	NT	U1H-B14-aa2-b-08-0-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2423	14928		3.24	0.0E+00	5453871	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2425	14928	27443	0.93	0.0E+00	BE910378.1	EST_HUMAN	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2426	14929	27444	7.9	0.0E+00	7657468	NT	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2427	14930	27445	0.89	0.0E+00	8923340	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2428	14931	27446	3.79	0.0E+00	U93239.1	NT	Homo sapiens hypodermal protein FLJ20366 (FLJ20366), mRNA
2433	14936	27451	2.76	0.0E+00	BE889490.1	EST_HUMAN	Human Sec62 (Sec62) mRNA, complete cds
2438	14940	27457	3.23	0.0E+00	BE876511.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2438	14940	27458	3.23	0.0E+00	BE876511.1	EST_HUMAN	601489241F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3891371 5'
2439	14941	27459	2.94	0.0E+00	AF114027.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2441	14943	27462	0.91	0.0E+00	AF24605.1	NT	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF6
2469	14970	27483	2.97	0.0E+00	AU143277.1	EST_HUMAN	Homo sapiens adiclin mRNA, complete cds
2469	14970	27484	2.97	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2470	14971	27485	31.4	0.0E+00	BE292896.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2470	14971	27485	31.4	0.0E+00	BE292896.1	EST_HUMAN	601103312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2470	14971	27488	31.4	0.0E+00	BE292898.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987855 5'
2471	14972	27487	4.27	0.0E+00	BF223041.1	EST_HUMAN	7q27h12.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE: 3' similar to TRC00246 O00246
2474	14975	27489	7.9	0.0E+00	AF245505.1	NT	HYPOTHETICAL 9.3 KD PROTEIN:
2505	15008	27517	1.25	0.0E+00	BE296613.1	EST_HUMAN	Homo sapiens adicben mRNA, complete cds
2523	15271	27538	15.7	0.0E+00	AB037836.1	NT	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3628169 5'
2523	15271	27539	15.7	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2524	15023		1.78	0.0E+00	BF513635.1	EST_HUMAN	UJ-H-BW1-emp-4-12-O-U1 st NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2530	15029	27545	0.99	0.0E+00	BF672818.1	EST_HUMAN	602162853F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293612 5'
2532	15031		19.64	0.0E+00	BE516895.1	EST_HUMAN	601270873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621788 5'
2538	15036	27552	1.48	0.0E+00	BF204131.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2538	15038	27553	1.48	0.0E+00	BF204131.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2542	15040	27556	12.55	0.0E+00	AB037742.1	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2543	15041	27557	15.77	0.0E+00	A1571737.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2544	15042	27558	4.04	0.0E+00	5032160	NT	CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);
2546	15045	27562	4.25	0.0E+00	AB037859.1	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF21)
2549	15048	27563	3.62	0.0E+00	BE283328.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2557	15058		4.31	0.0E+00	BE792472.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3061389 6'
2559	15068	27573	1.44	0.0E+00	AB020710.1	NT	601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3839222 5'
2570	15068	27584	5.18	0.0E+00	4504686	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
2575	15342	27590	2.33	0.0E+00	4507720	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2581	15077		2.13	0.0E+00	U78027.1	NT	Homo sapiens titin (TTN) mRNA
2582	15078	27594	4.9	0.0E+00	AF173227.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2585	15081	27595	2.1	0.0E+00	AB011108.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2588	15084	27598	1.75	0.0E+00	AU133385.1	EST_HUMAN	Homo sapiens mRNA for KIAA0536 protein, partial cds
2589	15085	27599	1.88	0.0E+00	M69225.1	NT	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001984 5'
2592	15088	27602	4.64	0.0E+00	AU130403.1	EST_HUMAN	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2592	15088	27603	4.54	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2598	15094	27610	1.22	0.0E+00	BF000018.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2599	15095	27611	5.73	0.0E+00	BE383165.1	EST_HUMAN	7h15h05.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316089 3'
2600	15098		1.89	0.0E+00	BE531263.1	EST_HUMAN	601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
						EST_HUMAN	601270873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610287 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2636	15131	27643	8.29	0.0E+00	8922843	NT	Homo sapiens hypothetical protein FLJ11062 (FLJ11062), mRNA
2647	15140	27651	5.23	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2675	15168		13.71	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2676	15169	27677	1.68	0.0E+00	BE794884.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843591 5'
2683	15175	27688	2.2	0.0E+00	U36263.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2685	15177	27688	2.4	0.0E+00	7669517	NT	Homo sapiens neurogranin 1 (NRG1), transcript variant SMD, mRNA
2686	15178	27689	9.32	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2688	15180	27691	0.93	0.0E+00	AB051828.1	NT	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds
2694	15185	27697	18.86	0.0E+00	BE706376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945083 5'
2695	15186	27698	7.94	0.0E+00	BF680632.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 6'
2698	15348	27702	30.83	0.0E+00	BE863433.1	EST_HUMAN	601333485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689584 6'
2699	15189		3.07	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2701	15191	27705	5.09	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2701	15191	27706	5.09	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2702	15192	27707	2.13	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2702	15192	27708	2.13	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2703	15193	27709	1.2	0.0E+00	AF290196.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2704	15194		114.66	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'
2705	15195	27710	5.08	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250800-439-b08 TN0141 Homo sapiens cDNA
2705	15195	27711	5.08	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250800-439-b08 TN0141 Homo sapiens cDNA
2709	15199	27714	8.32	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2709	15199	27715	8.32	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2713	15203	27720	7.16	0.0E+00	BE747193.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2714	15204	27721	6.57	0.0E+00	N44974.1	EST_HUMAN	Y945h10.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR-A45773
2720	15210	27728	1.71	0.0E+00	BF037713.1	EST_HUMAN	A45773 kelch protein, long form - fruit fly;
2726	15218		1.7	0.0E+00	AL163201.2	NT	601462039F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865497 5'
2727	15217	27732	4.9	0.0E+00	BF514110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
2734	15224		0.97	0.0E+00	4503098	NT	UI-H-BW1-amiw-e-07-0JL.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2740	15230	27742	3.11	0.0E+00	BF577694.1	EST_HUMAN	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2746	15236	27760	2.33	0.0E+00	7427622	NT	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2750	15240	27763	14.69	0.0E+00	AV725534.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2750	15240	27764	14.69	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2752	15242		12.15	0.0E+00	AB78163.1	EST_HUMAN	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2755	15245	27759	3.38	0.0E+00	BF530661.1	EST_HUMAN	602071957F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214679 5'
2756	15246	27760	16.17	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'
2758	15248	27761	3.5	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2758	15248	27762	3.5	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2759	15249	27763	66.43	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860808 5'
2759	15249	27764	66.43	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860808 5'
2764	12785	25210	11.08	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3068 nt]
2767	15255		2.59	0.0E+00	AB033281.1	NT	Homo sapiens BTROP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2773	13314	25743	1.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2773	13314	25744	1.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2778	13610	26050	4.36	0.0E+00	4503202	NT	Homo sapiens ALR-like protein mRNA, partial cds
2778	13610	26051	4.36	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2782	15349	27771	3.25	0.0E+00	X86980.1	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2783	15350		1.4	0.0E+00	AF068624.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2784	15351		1.74	0.0E+00	AB040980.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
2785	15352	27772	3.11	0.0E+00	4502568	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2785	15352	27773	3.11	0.0E+00	4502568	NT	Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10) mRNA
2800	15357		1.17	0.0E+00	AJ238852.1	NT	Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10) mRNA
2801	15358	27778	3.33	0.0E+00	AL163201.2	NT	Homo sapiens partial rpl3 gene for ribosomal protein L3, U82 snRNA, U83a snRNA and U83b snRNA genes
2805	15362	27779	6.25	0.0E+00	M80902.1	NT	Homo sapiens chromosome 21 segment HS21C001
2809	15366		2.19	0.0E+00	X73428.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2810	15367		2.86	0.0E+00	AL163269.2	NT	H. sapiens l3 gene for HLH type transcription factor
2811	15368	27782	1.26	0.0E+00	7019584	NT	Homo sapiens chromosome 21 segment HS21C088
2811	15368	27783	1.26	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2811	15368	27784	1.26	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2813	15370	27785	12.11	0.0E+00	M89478.1	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2816	15372	27788	35.17	0.0E+00	D50637.1	NT	Human transglutaminase mRNA, complete cds
2816	15372	27789	35.17	0.0E+00	D50637.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2819	15373	27790	4.3	0.0E+00	AL086857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2819	15373	27790	4.3	0.0E+00	AL086857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes

Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2820	15375		7.14	0.0E+00	Y10658.1	NT	H.sapiens mRNA for nuclear DNA helicase II
2821	15377		1.01	0.0E+00	AF152303.1	NT	Homo sapiens protodactherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2822	15378	27791	139.19	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2822	15378	27792	139.19	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2834	15390	27803	3.28	0.0E+00	4507280	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2837	15393	27807	1.55	0.0E+00	AL047599.1	EST_HUMAN	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2838	15394	27808	1.44	0.0E+00	7681863	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2838	15394	27809	1.44	0.0E+00	7681863	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2839	15395		2.78	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2841	15397	27811	8.15	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2841	15397	27812	6.15	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2846	15402	27820	0.63	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2846	15402	27821	0.63	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2849	15405	27825	2.44	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2849	15405	27826	2.44	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2850	15406	27827	1.86	0.0E+00	AA215579.1	EST_HUMAN	z86b11.31 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element
2857	15412		4.55	0.0E+00	Y19210.1	NT	Homo sapiens hrb5 gene for hair keratin, exons 1 to 9
2860	15415	27836	1.29	0.0E+00	4758278	NT	Homo sapiens EphA4 (EPHA4) mRNA
2863	15418	27841	68.66	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2865	15420	27843	1.16	0.0E+00	P62740	SWISSPROT	ZINC FINGER PROTEIN 132
2866	15421	27844	1.42	0.0E+00	AF162338.1	NT	Homo sapiens protodactherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2874	15429	27848	1.05	0.0E+00	AI209084.1	EST_HUMAN	qg49104.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1838527 3' similar to SW:CB20_HUMAN P62298 20 KD NUCLEAR CAP BINDING PROTEIN ;
2882	15437	27856	3.06	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2882	15437	27857	3.06	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2883	15438	27858	6.19	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2883	15438	27859	6.19	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2885	15440	27861	3.39	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2885	15440	27862	3.39	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2886	15441	27863	5.77	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2886	15441	27864	5.77	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2891	15445	27868	1.81	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2891	15445	27869	1.81	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17293 PROTEIN. ;
2899	15454	27880	3.56	0.0E+00	4505084	NT	Q9VLN1 CG17293 PROTEIN. ;
2899	15454	27881	3.56	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2907	15462	27886	2.17	0.0E+00	4758827	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2908	15463		1.08	0.0E+00	X98494.1	NT	Homo sapiens neurexin III (NRXN3) mRNA
2911	15466	27889	1.42	0.0E+00	AB033034.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2913	15468	27891	10.6	0.0E+00	AF106275.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
2927	15482		1.24	0.0E+00	AI149880.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1a variant 4 (ILT1a) gene, exon 6
2936	15491	27912	1.2	0.0E+00	AF281074.1	NT	qf43f09.x1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
2936	15491	27913	1.2	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
2937	15492	27914	2.77	0.0E+00	AB004884.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
2948	15503	27922	1.48	0.0E+00	7682273	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2949	15504	27923	1.79	0.0E+00	6729766	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2949	15504	27924	1.79	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2960	15515	27935	0.7	0.0E+00	AF114488.1	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2980	15516	27936	0.7	0.0E+00	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2985	15540		0.7	0.0E+00	AL163248.2	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2987	15542	27958	1.04	0.0E+00	M74099.1	NT	Homo sapiens chromosome 21 segment HS21C048
2986	15551	27963	0.66	0.0E+00	4508882	NT	Human displacement protein (GCAAT) mRNA
2989	15554	27967	0.72	0.0E+00	AW676268.1	EST_HUMAN	Homo sapiens semenogelin I (SEMGI) mRNA
3004	15559		4.16	0.0E+00	AF195953.1	NT	EST388375 MAGE resequences, MAGN Homo sapiens cDNA
3007	15562	27976	87.23	0.0E+00	5579469	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3007	15562	27976	87.23	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3009	15564		6.89	0.0E+00	AL359403.1	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3014	15569	27981	2.84	0.0E+00	AF017433.1	NT	isoform 2 of a novel human mRNA from chromosome 22
							Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3017	15572		2.45	0.0E+00	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α -
3038	15593	28005	7.57	0.0E+00	X03529.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (Ig-LC16.1)
3044	15598		1.6	0.0E+00	AF199355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3048	15602	28012	1.47	0.0E+00	AF084599.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3067	15621	28029	3.26	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3068	15622	28029	5.39	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3073	15627	28033	4.24	0.0E+00	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3074	15628	28034	1.36	0.0E+00	AF042075.1	NT	Homo sapiens ciliary receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3101	15654	28068	2.84	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3109	15662	28074	52.59	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3112	15665	28077	1.65	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3112	15665	28078	1.65	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3119	15672	28085	22.34	0.0E+00	T94870.1	EST_HUMAN	ye32f03.s1 Stralagene lung (#337210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S29539
3134	15687	28103	1.15	0.0E+00	BF243336.1	EST_HUMAN	S29539 BASIC PROTEIN, 23K -;
3139	15692	28110	7.81	0.0E+00	X98922.1	NT	601876507F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4107433 5'
3139	15692	28111	7.81	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3140	15693	28112	0.85	0.0E+00	A1695950.1	EST_HUMAN	H. sapiens mRNA for gamma-glutamyltransferase
3149	15702	28121	1.49	0.0E+00	4758827	NT	tu38g09.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICDI
3149	15702	28122	1.49	0.0E+00	4758827	NT	P03967 RAS-LIKE PROTEIN RASD ;
3158	15709	28130	12.29	0.0E+00	4504658	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3175	15728	28148	3.08	0.0E+00	M28699.1	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3179	15732	28151	3.21	0.0E+00	4502098	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3185	15738	28159	0.8	0.0E+00	4758055	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3185	15738	28160	0.8	0.0E+00	4758055	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3187	15740	28161	92.56	0.0E+00	AA774783.1	EST_HUMAN	Homo sapiens GREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3195	15748	28169	7.75	0.0E+00	AF286598.1	NT	Homo sapiens GREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3195	15748	28170	7.75	0.0E+00	AF286598.1	NT	ae87b11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3207	15759	28177	1.63	0.0E+00	4557590	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3214	15766	28186	0.98	0.0E+00	4507720	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3222	15774		7.43	0.0E+00	M65189.1	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
						NT	Homo sapiens titin (TTN) mRNA
						NT	Human connexin 43 processed pseudogene
3223	15775	28193	1.59	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing Imanashin-X (Imanashin-X) gene, partial cds; cytchrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, heilcse (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3226	15778	28196	5.04	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3229	15781	28108	2.62	0.0E+00	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3229	15781	28109	2.62	0.0E+00	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3237	17981	28206	2.02	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3237	17981	28207	2.02	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3253	15804	28221	2.91	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3254	15805	28222	0.87	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3267	15818	28236	2.08	0.0E+00	7667038	NT	Homo sapiens death receptor 8 (DR8), mRNA
3278	15828	28248	0.78	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3282	15841	28259	10.16	0.0E+00	AI589294.1	EST_HUMAN	tr56f08.x2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:222835 3' similar to SW:RL11_RAT
3285	15844	28262	2.65	0.0E+00	AW955400.1	EST_HUMAN	P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element
3303	15851	28269	2.56	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3303	15851	28270	2.56	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3304	15852	28271	0.98	0.0E+00	7667213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3304	15852	28272	0.98	0.0E+00	7667213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3307	15855	28274	1.58	0.0E+00	4502562	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3307	15855	28275	1.58	0.0E+00	4502562	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3311	15859	28278	12.71	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3313	15861	28280	0.94	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3320	15867	28286	0.78	0.0E+00	BE779039.1	EST_HUMAN	601484895F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5'
3333	15880	28301	0.65	0.0E+00	AI632569.1	EST_HUMAN	wb10f04.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3868246 5'
3374	15921	28339	4.28	0.0E+00	AU123664.1	EST_HUMAN	ZINC FINGER PROTEIN
3383	15929	28343	1.09	0.0E+00	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3384	15930	28344	1.25	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1a isoform (CACNA1I) mRNA, complete cds
3389	15935		1.15	0.0E+00	AW897015.1	EST_HUMAN	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3402	15947	28359	1.66	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3402	15947	28360	1.66	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3403	15948	28361	0.94	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3405	15950	28362	2.06	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3414	15178	27689	4.9	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
3418	15962	28373	1.19	0.0E+00	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA

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3416	15983	28374	2.62	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3420	15984	28375	1.16	0.0E+00	5453995	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3420	15984	28376	1.16	0.0E+00	5453995	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3423	15987	28380	6.05	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and InoA, InoB, and InoC incompatibility determinants
3425	15989	28382	1.18	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3428	15972	28385	1.56	0.0E+00	4557746	NT	Homo sapiens met proto-oncogene (hepatocellular growth factor receptor) (MET) mRNA
3432	15976	28389	4.63	0.0E+00	A1935159.1	EST_HUMAN	wp14d10.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2404819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE ;
3432	15978	28390	4.63	0.0E+00	A1935159.1	EST_HUMAN	wp14d10.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2404819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE ;
3436	15980	28395	3.72	0.0E+00	A1278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3442	15986	28403	36.33	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3442	15986	28404	36.33	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3447	15991	28410	2.7	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3452	15998	28416	6.63	0.0E+00	U43293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3457	16001	28418	1.2	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3457	16001	28420	1.2	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3461	16005	28425	4.47	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3461	16005	28426	4.47	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3469	16013	28435	1.12	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3475	16018	28437	1.96	0.0E+00	AJ010770.1	NT	Homo sapiens hyperton gene, exons 1-50
3477	16020	28439	1.03	0.0E+00	AA626677.1	EST_HUMAN	ab51f12.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3477	16020	28440	1.03	0.0E+00	AA626677.1	EST_HUMAN	ab51f12.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3477	16020	28441	1.03	0.0E+00	AA626677.1	EST_HUMAN	ab51f12.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3480	16023	28444	1.18	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) mRNA
3484	16027	28448	3.67	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3484	16027	28449	3.67	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3487	16030	28452	0.94	0.0E+00	4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNK2) mRNA
3490	16033	28455	1.13	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTF AND CNC HOMOLOG 1) (HA2303)
3494	16037	28458	1.01	0.0E+00	A1984007.1	EST_HUMAN	ts35g12.x1 Sources_NihMpu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00488 O00488 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3497	16040	28461	2.19	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3515	16058	28479	0.67	0.0E+00	AA456282.1	EST_HUMAN	z69h04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3515	16058	28480	0.67	0.0E+00	AA456282.1	EST_HUMAN	z69h04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3522	16085	28488	1.31	0.0E+00	AB029019.1	NT	Homo sapiens mRNA for KIAA1086 protein, partial cds
3524	16067	28489	1.07	0.0E+00	AV701869.1	EST_HUMAN	AV701869 ADB Homo sapiens cDNA clone ADBDAH06 5'
3526	16069	28480	0.77	0.0E+00	4508884	NT	Homo sapiens semomogalin II (SEM62) mRNA
3528	16071		1.71	0.0E+00	AF079868.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3537	16080	28498	1.36	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X
3540	16082	28501	1	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3553	16095	28512	0.91	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3564	16106	28520	1.36	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3564	16106	28521	1.38	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3565	16107		0.74	0.0E+00	AI091907.1	EST_HUMAN	cx77c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1682366 3' similar to WP.T1084.4 CE13742;
3567	16109	28524	2.4	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTNSA3), mRNA
3573	16115		5.28	0.0E+00	AW652217.1	EST_HUMAN	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
3577	16119	28535	1.1	0.0E+00	4504294	NT	Homo sapiens H3 histone family, member K (H3FK), mRNA
3581	16123		0.94	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCCLC) gene, partial cds
3582	16124	28536	9.5	0.0E+00	BF676393.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248598 5'
3587	16129		1.14	0.0E+00	AA988715.1	EST_HUMAN	cx94h06.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1594043 3' similar to contains MER29.b2
3597	16138	28551	0.85	0.0E+00	AW937977.1	EST_HUMAN	MER29 repetitive element;
3610	16150	28558	0.81	0.0E+00	BF672054.1	EST_HUMAN	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3610	16150	28559	0.81	0.0E+00	BF672054.1	EST_HUMAN	602162486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293846 5'
3611	16151		1.15	0.0E+00	4828987	NT	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293846 5'
3613	16153	28561	0.8	0.0E+00	AW664693.1	EST_HUMAN	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3613	16153	28562	0.8	0.0E+00	AW664693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978024 3'
3617	16167	28568	1.25	0.0E+00	4826763	NT	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978024 3'
3619	16150	28569	1.08	0.0E+00	7682319	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3628	16168	28577	0.93	0.0E+00	4557752	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3628	16168	28578	0.93	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3647	16187	28593	2.56	0.0E+00	D87327.1	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3650	16190		6.76	0.0E+00	7669491	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3667	16207	28612	9.4	0.0E+00	AB028542.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3670	16210	28614	4.07	0.0E+00	AF124250.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3670	16210	28614	4.07	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3670	16210	28615	4.07	0.0E+00	AF124260.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3676	16216	28623	4.08	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g06f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3678	16218	28624	4.08	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g06f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3679	16219	28626	1.48	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3679	16219	28627	1.48	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3682	16222	28630	1.03	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281089-005-605 CT0222 Homo sapiens cDNA
3684	16224	28632	2.14	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3686	16226	28634	1.68	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0768 protein, partial cds
3688	16228	28636	1.33	0.0E+00	O14887	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3689	16229	28637	0.64	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3689	16229	28638	0.84	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3701	16241	28646	5.84	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-0-J1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3701	16241	28647	5.84	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-0-J1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3728	16268	28672	1.16	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen $\alpha 1$ chain, exon 6
3729	16269	28673	1.15	0.0E+00	AA463659.1	EST_HUMAN	aa06g01.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:812498 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB4. [1]:
3733	16273	28677	0.79	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3736	16276	28678	7.84	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3746	16285	28689	0.99	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3754	16293	28695	1.04	0.0E+00	AA042813.1	EST_HUMAN	Zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
3780	16299	28700	8.99	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3763	16302	28703	42.7	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3827	16364	28763	1.29	0.0E+00	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
3828	16366	28765	0.72	0.0E+00	AF196696.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3830	16367	28765	2.5	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3833	16370	28769	1.59	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3834	16371	28770	1.59	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3834	16371	28771	1.35	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3838	16375	28776	1.34	0.0E+00	4769011	NT	Homo sapiens RAB9, member RAS oncogene family (RAB9) mRNA
3839	16376	28777	1	0.0E+00	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3841	16378	28779	1.05	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3841	16378	28780	1.05	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGOT1) gene, partial cds
3842	16379	28781	1.55	0.0E+00	A377898.1	EST_HUMAN	test210.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3843	16380		2.41	0.0E+00	AF152498.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3844	16381	28782	1.55	0.0E+00	4768189	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
3848	16383	28783	14.33	0.0E+00	S78885.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3847	16384	28784	2.38	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3848	16385	28785	3.2	0.0E+00	7682183	NT	Homo sapiens KIA00589 gene product (KIA00589), mRNA
3850	16387	28786	1.32	0.0E+00	AF068601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3850	16387	28787	1.32	0.0E+00	AF068601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3858	16392	28793	1.13	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3860	16396	28799	8.04	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3860	16398	28800	8.04	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3862	16398	28803	4.84	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3863	16399	28804	0.66	0.0E+00	AF114488.1	NT	Homo sapiens intercedin short isoform (ITSN) mRNA, complete cds
3866	16402	28806	1.29	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3869	16405	28809	0.94	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3870	16406	28810	2.61	0.0E+00	4759171	NT	Homo sapiens SC35-Interacting protein 1 (SRRP129), mRNA
3872	16408	28812	0.89	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
3883	16418	28822	2.51	0.0E+00	A1864727.1	EST_HUMAN	wk01f01.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340
3886	16421	28826	31.31	0.0E+00	4508742	NT	O43340 R28830_2, contains element PTR7 repetitive element;
3891	16426	28832	1.71	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3897	16432	28839	1.33	0.0E+00	6005887	NT	DKFZP434N0413_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0413 5'
3897	16432	28840	1.33	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3899	16434	28842	3.22	0.0E+00	4504138	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3900	16435		2.36	0.0E+00	4505078	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3904	16439	28845	1.23	0.0E+00	AF149412.1	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3916	16451	28858	1.77	0.0E+00	4506756	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3920	16455	28862	4.03	0.0E+00	4585642	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3929	16464	28872	2.64	0.0E+00	BF355295.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3931	16466	28874	1.4	0.0E+00	AW888221.1	EST_HUMAN	Homo sapiens zinc finger protein (KIA00412) mRNA
							RC3-H10860-170800-011-a12 HT0860 Homo sapiens cDNA
							MXRA5 Human matrix tissue expression library/Homo sapiens cDNA clone Incyte 1989728 similar to MXRA5
							Matrix remodeling associated gene 5

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3931	16468	28975	1.4	0.0E+00	AW898221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1998728 similar to MXRA5 Matrix remodelling associated gene 6
3937	16472	28981	2.4	0.0E+00	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
3940	16475	28984	1.35	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3940	16475	28985	1.35	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3945	16480	28980	4.73	0.0E+00	BE378602.1	EST_HUMAN	607236966F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3608800 5'
3953	16488	28987	0.94	0.0E+00	AW580740.1	EST_HUMAN	PM3-L T0031-100100-003-h09 LT0031 Homo sapiens cDNA
3954	16489	28988	1.08	0.0E+00	5360215	NT	Homo sapiens kloronate 2-sulfatase (Huntar syndrome) (IDS), transcript variant 1, mRNA
3989	16523	28926	5.41	0.0E+00	AF116185.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3989	16523	28928	5.41	0.0E+00	AF116185.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3999	16533		5	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4001	16535		6.73	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4007	16541	28939	1.09	0.0E+00	AL118494.1	NT	Novel human gene mapping to chromosome 20
4011	16544	28941	3.26	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4019	16552	28949	1.69	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
4031	16564		100.63	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4036	16569		1.07	0.0E+00	AI657076.1	EST_HUMAN	t55g08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:060309 O60309 KIAA0563 PROTEIN ;
4039	16571	28963	1.76	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4040	16572	28964	1.79	0.0E+00	U09366.1	NT	Human zinc finger protein ZNF133
4058	16589	28981	11.47	0.0E+00	AB015610.1	NT	Chlorobacterium aethiops mRNA for ribosomal protein S4X, complete cds
4067	16598		4.05	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
4081	16612	29000	2.2	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4082	16613	29001	3.35	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4082	16613	29002	3.35	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4088	16619	29007	11.37	0.0E+00	5032028	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4088	16619	29008	11.37	0.0E+00	5032028	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4100	16631	29020	0.64	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylamidimidazole synthetase (GART) mRNA
4106	16638	29024	0.44	0.0E+00	4883306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4107	16637	29025	1.86	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4110	16640	29026	0.85	0.0E+00	4769807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4111	16641	29027	9.99	0.0E+00	11418297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4112	16642	29028	3.12	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes

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Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4118	16849	28035	2.7	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4128	13702	26141	1.47	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4128	13702	26142	1.47	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4134	16863	29049	1.51	0.0E+00	5801905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
4135	16864	29050	1.04	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
4135	16864	29051	1.04	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
4137	16069	28490	1.16	0.0E+00	4506884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
4139	16667	28053	0.91	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4139	16667	28054	0.91	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4144	16672	29058	0.77	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4151	16878	29097	6.4	0.0E+00	A1982597.1	EST_HUMAN	wu04004.x1 NCI CGAP GCG Homo sapiens cDNA clone IMAGE:2515976 3'
4161	16879	29088	6.4	0.0E+00	A1982597.1	EST_HUMAN	wu04004.x1 NCI CGAP GCG Homo sapiens cDNA clone IMAGE:2515976 3'
4164	16881	29070	0.83	0.0E+00	BE184858.1	EST_HUMAN	MR1-HT0707-100500-001-402 HT0707 Homo sapiens cDNA
4154	16881	29071	0.93	0.0E+00	BE184858.1	EST_HUMAN	MR1-HT0707-100500-001-402 HT0707 Homo sapiens cDNA
4159	16886		5.58	0.0E+00	BE274217.1	EST_HUMAN	60120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867690 5'
4165	16892	29078	1.04	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4165	16892	29079	1.04	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4167	16894	29081	2.36	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4173	16700		5.58	0.0E+00	AW675599.1	EST_HUMAN	ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900085 3' similar to SW:TH12_BOVIN
4178	18705	29094	1.41	0.0E+00	AW408788.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4179	18708	29095	1.68	0.0E+00		NT	UI-HF-BM0-eda-o-02-Q-UJr1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3083147 5'
4179	18708	29096	1.68	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
4188	18715		2.51	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4200	18725	29113	1.12	0.0E+00	AB037739.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
4208	18733	29122	11.16	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;
4208	18733	29123	11.16	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;
4211	18736	29127	2.74	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4236	18760	29148	1.18	0.0E+00	7661869	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4239	18764	29148	1.11	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DPLI) (DSP) mRNA
4239	18764	29149	1.11	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DPLI) (DSP) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4248	16771		0.82	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4247	16772	29158	1.05	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
4276	16800	29183	1.03	0.0E+00	AJ010770.1	NT	Homo sapiens hyperon gene, exons 1-50
4280	16816	29199	4.74	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
4295	16820	29203	1.01	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4295	16820	29204	1.01	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4304	16829	29218	0.94	0.0E+00	AW693689.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4309	16867	29286	1.45	0.0E+00	BE776039.1	EST_HUMAN	60148498F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868248 5'
4312	16836	29225	1.07	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4312	16836	29228	1.07	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4314	16838	29228	3.75	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fbl4 (FBL4) mRNA, partial cds
4322	16845		2.65	0.0E+00	AI189844.1	EST_HUMAN	qdz106.x1 Soares, placenta, 8to9weeks, 2Nbl-P8to9W Homo sapiens cDNA clone IMAGE:1724578 3'
4326	16848		4.85	0.0E+00	U14620.1	NT	similar to contains MER20 b2 MER20 repetitive element ;
4330	16852	29238	0.95	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
4347	16869	29253	1.05	0.0E+00	8563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4347	16869	29254	1.05	0.0E+00	8563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4354	16876	29260	0.97	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4354	16876	29261	0.97	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4363	16885	29268	14.08	0.0E+00	6812281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4382	16904		1.02	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-38 (CX38) gene, complete cds
4386	16908	29281	12.33	0.0E+00	U03901.1	NT	Human Ig light chain VL1 region germline (humV1c2c) gene, partial cds
4392	16914	29288	4.75	0.0E+00	L14591.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4396	16918	29303	4.29	0.0E+00	Z80780.1	NT	H. sapiens H2B1h gene
4396	16918	29304	4.29	0.0E+00	Z80780.1	NT	H. sapiens H2B1h gene
4397	16919	29305	2.89	0.0E+00	AW166933.1	EST_HUMAN	xg8e10.x1 NCJ CGAP U14 Homo sapiens cDNA clone IMAGE:2633514 3' similar to TR:P97365 P97365
4403	16925	29311	1.05	0.0E+00	X60483.1	NT	ZINC FINGER PROTEIN 64 ;
4403	16925	29312	1.05	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4408	16929	29318	9.97	0.0E+00	7662091	NT	H. sapiens H4/d gene for H4 histone
4408	16929	29318	9.97	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA

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4408	16929	29319	9.97	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4418	16939	29330	4.97	0.0E+00	X82338.1	NT	Homo sapiens Menkes disease gene, exon 4
4421	16942	29334	16.36	0.0E+00	4885128	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4422	16943	29335	1.14	0.0E+00	AJ271798.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4423	16944		1.02	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment H321C007
4428	16947	29337	1.15	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4482	16982	29368	3.41	0.0E+00	7019458	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4472	16992		7.21	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4478	16998	29379	1.51	0.0E+00	AJ248765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4478	16998	29380	1.61	0.0E+00	AJ248766.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4482	17001	29388	0.73	0.0E+00	W26178.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4482	17001	29387	0.73	0.0E+00	W26179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4502	17020		2.33	0.0E+00	AF200629.1	NT	Homo sapiens HPS1 gene, intron 6
4523	17041	29420	0.7	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Col8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F205 5'
4523	17041	29421	0.7	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Col8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F205 5'
4526	17044		0.62	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4538	17056	29439	121.33	0.0E+00	AW084964.1	EST_HUMAN	xc68e08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589448 3' similar to SW:AHNK_HUMAN
4540	17067		3.98	0.0E+00		NT	Q09868 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ;
4542	17059	29442	2.36	0.0E+00	AI696888.1	EST_HUMAN	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4543	17060	29443	1.49	0.0E+00	AF016050.1	NT	wc66b02.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2322603 3' similar to contains MER22.b2
4548	17063		5.68	0.0E+00	AL163207.2	NT	PTTR5 repetitive element ;
4548	17065	29447	1.55	0.0E+00	AW381570.1	EST_HUMAN	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4554	17071	29454	2.41	0.0E+00	AJ278120.1	NT	Homo sapiens chromosome 21 segment HS21C007
4554	17071	29455	2.41	0.0E+00	AJ278120.1	NT	PM1-HT0305-101198-002-403 HT0305 Homo sapiens cDNA
4556	17073	29457	2.75	0.0E+00	AF108830.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4558						NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4558						NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4561	17078	29463	1.01	0.0E+00	4506952	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminidase: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
4566	17083	29469	1.19	0.0E+00	AF111163.1	NT	(SIAT8) mRNA
4566	17083	29470	1.19	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4575	17088	29479	3.71	0.0E+00	6005973	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4580	17096	29484	3.88	0.0E+00	AF208161.1	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
						NT	Homo sapiens synovial precursor, mRNA, complete cds

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4585	17101	28481	3.54	0.0E+00	AF162337.1	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4588	17104	28495	1.34	0.0E+00	6454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4600	17116	29504	44.89	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4608	17124	29509	0.77	0.0E+00	4505018	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4614	17130	29515	1.3	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4617	17133	29518	1.09	0.0E+00	4502558	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4620	17136		1.1	0.0E+00	BE971908.1	EST_HUMAN	601447932F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852127 5'
4623	17139		3.79	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphatase (IDS) gene, complete cds
4625	17141	29521	12.38	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4625	17141	29522	12.38	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4642	17158	29537	4.37	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 6
4645	17161	29540	13.83	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4646	17161	29541	13.83	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4655	17171		0.64	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4667	17183		1.45	0.0E+00	AA174072.1	EST_HUMAN	zo18g08.s1 Stratiagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:609854 3'
4670	17186		2.33	0.0E+00	7667410	NT	Homo sapiens cdx (odd Ozten-m, Drosophila) homolog 1 (ODZ1), mRNA
4672	17188		1.76	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4673	17189	29556	1.39	0.0E+00	H92741.1	EST_HUMAN	y92b01.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4673	17188	29557	1.39	0.0E+00	H92741.1	EST_HUMAN	y92b01.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4674	17190	29558	4.61	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4675	17191	29559	4.97	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4676	17192		1.8	0.0E+00	AB037521.1	NT	Homo sapiens gene for neuretic protein, partial cds
4682	17198	29576	1.06	0.0E+00	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4685	17201	29579	2.03	0.0E+00	AL162331.1	NT	Novel human gene mapping to chromosome 1
4687	17203	29581	7.63	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4687	17203	29582	7.63	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4688	17204	29583	1.36	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4703	17219	29601	10.36	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4709	17225	29609	3.09	0.0E+00	BE081827.1	EST_HUMAN	QV2-BT0635-160400-142-H05 BT0635 Homo sapiens cDNA
4714	17230		1.86	0.0E+00	AF086641.1	NT	Homo sapiens truncated terascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region

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4723	17239	29820	1.87	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4723	17239	29821	1.87	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4724	17240	29822	2.51	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1398 protein, partial cds
4724	17240	29823	2.51	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1398 protein, partial cds
4725	17241	29824	2.13	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4728	17245	29827	1.34	0.0E+00	AW294800.1	EST_HUMAN	UI-H-B12-ah1-c-05-0-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726792 3'
4729	17245	29828	1.34	0.0E+00	AW294800.1	EST_HUMAN	UI-H-B12-ah1-c-05-0-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726792 3'
4730	17246	29829	3.98	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4730	17246	29830	3.98	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4732	17249	29169	2.11	0.0E+00	T66945.1	EST_HUMAN	ya83g04.i2 Stratagene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:68310 5'
4732	17249	29169	2.11	0.0E+00	T66945.1	EST_HUMAN	ya83g04.i2 Stratagene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:68310 5'
4736	17250		1.95	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505821 5'
4742	17256	29836	0.71	0.0E+00	BE390050.1	EST_HUMAN	601285246F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607087 5'
4758	17272	29655	2.58	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EV12B), mRNA
4758	17272	29656	2.58	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EV12B), mRNA
4759	17273	29857	1.09	0.0E+00	U66651.1	NT	Mus musculus neurexophilin 1 (Nrxh1) gene, large exon and 3' end of the intron, and partial cds
4764	17278	29681	68.33	0.0E+00	M80802.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4767	17281	29684	4.48	0.0E+00	M69197.1	NT	Human haptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
4767	17281	29685	4.48	0.0E+00	M69197.1	NT	Human haptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
4771	17285	29670	2.18	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NCTR) gene, complete cds
4774	17288	29872	2.3	0.0E+00	7662181	NT	Homo sapiens KIAA0963 gene product (KIAA0963), mRNA
4785	17289	29883	1.07	0.0E+00	AL08857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4803	17317	29894	0.89	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4803	17317	29895	0.89	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4813	17325	29704	1.13	0.0E+00	AF028601.1	NT	Homo sapiens alpha-3 type IX collagen (COL3A3) gene, promoter region, and exons 1-28
4816	17328	29707	23.29	0.0E+00	7016320	NT	Homo sapiens protein0008 (AD013), mRNA
4816	17328	29708	23.28	0.0E+00	7016320	NT	Homo sapiens protein0008 (AD013), mRNA
4838	17350	29733	1.81	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-ajw-c-04-0-UI.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
4843	17355	29740	1.05	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4845	17357		1.11	0.0E+00	AF083242.1	NT	Homo sapiens HSP G924-iso mRNA, complete cds
4858	17370		2.52	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
4859	17371		0.62	0.0E+00	AW339253.1	EST_HUMAN	x289d06.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871371 3'
4893	17405	29776	0.94	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4893	17405	29777	0.94	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4900	17411		3.58	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4903	17414	29786	0.97	0.0E+00	X87205.1	NT	M fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4905	17416	29788	2.88	0.0E+00	AF084478.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCH9) mRNA, complete cds
4906	17417	29789	1.63	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4907	17418	29790	5.23	0.0E+00	4503768	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4909	17420	29792	27.61	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4910	17421	29793	1.47	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4912	17423	29795	1.07	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp782E1312 (DKFZp782E1312), mRNA
4917	17428	29801	3.47	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4920	17431	29804	1.92	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4920	17431	29805	1.92	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4922	17433	29807	1.95	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4922	17433	29808	1.95	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4925	17436	29811	1.98	0.0E+00	M55682.1	NT	Human collagenase type IV (CLG4) gene, exon 2
4928	17437	29812	2.69	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4950	17461	29837	2.35	0.0E+00	X92841.1	NT	H. sapiens MICA gene
4953	17464	29840	4.68	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4954	17465	29841	2.03	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4955	17466	29842	2.6	0.0E+00	6877648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA
4958	17467	29843	3.03	0.0E+00	6174560	NT	Homo sapiens meningioma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA
4957	17468	29844	1.33	0.0E+00	BE007935.1	EST HUMAN	QV0-BN0147-280400-213-g11 BN0147 Homo sapiens cDNA
4957	17468	29845	1.33	0.0E+00	BE007935.1	EST HUMAN	QV0-BN0147-280400-213-g11 BN0147 Homo sapiens cDNA
4959	17470	29847	2.93	0.0E+00	4768189	NT	Homo sapiens desmoplakin (DPI, DPLI) (DSP) mRNA
4961	17472	29849	1.27	0.0E+00	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
4962	17473	29850	1.51	0.0E+00	6174560	NT	Homo sapiens meningioma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA
4962	17473	29851	1.51	0.0E+00	6174560	NT	Homo sapiens meningioma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA
4963	17474	29852	2.64	0.0E+00	7705546	NT	Homo sapiens zinc-finger DNA-binding protein (HUMFOX1), mRNA
4964	17475		15.71	0.0E+00	AJ010442.1	NT	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RhD, therad 7
4968	17479	29857	58.86	0.0E+00	AF055066.1	NT	Homo sapiens MHC class 1 region
4970	17481		2.67	0.0E+00	4505508	NT	Homo sapiens oploid receptor, delta 1 (OPRD1) mRNA
4971	17482	29860	3.52	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4975	17488	28884	4.6	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4990	17500	28875	2.1	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPs) mRNA
5007	17517	28890	2.58	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
5007	17517	28891	2.58	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
5014	17524	28898	0.93	0.0E+00	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
5014	17524	28900	0.93	0.0E+00	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
5018	17528	28902	1	0.0E+00	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5028	17538	28909	0.88	0.0E+00	BF630735.1	EST_HUMAN	602072064F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215039 5'
5028	17538	28910	0.98	0.0E+00	BF630735.1	EST_HUMAN	602072064F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215039 5'
5040	17550	28921	1.48	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5047	17557	28926	1.58	0.0E+00	AW452728.1	EST_HUMAN	U1-H-B13-alc-f-02-Q-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068691 3'
5050	17560	28928	1.29	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
5050	17560	28930	1.29	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
5058	17568	28936	1.78	0.0E+00	8822926	NT	Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA
5064	17574	28943	0.91	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BF-SP1) mRNA
5068	17578	28947	6.87	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
5079	17589	28957	1.15	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5081	17591	28957	3.17	0.0E+00	BE408863.1	EST_HUMAN	601303729F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:36838118 5'
5086	17596	28963	3.14	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DP1) (DSP) mRNA
5095	17605	28968	0.97	0.0E+00	AB028866.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
5110	17618	28980	1.92	0.0E+00	8823441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5110	17618	28981	1.92	0.0E+00	8823441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5126	17632	28993	0.75	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5126	17632	28994	0.75	0.0E+00	AA601246.1	EST_HUMAN	E239140 SPALT PROTEIN; no14g09.s1 NCL_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5128	17632	28995	0.75	0.0E+00	AA601246.1	EST_HUMAN	E239140 SPALT PROTEIN; no14g09.s1 NCL_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5128	17633	28996	1.8	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
5128	17633	28997	1.8	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
5138	17640	30003	0.99	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5154	17658	30020	1.69	0.0E+00	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5159	17683	30024	1.23	0.0E+00	U53598.1	NT	Homo sapiens MHG class 1 region
5171	17675		1.62	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5176	17680		44.86	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5181	17685	30044	1.08	0.0E+00	AA084272.1	EST_HUMAN	zn03g10.t1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:548402 5'
5181	17685	30045	1.08	0.0E+00	AA084272.1	EST_HUMAN	zn03g10.t1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:548402 5'
5182	17686	30046	12.5	0.0E+00	S71446.1	NT	SCN1A=brain type I sodium channel alpha-subunit (IIIS6 transmembrane region) [human, placenta, Genomio, 1586 nt]
5216	17719	30085	3.35	0.0E+00	X52988.1	NT	Bacillus amyloqueliciens sacB gene for levansucrase (EC 2.4.1.10)
5246	17746	30113	5.68	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5246	17747	30114	5.58	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5246	17747	30115	1.14	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5266	17767	30126	1.02	0.0E+00	AA683288.1	EST_HUMAN	ae92b04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020367 3'
5267	17768	30137	0.84	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
5275	17776	30142	1.05	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
5279	17780	30148	0.98	0.0E+00	7657193	NT	Homo sapiens hypothetical protein (HS747E2A), mRNA
5281	17791	30156	2.17	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5281	17791	30157	2.17	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5300	17800	30168	0.76	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
5318	17818	30181	0.73	0.0E+00	5902091	NT	Homo sapiens solute carrier family 5 (inorganic transporters), member 3 (SLC5A3), mRNA
5331	17830	30188	0.93	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5331	17830	30189	0.93	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5352	17851	30208	1.46	0.0E+00	AF165592.1	NT	Homo sapiens core1 UDP-galactose 4-epimerase/alpha-R beta 1,3-galactosyltransferase (GT4ALT1) mRNA, complete cds
5353	17852	30209	1.91	0.0E+00	4757889	NT	Homo sapiens chromosome 8 open reading frame 1 (C8ORF1) mRNA
5355	17854	30211	1.73	0.0E+00	AF196658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5380	17858	30216	0.89	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
5381	17859	30217	2.07	0.0E+00	5360213	NT	Homo sapiens glypican 3 (GPC3) mRNA
5386	17866	30226	1.1	0.0E+00	AB831858.1	EST_HUMAN	wf52g05.x1 NC1 CGAP Cot8 Homo sapiens cDNA clone IMAGE:2393912 3'
5372	17870	30230	1.44	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
5372	17870	30231	1.44	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
5373	17871	30232	0.99	0.0E+00	7682117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
5376	17874		1.31	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1613 protein, partial cds
5396	17893	30250	1.53	0.0E+00	X76050.1	NT	H. sapiens mRNA for YRRM2
5404	17900	30255	2.17	0.0E+00	AI285302.1	EST_HUMAN	ql60c01.x1 NC1 CGAP Co8 Homo sapiens cDNA clone IMAGE:1873344 3'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5416	17912	30263	10.04	0.0E+00	AV763053.1	EST_HUMAN	AV763053 MDS Homo sapiens cDNA clone MDSBEC05 6'
5416	17912	30264	10.04	0.0E+00	AV763053.1	EST_HUMAN	AV763053 MDS Homo sapiens cDNA clone MDSBEC05 5'
5419	17914	30265	1.03	0.0E+00	BE144725.1	EST_HUMAN	CM0-HT0178-051099-084-e05 HT0178 Homo sapiens cDNA
5423	17918	30266	1.29	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5423	17918	30270	1.29	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5424	17919	30271	1.65	0.0E+00	11423143	NT	Homo sapiens hypothetical protein LOC57821 (LOC57821), mRNA
5431	17926	30277	9.77	0.0E+00	D61628.1	EST_HUMAN	HUM424F12B Clontech human fetal brain polyA+ mRNA (#8635) Homo sapiens cDNA clone GEN-424F12 5'
5435	17930	30284	3.34	0.0E+00	4788827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
5447	17942	30291	2.65	0.0E+00	7657442	NT	Homo sapiens protocadherin 11 (PCDH11), mRNA
5447	17942	30292	2.65	0.0E+00	7657442	NT	Homo sapiens protocadherin 11 (PCDH11), mRNA
5457	17952	30302	1.06	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
5465	17960	30308	1.13	0.0E+00	AK024487.1	NT	Homo sapiens mRNA for FLJ00060 protein, partial cds
5484	17979	30323	1.13	0.0E+00	AA701913.1	EST_HUMAN	zib4p10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435647 3' similar to gb:U07290_cds1 ZINC FINGER PROTEIN HF.12 (HUMAN);
5484	17979	30324	1.13	0.0E+00	AA701913.1	EST_HUMAN	zib4p10.e1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435647 3' similar to gb:U07290_cds1 ZINC FINGER PROTEIN HF.12 (HUMAN);
5491	18001		3.44	0.0E+00	AF093093.1	NT	Homo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5502	18093	30335	4.74	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5502	18093	30336	4.74	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5525	18115	30472	1.34	0.0E+00	AI934954.1	EST_HUMAN	wc06p08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
5528	18118	30475	1.5	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PCDH13), mRNA
5543	18133	30480	3.62	0.0E+00	BE931080.1	EST_HUMAN	RC3-GN0076-310800-013-b03 GN0076 Homo sapiens cDNA
5547	18137	30494	3.22	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5547	18137	30495	3.22	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5566	18145	30506	2.68	0.0E+00	X56163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
5566	18145	30507	2.68	0.0E+00	X56163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
5639	18226	30626	7.29	0.0E+00	BE675488.1	EST_HUMAN	719c08.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:3294250 3'
5640	18227	30627	1.94	0.0E+00	BE220753.1	EST_HUMAN	h88a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165184 3' similar to SW:Y054_HUMAN
5641	18228	30628	1.8	0.0E+00	BE794412.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN KIAA0084.
5641	18228	30629	1.8	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5641	18228	30629	1.8	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5642	18229	30630	0.73	0.0E+00	AI189142.1	EST_HUMAN	cd04a04.x1 Soares placenta_81c6weeks_2NbHP81c9W Homo sapiens cDNA clone IMAGE:1722702 3' similar to SW:T2D3_DROME P49848 TRANSCRIPTION INITIATION FACTOR TFIID 85 KD SUBUNIT ;
5646	18233	30633	6.47	0.0E+00	M29808.1	NT	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5660	18237	30636	0.96	0.0E+00	AI791363.1	EST_HUMAN	ch68a09.y5 NCI CGAP_K4d5 Homo sapiens cDNA clone IMAGE:1472152 5' similar to gb:M18512 IG
5660	24590	30644	4.85	0.0E+00		EST_HUMAN	HEAVY CHAIN PRECURSOR V-J REGION (HUMAN);
5670	18265		3.29	0.0E+00	11421038	NT	Homo sapiens Sp4 transcription factor (SP4), mRNA
5671	18266	30655	0.69	0.0E+00	BF665962.1	EST_HUMAN	602118928F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4276264 5'
5671	18266	30656	0.69	0.0E+00	AU134408.1	EST_HUMAN	AU134408 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5677	18262	30663	0.89	0.0E+00	BE538857.1	EST_HUMAN	AU134408 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5686	18271	30691	1.32	0.0E+00	BE292784.1	EST_HUMAN	601061489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5691	18276	30697	1.17	0.0E+00	BF626328.1	EST_HUMAN	601106891F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2988310 5'
5691	18276	30698	1.17	0.0E+00	BF626328.1	EST_HUMAN	602071372F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5711	18760	32553	2.02	0.0E+00	4857384	NT	602071372F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5714	18297	30726	0.91	0.0E+00	AB007935.1	NT	Homo sapiens Bcl-2 protein, partial cds
5714	18297	30726	0.91	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
5719	18301	30731	5.11	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5719	18301	30732	5.11	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 8 (DNAH8) mRNA, complete cds
5733	18315	30748	0.89	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5733	18315	30749	0.89	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5749	18331	30785	2.02	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5755	18336	30791	0.91	0.0E+00	Z38133.1	NT	H sapiens mRNA for myosin
5775	18358	30815	0.81	0.0E+00	D81584.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05 5'
5775	18358	30816	0.81	0.0E+00	D81584.1	EST_HUMAN	5'
5778	18359	30820	3.18	0.0E+00	BF629831.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05 5'
5778	18359	30821	3.18	0.0E+00	BF629831.1	EST_HUMAN	602042322F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179888 5'
5783	18364	30825	2.94	0.0E+00	BF313139.1	EST_HUMAN	602042322F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179888 5'
5794	18376	31033	4.42	0.0E+00	11434392	NT	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5811	18391	31052	4.19	0.0E+00	AI828181.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
							wc95b02.x1 NCI CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2463061 3' similar to TR:O76054
							Q75054 KIAA0468 PROTEIN ;

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5811	18391	31053	4.19	0.0E+00	A1928181.1	EST_HUMAN	wc95b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:075054
5820	18409	31076	1.25	0.0E+00	BE260777.1	EST_HUMAN	O75054 KIAA0466 PROTEIN ;
5838	18418		5.07	0.0E+00	AW867316.1	EST_HUMAN	G01160262F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502809 5'
5854	18433	31105	2.44	0.0E+00	BE292889.1	EST_HUMAN	MRO-SN0037-030-400-001-h07 SN0037 Homo sapiens cDNA
5854	18433	31108	2.44	0.0E+00	BE292889.1	EST_HUMAN	G01105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987803 5'
5875	18454	31128	1.94	0.0E+00	11420819	NT	G01105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987803 5'
5875	18454	31129	1.94	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5883	18462	31137	4.08	0.0E+00	AF064254.1	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5883	18462	31138	4.08	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5880	18469	31148	3.14	0.0E+00	AJ224639.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5890	18469	31149	3.14	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5921	18489	31180	0.72	0.0E+00	A198515.1	EST_HUMAN	q94g10.x1 Soares_plicenta_8to9weeks_2vhrIP8to9W Homo sapiens cDNA clone IMAGE:1757730 3'
5925	18503	31188	7.91	0.0E+00	M85718.1	EST_HUMAN	similar to SW:CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR ;
5932	18510	31195	3.94	0.0E+00	AW405472.1	EST_HUMAN	EST02238 Fetal brain, Striatum (cat936206) Homo sapiens cDNA clone HFBGM48
5945	18522	31205	1.3	0.0E+00	Z28269.1	NT	UI-HF-BLD-adh-4-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'
5957	18533	31215	1.97	0.0E+00	AW361877.1	EST_HUMAN	H.sapiens lscform 1 gene for L-type calcium channel, exon 14 adnd 15
5957	18533	31216	1.97	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5957	18533	31217	1.97	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5960	18538	31220	0.59	0.0E+00	AB035266.1	NT	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5960	18538	31221	0.59	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neuroxin II, complete cds
5962	18538	31224	1.92	0.0E+00	U36281.1	NT	Homo sapiens mRNA for neuroxin II, complete cds
5997	18571	31257	1	0.0E+00	AB046861.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
6059	18631	31323	4.62	0.0E+00	AA195905.1	EST_HUMAN	Homo sapiens mRNA for KIAA1641 protein, partial cds
6060	18632	31324	1.7	0.0E+00	AJ006345.1	NT	z96b11.r1 Striatum muscle 937209 Homo sapiens cDNA clone IMAGE:627633 5' similar to gb-X03740
6060	18632	31325	1.7	0.0E+00	AJ006345.1	NT	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
6069	18641	31337	1.3	0.0E+00	AJ207616.1	EST_HUMAN	Homo sapiens KVLQ11 gene
6091	18660	31354	4.88	0.0E+00	11416801	NT	Homo sapiens KVLQ11 gene
6098	18665	31357	2.14	0.0E+00	BE781173.1	EST_HUMAN	HA2881 Human fetal liver cDNA library Homo sapiens cDNA
6106	18676	31370	1.1	0.0E+00	9898943	NT	Homo sapiens protocadherin beta 2 (PCDH2), mRNA
6107	18676	31371	8.18	0.0E+00	BE60082.1	EST_HUMAN	Homo sapiens protocadherin beta 2 (PCDH2), mRNA
6108	18677	31372	1.66	0.0E+00	10048478	NT	G011684032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938551 5'
							Homo sapiens anilloide-sensitve cation channel 1, neuronal (degenerin) (ACCN1), mRNA
							G01345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677643 5'
							Mus mucleus aozinin (Aoz), mRNA

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6109	18678	31373	3.13	0.0E+00	U66981.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
6109	18678	31374	3.13	0.0E+00	U66981.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
6120	18698	31395	2.52	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184321 5'
6133	18702	31398	1.11	0.0E+00	AF142621.1	NT	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
6134	18703	31399	3.18	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347483 5'
6148	18714	31416	0.79	0.0E+00	BE503096.1	EST_HUMAN	h283d11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214581 3' similar to TR:Q82084 Q82084 PHOSPHOLIPASE C NEIGHBORING
6151	18719	31423	1.87	0.0E+00	BF568905.1	EST_HUMAN	602105852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
6156	18724	31427	0.91	0.0E+00	AA454642.1	EST_HUMAN	z899d06.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811883 3'
6192	18760	31461	1.82	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6194	18760	31463	5.2	0.0E+00	BE828144.1	EST_HUMAN	RC5-E10027-210600-022-G10 E10027 Homo sapiens cDNA
6199	18765	31468	1.28	0.0E+00	BE958638.1	EST_HUMAN	601649287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5'
6205	18771	31476	0.44	0.0E+00	AJ289880.1	NT	Homo sapiens KIA0851 gene (partial), X73 gene and LZTFL1 gene
6218	18784	31489	0.56	0.0E+00	BE673986.1	EST_HUMAN	7d72e11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN
6218	18784	31490	0.56	0.0E+00	BE673986.1	EST_HUMAN	P51843 ORPHAN NUCLEAR RECEPTOR DAX-1, [1];
6223	18789	31496	0.73	0.0E+00	AW276760.1	EST_HUMAN	7d72e11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN
6235	18799	31510	0.91	0.0E+00	BF031742.1	EST_HUMAN	P51843 ORPHAN NUCLEAR RECEPTOR DAX-1, [1];
6235	18799	31511	0.91	0.0E+00	BF031742.1	EST_HUMAN	XP05103.x1 NCL_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335 GUANYLATE KINASE ASSOCIATED PROTEIN, [1];
6247	18811	31528	0.76	0.0E+00	AW470846.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6261	18825	31538	1.05	0.0E+00	BF155670.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6261	18825	31539	1.05	0.0E+00	BF155670.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6269	18832	31545	1.67	0.0E+00	W33069.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6269	18832	31546	1.67	0.0E+00	W33069.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6270	18833		2.84	0.0E+00	AF012616.1	NT	h344d08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875595 3' similar to TR:Q9Z1N3
6274	18837	31552	3.21	0.0E+00	BE280197.1	EST_HUMAN	Q9Z1N3 MYOSIN-RHO GAP PROTEIN, MYR 7, [1];
6280	18842	31560	2.4	0.0E+00	BE889610.1	EST_HUMAN	QV4-HT0894-280900-399-a10 HT0894 Homo sapiens cDNA
6282	18844	31563	0.81	0.0E+00	BE388673.1	EST_HUMAN	QV4-HT0894-280900-399-a10 HT0894 Homo sapiens cDNA
6297	18869	31581	0.74	0.0E+00	AW752848.1	EST_HUMAN	z808d06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
							z808d06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
							z808d06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
							Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
							601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
							601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
							601286320F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3913085 5'
							IL3-CT0220-111199-028-E04 CT0220 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6300	18861	31583	1.32	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6300	18861	31584	1.32	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6301	18862	31585	1.16	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980200 5'
6301	18862	31586	1.16	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980200 5'
6301	18862	31587	1.16	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980200 5'
6317	24608	31604	12.1	0.0E+00	9789986	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCNK2), mRNA
6320	18880	31607	1.39	0.0E+00	AA193508.1	EST_HUMAN	z440h01.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42894 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5.;
6320	18880	31608	1.39	0.0E+00	AA193508.1	EST_HUMAN	z440h01.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42894 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5.;
6343	18901	31633	10.28	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6343	18901	31634	10.28	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6345	18903	31636	0.45	0.0E+00	AW853983.1	EST_HUMAN	RC3-CT0254-110300-027-a09 CT0254 Homo sapiens cDNA
6345	18903	31637	0.45	0.0E+00	AW853983.1	EST_HUMAN	RC3-CT0254-110300-027-a09 CT0254 Homo sapiens cDNA
6386	18943	31680	1.22	0.0E+00	BE258330.1	EST_HUMAN	601114823F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3355565 5'
6396	18963	31688	1.14	0.0E+00	BE169561.1	EST_HUMAN	QV0-HT0368-090200-089-609 HT0368 Homo sapiens cDNA
6406	18963	31698	0.56	0.0E+00	M38107.1	NT	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
6444	19000	31732	1.68	0.0E+00	BE379007.1	EST_HUMAN	601238276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608480 5'
6450	19006	31738	1.51	0.0E+00	AU197772.1	EST_HUMAN	AU197772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
6472	18027	31764	3.98	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
6501	19055	31796	4.88	0.0E+00	AA204740.1	EST_HUMAN	zq81d03.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:848005 5' similar to
6502	19056	31797	3.92	0.0E+00	11545913	NT	TR:G854185 G854185 LEUKOCYTE SURFACE PROTEIN.;
6502	19056	31798	3.92	0.0E+00	11545913	NT	Homo sapiens xylotransferase II (XT2), mRNA
6523	19076	31817	0.63	0.0E+00	U07223.1	NT	Homo sapiens xylotransferase II (XT2), mRNA
6541	19093	31834	1.56	0.0E+00	11426397	NT	Human betaz2-chimaerin mRNA, complete cds
6545	19097	31839	3.04	0.0E+00	BE257173.1	EST_HUMAN	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6562	19113		0.9	0.0E+00	AI66048.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
6566	19117	31860	1.44	0.0E+00	L35930.1	NT	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
6575	19126	31868	1.07	0.0E+00	BE787385.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
6575	19126	31869	1.07	0.0E+00	BE787385.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'

Table 4
Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6588	19137	31884	0.6	0.0E+00	A1198025.1	EST_HUMAN	q150b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT ;
6589	19137	31885	0.6	0.0E+00	A1198025.1	EST_HUMAN	q150b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT ;
6589	19140	31887	1.02	0.0E+00	BF357123.1	EST_HUMAN	q150b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT ;
6597	19148	31897	1.19	0.0E+00	11435630	NT	MRO-HT0923-220800-102-b05 HT0923 Homo sapiens cDNA Homo sapiens peptide transporter 3 (LOC51296), mRNA
6607	19158	31908	0.7	0.0E+00	D55649.1	NT	Human mRNA for alpha mannosidase II isozyme, complete cds
6627	19176	31930	0.99	0.0E+00	AW178142.1	EST_HUMAN	IL3-HT0092-010899-014-A04 HT0062 Homo sapiens cDNA
6648	19196	31947	0.82	0.0E+00	BE674644.1	EST_HUMAN	7602c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302 3' similar to SW:Y176_HUMAN Q14681 HYPOTHETICAL PROTEIN KIAA0176 ;
6654	19202	31953	1.07	0.0E+00	7662039	NT	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6658	19216		7.98	0.0E+00	AV650020.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLC0409 3'
6677	19225	31974	3.66	0.0E+00	AW57598.1	EST_HUMAN	UI-HF-BL0-acc-g-12-Q-J1.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
6680	19228	31977	3.92	0.0E+00	H01255.1	EST_HUMAN	Y27503.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5'
6690	19238	31988	0.52	0.0E+00	11426233	NT	Homo sapiens anion-exchange sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
6695	19242	31993	1.97	0.0E+00	X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
6697	19244	31995	0.9	0.0E+00	AA456375.1	EST_HUMAN	aat14607.r1 Scores_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:819252 5'
6698	19246	31998	1.18	0.0E+00	AI612841.1	EST_HUMAN	t257d08.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292687 3' similar to SW:NTOS_HUMAN P53798 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2 ;
6704	19251	32002	4.33	0.0E+00	BE735989.1	EST_HUMAN	601305388F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639816 5'
6704	19251	32003	4.33	0.0E+00	BE735989.1	EST_HUMAN	601305388F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639816 5'
6708	19255	32009	0.81	0.0E+00	AW748596.1	EST_HUMAN	MRO-BT0284-221199-002-f11 BT0284 Homo sapiens cDNA
6708	19255	32010	0.81	0.0E+00	AW748596.1	EST_HUMAN	MRO-BT0284-221199-002-f11 BT0284 Homo sapiens cDNA
6709	19256		0.77	0.0E+00	U77829.1	NT	Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
6711	19258	32012	15.18	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6711	19258	32013	15.18	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6716	19262	32019	0.89	0.0E+00	BE780483.1	EST_HUMAN	601498712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
6717	19263	32020	0.95	0.0E+00	X92217.1	NT	H.sapiens germ-line immunoglobulin heavy chain, variable region, (13-2)
6735	19280	32042	1.83	0.0E+00	AI689483.1	EST_HUMAN	ws25c07.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498220 3'
6750	19294	32058	2.83	0.0E+00	BE293153.1	EST_HUMAN	601106344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987983 5'
6760	19294	32058	2.83	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987983 5'
6794	19327	32095	0.42	0.0E+00	BE867657.1	EST_HUMAN	601443175F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847291 5'
6799	19332	32102	0.46	0.0E+00	BF057438.1	EST_HUMAN	7k43h05.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3478498 3' similar to TR:O14553 O14553 R31240_1 ;

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6827	19388	32145	1.39	0.0E+00	AW406348.1	EST_HUMAN	UIHF-BLO-acc-h-02-0-JL1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059831 5'
6827	19388	32146	1.39	0.0E+00	AW406348.1	EST_HUMAN	UIHF-BLO-acc-h-02-0-JL1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059831 5'
6861	19401	32177	11.06	0.0E+00	AV719444.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GLCEHC08 5'
6870	19410	32184	0.79	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3951301 5'
6870	19410	32185	0.79	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3951301 5'
6873	19413	32188	2.3	0.0E+00	AF190880.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant Cav1.1a (CACNA1G) mRNA, complete cds
6876	19416	32191	0.47	0.0E+00	L48948.1	NT	Homo sapiens tuberin (TSC2) gene, exons 38, 39, 40 and 41
6878	19418	32192	1.13	0.0E+00	11420658	NT	Homo sapiens transformation/transcription domain-associated protein (TRRAP), mRNA
6885	19425	32199	4.3	0.0E+00	AW163940.1	EST_HUMAN	601681150F1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206
6885	19426	32200	4.3	0.0E+00	AW163940.1	EST_HUMAN	601681150F1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206
6889	19429	32203	0.94	0.0E+00	W37163.1	EST_HUMAN	Z620e06.r1 Soares fetal lung, NbHL19W Homo sapiens cDNA clone IMAGE:302628 5' similar to SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45
6889	19429	32204	0.94	0.0E+00	W37163.1	EST_HUMAN	Z620e06.r1 Soares fetal lung, NbHL19W Homo sapiens cDNA clone IMAGE:302628 5' similar to SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45
6907	19446	32224	1.44	0.0E+00	BE794853.1	EST_HUMAN	601599371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
6914	19453	32231	5.52	0.0E+00	BE799873.1	EST_HUMAN	601599371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
6915	19454	32232	0.84	0.0E+00	BE767955.1	EST_HUMAN	QV1-GN0085-140800-318-h02.GN0085 Homo sapiens cDNA
6915	19454	32233	0.84	0.0E+00	BE767955.1	EST_HUMAN	QV1-GN0085-140800-318-h02.GN0085 Homo sapiens cDNA
6919	19458	32236	6.72	0.0E+00	BE889813.1	EST_HUMAN	601612058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6919	19459	32237	6.72	0.0E+00	BE889813.1	EST_HUMAN	601612058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6928	19467	32245	5.1	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
6933	19472	32249	2.65	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6933	19472	32250	2.65	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6939	19478	32257	3.77	0.0E+00	6005993	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
6942	19480	32259	6.52	0.0E+00	AI638412.1	EST_HUMAN	tt31f11.x1 NCL_GGAP_G08 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE
6944	19482	32261	1.65	0.0E+00	L3282.1	NT	P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR ;
6957	19494	32274	0.87	0.0E+00	AW505430.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
6959	19496	32275	4.36	0.0E+00	AA434584.1	EST_HUMAN	UIHF-BNO-ama-c-01-0-JL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
6975	19512		1.2	0.0E+00	BE217200.1	EST_HUMAN	zw52c03.r1 Soares fetal lung, NbHL19W Homo sapiens cDNA clone IMAGE:773668 5'
6980	19517	32289	1.58	0.0E+00	BE925876.1	EST_HUMAN	601865317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'

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Single Exon Probes Expressed In Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7016	19551	32337	0.57	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
7016	19551	32338	0.87	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
7016	19552		0.53	0.0E+00	AJ230823.1	EST_HUMAN	AJ230823 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D7 3'
7017	19553	32340	0.7	0.0E+00	AW611864.1	EST_HUMAN	hg82e04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952126 3'
7037	19572	32363	1.81	0.0E+00	AU125928.1	EST_HUMAN	AU125928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
7039	19574	32366	0.74	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
7039	19574	32368	0.74	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
7063	19597	32392	1.28	0.0E+00	BE142363.1	EST_HUMAN	GMO-HT0143-270969-062-d08 HT0143 Homo sapiens cDNA
7087	19621	32416	0.93	0.0E+00	BE006012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
7087	19621	32417	0.93	0.0E+00	BE006012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
7115	19648	32444	0.51	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
7117	19650	32446	8.69	0.0E+00	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7119	19652	32448	1.54	0.0E+00	BF085667.1	EST_HUMAN	IL5-GN0032-180800-145-d07 GN0032 Homo sapiens cDNA
7160	19873	32686	3.68	0.0E+00	AX190755.1	EST_HUMAN	zp88e03.t1 Stratiogene HeLa cell s3 637218 Homo sapiens cDNA clone IMAGE:627292 5'
7172	19885	32710	0.99	0.0E+00	U39573.1	NT	Human salivary peroxidase mRNA, complete cds
7176	19889	32712	0.7	0.0E+00	BE571987.1	EST_HUMAN	7a49b07.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z285 Q9Z285
7188	19899	32726	7.16	0.0E+00	A1940621.1	EST_HUMAN	TEKTN. ;
7188	19899	32727	7.16	0.0E+00	A1940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
7202	19913	32743	2.24	0.0E+00	11435828	NT	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
7217	19829	32648	0.82	0.0E+00	AL042443.1	EST_HUMAN	Homo sapiens CD6 antigen (CD6), mRNA
7218	19830	32647	1.79	0.0E+00	X56163.1	NT	DKFZp434D2021_11 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D2021 5'
7221	19833	32650					H. sapiens Immunoglobulin, heavy chain gene, variable region
7226	19838	32655	0.78	0.0E+00	A168270.1	EST_HUMAN	co10d01.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1565761 3' similar to TR:Q26623 Q26623 TEKTN C1. ;
7250	18024	30407	0.91	0.0E+00	BE734087.1	EST_HUMAN	601567370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'
7259	18033	30416	1.47	0.0E+00	BE556381.1	EST_HUMAN	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682287 5'
7259	18033	30417	15.9	0.0E+00	BE687899.1	EST_HUMAN	601443667F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3847697 5'
7259	18033	30417	15.9	0.0E+00	BE687899.1	EST_HUMAN	601443667F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3847697 5'
7267	19772	32579	2.84	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
7267	19772	32580	2.84	0.0E+00	BE550162.1	EST_HUMAN	Q08379 GOLGIN-95 ;
7267	19772	32580	2.84	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7281	19768	32595	0.73	0.0E+00	BF700780.1	EST_HUMAN	602128566F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285532 5'
7286	19800	32611	1.54	0.0E+00	BF088376.1	EST_HUMAN	GM1-HT0877-060900-397-q11 HT0877 Homo sapiens cDNA
7302	19808	32618	1.54	0.0E+00	AA195108.1	EST_HUMAN	z34g03.r1 Soares_NhiMPu_S1 Homo sapiens cDNA clone IMAGE:685332 5'
7303	19807	32619	0.41	0.0E+00	AW391684.1	EST_HUMAN	MR3-ST0220-161290-028-g08 ST0220 Homo sapiens cDNA
7311	19723		13.17	0.0E+00	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
7313	19726	32627	1.19	0.0E+00	11431474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
7315	19727	32630	0.53	0.0E+00	BE313075.1	EST_HUMAN	601150662F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503391 5'
7316	19727	32631	0.53	0.0E+00	BE313075.1	EST_HUMAN	601150662F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503391 5'
7330	16742	32545	3.41	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310078 5'
7338	19760	32653	0.72	0.0E+00	4557394	NT	Homo sapiens Bloom syndrome (BLM) mRNA
7346	19768		2.15	0.0E+00	J03069.1	NT	Human MYCL2 gene, complete cds
7355	19812	32624	1.58	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7355	19812	32625	1.69	0.0E+00	AF217299.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7356	19813	32626	1.16	0.0E+00	M38113.1	NT	Homo neurofibromatosis type 1 gene, exon x3
7369	18039	30423	3.58	0.0E+00	11420776	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
7370	18040	30424	0.61	0.0E+00	AI419969.1	EST_HUMAN	tg53c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112490 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN. ;
7370	18040	30425	0.61	0.0E+00	AI419969.1	EST_HUMAN	tg53c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112490 3' similar to SW:OXYB_HUMAN P22069 OXYSTEROL-BINDING PROTEIN. ;
7375	18045	30429	0.77	0.0E+00	BE256708.1	EST_HUMAN	601155156F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3366330 5'
7387	18056	30395	0.43	0.0E+00	AI650911.1	EST_HUMAN	wf21c09.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:MT4297 HOMEBOX PROTEIN HOX-A4 (HUMAN); contains PTR5.b1 MER22 REPETITIVE element;
7387	18056	30396	0.43	0.0E+00	AI650911.1	EST_HUMAN	wf21c09.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:MT4297 HOMEBOX PROTEIN HOX-A4 (HUMAN); contains PTR5.b1 MER22 REPETITIVE element;
7398	18087	30357	1.19	0.0E+00	AU118478.1	EST_HUMAN	AU118478 HEMBA1 Homo sapiens cDNA clone HEMBA1003078 5'
7401	18070	30361	6.26	0.0E+00	BE262841.1	EST_HUMAN	601148854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501828 5'
7402	18071	30362	2.96	0.0E+00	Z37978.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7402	18071	30363	2.96	0.0E+00	Z37978.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7403	18072	30384	3.35	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7403	18072	30365	3.35	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7410	18079	30372	1.44	0.0E+00	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7412	19081	30374	0.55	0.0E+00	BF130916.1	EST_HUMAN	601819722F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4051709 5'
7417	19922	32752	0.6	0.0E+00	BE762770.1	EST_HUMAN	QV3-NT0022-140600-223-01 NT0022 Homo sapiens cDNA
7423	19928	32759	2.6	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7425	19930	32761	0.82	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7425	19930	32762	0.62	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7429	19934	32767	4.01	0.0E+00	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
7434	19938	32771	0.71	0.0E+00	AW502362.1	EST_HUMAN	UI-HF-BR0p-aka-d-10-0-UJL1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7434	19938	32772	0.71	0.0E+00	AW502362.1	EST_HUMAN	UI-HF-BR0p-aka-d-10-0-UJL1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7445	19948	32782	0.91	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211.1_1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434D2211 5'
7445	19948	32783	0.91	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211.1_1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434D2211 5'
7455	19958	32792	5.37	0.0E+00	BF308996.1	EST_HUMAN	601869823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7461	19963	32797	2.56	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
7505	19709	32510	1.17	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7611	19714	32617	0.51	0.0E+00	AW513069.1	EST_HUMAN	xc40ec2.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2706458 3' similar to TR:O94895 O94895 KIAA0803 PROTEIN;
7547	19997	32837	0.82	0.0E+00	AB028893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7547	19997	32838	0.82	0.0E+00	AB028893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7552	20002	32844	0.99	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7552	20002	32845	0.99	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7558	20008	32851	1.35	0.0E+00	AW954806.1	EST_HUMAN	EST368876 MAGC resequences, MAGC Homo sapiens cDNA
7559	20009	32852	0.79	0.0E+00	BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354568 5'
7573	20023	32866	0.94	0.0E+00	L01973.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7581	20030	32876	0.81	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7581	20030	32877	0.81	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7587	20036	32884	2.17	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001556 5'
7604	20053	32905	0.97	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7606	20055	32907	0.5	0.0E+00	AA312125.1	EST_HUMAN	EST182818 Jurkat T-cells VI Homo sapiens cDNA 5' and
7612	20061		2.69	0.0E+00	AU143708.1	EST_HUMAN	AU143708 Y78AA1 Homo sapiens cDNA clone Y78AA1002365 5'
7613	20062	32914	1.07	0.0E+00	4758839	NT	Homo sapiens neflin 1 (NTN1), mRNA
7623	20072	32924	1.38	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7623	20072	32925	1.38	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7645	18093	30335	2.62	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7645	18093	30336	2.62	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7657	20103	32854	0.82	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7657	20103	32855	0.82	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7670	20116	32869	4.35	0.0E+00	11436639	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7670	20116	32870	4.35	0.0E+00	11436639	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7685	20130	32884	0.52	0.0E+00	AF227744.1	NT	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform as (CACNA1G) mRNA, complete cds
7707	20152	33009	45.04	0.0E+00	A1128344.1	EST_HUMAN	qc87a07.x1 Soares_placenta_8to9weeks_2N6HP8b9W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ;contains element HGR repetitive element ;
7707	20152	33010	45.04	0.0E+00	A1128344.1	EST_HUMAN	qc87a07.x1 Soares_placenta_8to9weeks_2N6HP8b9W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ;contains element HGR repetitive element ;
7710	20155	33013	0.75	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7710	20155	33014	0.75	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7713	20158	33017	5.32	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7713	20158	33018	5.32	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7717	20182		15.18	0.0E+00	BF337376.1	EST_HUMAN	602035086F1 NCI CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4182839 5'
7719	20164	33021	3.02	0.0E+00	AA128453.1	EST_HUMAN	zn60109.t1 Stratagene muscle 637209 Homo sapiens cDNA clone IMAGE:562801 5' similar to TR:G806562 G806562 NEBULIN ;
7724	20168	33027	0.69	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7724	20168	33028	0.69	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7735	20179	33040	0.88	0.0E+00	AJ270896.1	NT	Homo sapiens partial mRNA for LTRPC5 protein (LTRPC5 gene)
7772	20214	33077	1.24	0.0E+00	BE285489.1	EST_HUMAN	601174576F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528784 5'
7774	20216	33078	1.1	0.0E+00	11427865	NT	Homo sapiens hypothetical protein (FLJ20281), mRNA
7777	20219		1.52	0.0E+00	AU118607.1	EST_HUMAN	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'
7778	20220	33081	2.21	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7778	20220	33082	2.21	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7780	20232	33092	0.94	0.0E+00	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
7789	20241	33098	11.28	0.0E+00	KT0172.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
7801	20243	33100	7.8	0.0E+00	U45448.1	NT	Human P2X1 receptor mRNA, complete cds
7801	20243	33101	7.8	0.0E+00	U45448.1	NT	Human P2X1 receptor mRNA, complete cds
7815	20257	33117	1.05	0.0E+00	AW956603.1	EST_HUMAN	EST1368573 MAGE resequences, MAGD Homo sapiens cDNA
7817	20259	33119	0.57	0.0E+00	BE672445.1	EST_HUMAN	7a60108.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:3223167 3' similar to gb:M54911_ma1 IG HEAVY CHAIN PRECURSOR V-J REGION (HUMAN);

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7818	20260	33120	2.82	0.0E+00	AW050516.1	EST_HUMAN	EST1362588 IMAGE resequences, MAGA Homo sapiens cDNA
7847	20287	33149	0.82	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7847	20287	33150	0.82	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7847	20287	33151	0.82	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7872	20311		0.72	0.0E+00	M60354.1	NT	Human BTF3 protein homologue gene, complete cds
7873	20312	33178	0.65	0.0E+00	BE408293.1	EST_HUMAN	601302678F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637434 5'
7885	20324	33189	0.44	0.0E+00	AW402542.1	EST_HUMAN	U1HF-BK0-aae-g-07-0-JL1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3064924 5'
7904	20343		1.16	0.0E+00	R67430.1	EST_HUMAN	ym88h10.r1 Scores adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:166051 5'
7905	20344	33210	1.89	0.0E+00	AW239326.1	EST_HUMAN	x639a05.y1 NCI CGAP Lu31 Homo sapiens cDNA clone IMAGE:2878640 5' similar to TR:Q08050 Q08050
7927	20384		1.41	0.0E+00	AU117553.1	EST_HUMAN	HNF3/TFH TRANSCRIPTION FACTOR GENESIS ;
7929	20366	33231	3.97	0.0E+00	11427135	NT	U1HF1653 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5'
7950	20387	33254	1.81	0.0E+00	AA211663.1	EST_HUMAN	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7958	20394	33261	0.66	0.0E+00	BF229235.1	EST_HUMAN	z56602.r1 Stratagene muscle 637209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740
7863	20369	33269	0.73	0.0E+00	AW405627.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7969	20405	33275	0.65	0.0E+00	AW996499.1	EST_HUMAN	MRO-AN0083-270900-004-07 AN0083 Homo sapiens cDNA
7972	20408	33278	0.83	0.0E+00	L32832.1	NT	U1HF-BLO-abs-d-07-0-JL1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057469 5'
8002	20425	33291	0.43	0.0E+00	11420764	NT	QV3-BN0046-220300-128-e04 BN0046 Homo sapiens cDNA
8002	20435	33301	1.04	0.0E+00	BF306996.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
8012	20444	33314	1.08	0.0E+00	AU118787.1	EST_HUMAN	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
8047	20479	33353	0.82	0.0E+00	AW499551.1	EST_HUMAN	601899823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
8075	20503	33380	0.42	0.0E+00	AB002355.1	NT	601899823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
8076	20504	33381	4.07	0.0E+00	A1752561.1	EST_HUMAN	AU118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'
8076	20504	33382	4.07	0.0E+00	A1752561.1	EST_HUMAN	U1HF-BR0p-aj-e-10-0-JL1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3074778 5'
8148	20571	33447	0.51	0.0E+00	AA398959.1	EST_HUMAN	Human mRNA for KIAA0357 gene, partial cds
8148	20571	33448	0.51	0.0E+00	AA398959.1	EST_HUMAN	cn17405.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
8148	20572	33449	0.53	0.0E+00	AL046347.2	EST_HUMAN	cn17405.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
8166	20588	33468	1.27	0.0E+00	AF064205.1	NT	zu68b07.r1 Scores_NHT Homo sapiens cDNA clone IMAGE:743125 5'
							zu68b07.r1 Scores_NHT Homo sapiens cDNA clone IMAGE:743125 5'
							DKFZp434J087_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J087 5'
							Homo sapiens dynactin 1 (DC1N1) gene, alternatively spliced products, exons 7 through 32 and complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8168	20588	33469	1.27	0.0E+00	AF084205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
8174	20598	33480	0.98	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
8188	20610	33497	1.5	0.0E+00	BE439545.1	EST_HUMAN	HTM1-183F1 HTM1 Homo sapiens cDNA
8189	20611	33498	1.09	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorm) 5A (SEMA5A), mRNA
8207	20627	33515	0.45	0.0E+00	AW672785.1	EST_HUMAN	ba01608.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823108 5' similar to SW:P101_PIG 002698 PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT ;
8207	20627	33518	0.45	0.0E+00	AW672785.1	EST_HUMAN	ba01608.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823108 5' similar to SW:P101_PIG 002698 PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT ;
8214	20634	33523	0.49	0.0E+00	BF569805.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
8224	20643	33533	1.3	0.0E+00	AB255504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O75363 O75363 AIBC1 ;
8224	20843	33534	1.3	0.0E+00	AB255504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O75363 O75363 AIBC1 ;
8233	20652	33544	1.51	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
8239	20666	33547	1.08	0.0E+00	N76128.1	EST_HUMAN	za86e06.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299456 3'
8248	20665	33554	6.8	0.0E+00	BF217905.1	EST_HUMAN	601865465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
8253	20670	33560	0.57	0.0E+00	BF569882.1	EST_HUMAN	602185808F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310286 5'
8258	20675	33565	5.5	0.0E+00	AU129622.1	EST_HUMAN	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
8284	24647	33593	1.32	0.0E+00	AW069274.1	EST_HUMAN	cr42e08.x1 Jila bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e08 3'
8284	24647	33594	1.32	0.0E+00	AW069274.1	EST_HUMAN	cr42e08.x1 Jila bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e08 3'
8288	20704	33596	7.08	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8295	20711	33603	1.04	0.0E+00	AV758467.1	EST_HUMAN	AV758467 BM Homo sapiens cDNA clone BMFBGG05 5'
8298	20713	33605	6.86	0.0E+00	BE739870.1	EST_HUMAN	601593166F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
8298	20713	33606	6.86	0.0E+00	BE739870.1	EST_HUMAN	601593166F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
8299	20714	33607	0.85	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
8299	20714	33608	0.85	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
8300	20715	33609	1.71	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
8300	20715	33610	1.71	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
8327	20742	33636	0.52	0.0E+00	BF580287.1	EST_HUMAN	naab22e04.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3263214 3' similar to contains element TAR1 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8341	20756	33651	1.68	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
8341	20756	33652	1.68	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
8378	20782	33691	0.42	0.0E+00	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8381	20795	33693	0.49	0.0E+00	X92224.1	NT	H. sapiens germline immunoglobulin heavy chain, variable region, (8-1G1)
8384	20788	33696	0.51	0.0E+00	BE736034.1	EST_HUMAN	601305637F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640041 5'
8395	20809	33708	0.44	0.0E+00	AW956307.1	EST_HUMAN	EST368377 MAGE sequences, MAGD Homo sapiens cDNA
8405	20819						7a31a04.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:3220302 3' similar to gb:S67768
8428	20843	33743	0.47	0.0E+00	Y16795.1	NT	HYALURONIDASE PRECURSOR (HUMAN);
8431	20845	33745	0.47	0.0E+00	AJ404498.1	NT	Homo sapiens pshHsaA pseudogene
8431	20845	33746	0.47	0.0E+00	AJ404498.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
8439	20853	33754	0.46	0.0E+00	W52673.1	EST_HUMAN	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
8442	20856	33758	0.44	0.0E+00	11425128	NT	zc80f10.1 Pancreatic islet Homo sapiens cDNA clone IMAGE:336443 5'
8443	20857	33759	0.6	0.0E+00	AU117333.1	EST_HUMAN	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC83433), mRNA
8444	20858		0.81	0.0E+00	BE613963.1	EST_HUMAN	AU117333 HEMBA1 Homo sapiens cDNA clone HEMBA1001175 5'
8458	20871	33771	0.44	0.0E+00	AB001523.1	NT	601504084F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905733 5'
8470	20883	33781	0.43	0.0E+00	AW988044.1	EST_HUMAN	Homo sapiens gene for TMEH1 and PWP2, complete and partial cds
8471	20884	33782	0.53	0.0E+00	AH33435.1	EST_HUMAN	EST380119 MAGE sequences, MAGJ Homo sapiens cDNA
8501	20913	33808	0.5	0.0E+00	6995995	NT	HA2043 Human fetal liver cDNA library Homo sapiens cDNA
8501	20913	33809					Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8502	20914	33810	0.5	0.0E+00	6995995	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8521	20932	33829	0.43	0.0E+00	AW408410.1	EST_HUMAN	UI-HF-BKO-ey-h-04-0-UJ.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3055710 5'
8578	21013	33913	1.87	0.0E+00	AA149791.1	EST_HUMAN	UI-HF-BKO-abk-k-11-Q-UJ.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3056780 5'
8608	21041	33948	2.07	0.0E+00	BE736046.1	EST_HUMAN	zco1c08.1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:566410 5'
8619	21054	33960	7.24	0.0E+00	M34872.1	NT	601306659F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'
8619	21054	33961	7.24	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8645	21080	33987	2.28	0.0E+00	AA337551.1	EST_HUMAN	Human amyloid-beta protein (APP) gene, exon 11
8648	21083	33988	4.28	0.0E+00	AU142402.1	EST_HUMAN	z81b04.1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
8650	21085	33992	1.14	0.0E+00	BE388421.1	EST_HUMAN	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
8650	21085	33993	1.14	0.0E+00	BE388421.1	EST_HUMAN	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA100277 5'
							601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
							601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8682	21097	34003	1.08	0.0E+00	W95278.1	EST_HUMAN	z605d01.t1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
8682	21097	34004	1.08	0.0E+00	W95278.1	EST_HUMAN	z605d01.t1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
8683	21098		7.08	0.0E+00	BF873098.1	EST_HUMAN	602163008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284128 5'
8687	21102		1.18	0.0E+00	AU134114.1	EST_HUMAN	AU134114 OVARC1 Homo sapiens cDNA clone OVARC1001298 5'
8679	21114	34017	2.21	0.0E+00	BF525534.1	EST_HUMAN	602069832F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4212727 5'
8679	21114	34018	2.21	0.0E+00	BF525534.1	EST_HUMAN	602069832F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4212727 5'
8698	21133	34035	1.81	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P082.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P082 5'
8688	21133	34036	1.81	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P082.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P082 5'
8727	21182		1.31	0.0E+00	BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887773 5'
8742	21176	34079	1.34	0.0E+00	AW600849.1	EST_HUMAN	UI-HF-BNO-ak4-f01-q-Ul.t1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077498 5'
8750	21184	34083	14.28	0.0E+00	AW157233.1	EST_HUMAN	eu93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783789 3' similar to TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
8777	21211	34114	1.28	0.0E+00	11421722	NT	Homo sapiens centronal protein 2 (CEP2), mRNA
8781	21216	34118	1.17	0.0E+00	BE746597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8781	21215	34119	1.17	0.0E+00	BE746597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8781	21225	34131	1.21	0.0E+00	AJ271735.1	NT	Homo sapiens Xa1 pseudautosomal region, segment 1/2
8828	21280	34168	2.21	0.0E+00	BE674157.1	EST_HUMAN	7d76a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O85783 O85783 STAUFEN PROTEIN. ;
8828	21262	34168	1.75	0.0E+00	AI885971.1	EST_HUMAN	W60b10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P60281 MATRIX METALLOPROTEINASE-14 PRECURSOR ;
8837	21271	34179	1.49	0.0E+00	BE593650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8837	21271	34180	1.49	0.0E+00	BE593650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8844	21278	34189	1.88	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8844	21278	34180	1.88	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8845	21279	34181	0.95	0.0E+00	AA403192.1	EST_HUMAN	z66802.t1 Soares_fetal_heart_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:768619 5' similar to TR:G1304132 G1304132 TPRD. ;
8845	21279	34192	0.95	0.0E+00	AA403192.1	EST_HUMAN	z66802.t1 Soares_fetal_heart_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:768619 5' similar to TR:G1304132 G1304132 TPRD. ;
8877	21311		3.63	0.0E+00	AA398511.1	EST_HUMAN	z173a08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S66655 PROHIBITIN (HUMAN);
8883	21317	34228	1.84	0.0E+00	BE637593.1	EST_HUMAN	RC2-FN0084-120600-013-h07 FN0084 Homo sapiens cDNA
8884	21318	34230	1.7	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221289-046-c07 DT0045 Homo sapiens cDNA
8884	21318	34231	1.7	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221289-046-c07 DT0045 Homo sapiens cDNA
8900	21334	34247	1.46	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3886179 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8900	21334	34248	1.48	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855179 5'
8913	21347	34284	1.45	0.0E+00	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
8913	21347	34285	1.46	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8928	21362	34275	0.92	0.0E+00	AA502294.1	EST_HUMAN	nc25d10.s1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1138434
8937	21371		1.77	0.0E+00	BE890787.1	EST_HUMAN	G1138434 KIAA0187 PROTEIN.;
8956	21389	34301	2.25	0.0E+00	4758695	NT	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'
8956	21389	34302	2.25	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9009	21442	34352	1.74	0.0E+00	X98922.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9009	21442	34353	1.74	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
9009	21442	34354	1.74	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
9016	21449	34359	0.84	0.0E+00	U82978.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
9050	21482	34394	1.48	0.0E+00	AU131671.1	EST_HUMAN	AU131671 NT2RP3 Homo sapiens cDNA clone NT2RP3003016 5'
9060	21492		1.2	0.0E+00	AW513513.1	EST_HUMAN	xc46601.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POLYPROTEIN (HUMAN);
9082	21494	34403	3.18	0.0E+00	D92850.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-084C02 5'
9084	21516	34426	4.53	0.0E+00	BE378495.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
9089	21521	34429	2.69	0.0E+00	AA410646.1	EST_HUMAN	z332a04.t1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:724062 5'
9090	21522		1.88	0.0E+00	BF313946.1	EST_HUMAN	601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'
9097	21529	34436	1.6	0.0E+00	AW135873.1	EST_HUMAN	U1-H-B11-adr-e-12-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
9097	21529	34437	1.6	0.0E+00	AW135873.1	EST_HUMAN	U1-H-B11-adr-e-12-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
9122	21534	34458	2.35	0.0E+00	BE260272.1	EST_HUMAN	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5'
9125	21557	34461	2.51	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
9125	21557	34462	2.51	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
9125	21557	34463	2.51	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
9134	21566	34472	10.34	0.0E+00	AI468722.1	EST_HUMAN	tk13h11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:27150949 3'
9154	21586	34494	0.83	0.0E+00	AL449770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Starvides GS) Homo sapiens cDNA c80g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S
9159	21591	34498	11.14	0.0E+00	AA982627.1	EST_HUMAN	RIBOSOMAL PROTEIN L7A (HUMAN);
9165	21597	34506	2.02	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
9165	21597	34507	2.02	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
9184	21616	34527	1.55	0.0E+00	Y11107.3	NT	Homo sapiens ITGB4 gene for Integrin beta 4 subunit, exons 3-41
9186	21618	34529	1.8	0.0E+00	BE278917.1	EST_HUMAN	601155330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9194	21626		3.72	0.0E+00	AV718377.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAF11 5'
9199	21631	34540	2.98	0.0E+00	AW337277.1	EST_HUMAN	xw73c07.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X53587
9203	21636	34544	1.24	0.0E+00	AU124051.1	EST_HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
9207	21699	34610	6.03	0.0E+00	AW592233.1	EST_HUMAN	h448a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2836096 3'
9207	21699	34611	6.03	0.0E+00	AW592233.1	EST_HUMAN	h448a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2836096 3'
9297	21729	34637	0.91	0.0E+00	AV714784.1	EST_HUMAN	AV714784 DCB Homo sapiens cDNA clone DCBAUA08 5'
9304	21736	34642	3.26	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814 3'
9304	21736	34643	3.26	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814 3'
9307	21739	34646	1.63	0.0E+00	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
9309	21741	34649	2.39	0.0E+00	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9335	21767	34671	3.31	0.0E+00	11422857	NT	Homo sapiens tumor protein p73 (TP73), mRNA
9341	21773	34678	1.14	0.0E+00	K01241.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
9345	21777	34683	5.31	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
9345	21777	34684	5.31	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
9349	21781	34689	2.06	0.0E+00	AV660739.1	EST_HUMAN	AV660739 GLC Homo sapiens cDNA clone GLCGKG12 3'
9353	21785	34693	3.77	0.0E+00	7706838	NT	Homo sapiens polyesthrin-L (PKDL), mRNA
9358	21790	34698	1.01	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
9358	21790	34699	1.01	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
9375	21807	34717	4.79	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9375	21807	34718	4.79	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9388	21818	34734	1.87	0.0E+00	X14768.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
9394	21826	34741	1.45	0.0E+00	AI051395.1	EST_HUMAN	an28e04.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700094 3'
9398	21830	34744	2.13	0.0E+00	AI054607.1	EST_HUMAN	wq34at12.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473160 3' similar to SW:MGB3_HUMAN
9402	21834	34748	5.26	0.0E+00	9256595	NT	O16480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
9411	21843	34757	2.17	0.0E+00	AW958311.1	EST_HUMAN	Homo sapiens probocadherin alpha 8 (PCDH8), mRNA
9418	21850	34764	2.89	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
9428	21860	34777	1.21	0.0E+00	AU142652.1	EST_HUMAN	AU142652 Y79AA1 Homo sapiens cDNA clone Y79AA1000878 5'
9434	21866	34782	1.2	0.0E+00	11436995	EST_HUMAN	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
9435	21867		1.01	0.0E+00	BE410768.1	EST_HUMAN	601301676F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636163 5'
9445	21876	34795	1.49	0.0E+00	BF002024.1	EST_HUMAN	7987m12.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:Q8UH62

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9455	21886	34808	1.81	0.0E+00	AB011150.1	NT	Homo sapiens mRNA for KIAA0578 protein, partial cds
9456	21887	34807	5.14	0.0E+00	BE794823.1	EST_HUMAN	601588284F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3943463 5'
9463	21894	34815	1.28	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC.71 Homo sapiens cDNA clone IMAGE:3911986 5'
9463	21894	34816	1.28	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC.71 Homo sapiens cDNA clone IMAGE:3911986 5'
9477	21908	34829	0.82	0.0E+00	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9479	21910	34832	1.65	0.0E+00	AA344601.1	EST_HUMAN	EST60505 Gall bladder 1 Homo sapiens cDNA 5' end
9479	21910	34833	1.65	0.0E+00	AA344601.1	EST_HUMAN	EST60505 Gall bladder 1 Homo sapiens cDNA 5' end
9523	21938	34861	1.05	0.0E+00	AW673469.1	EST_HUMAN	ba64d08.y3 NIH_MGC.10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O60275 O60275
9523	21938	34862	1.05	0.0E+00	AW673469.1	EST_HUMAN	KIAA0522 PROTEIN;
9549	21983	34885	1.97	0.0E+00	BE207063.1	EST_HUMAN	ba08f06.y1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus
9549	21983	34886	1.97	0.0E+00	BE207063.1	EST_HUMAN	Bcl-xL mRNA, complete cds (MOUSE);
9559	22122	35049	1.83	0.0E+00	BF348013.1	EST_HUMAN	ba08f06.y1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus
9580	22003	34930	3.39	0.0E+00	BE712515.1	EST_HUMAN	Bcl-xL mRNA, complete cds (MOUSE);
9609	22089	35017	1.02	0.0E+00	5803069	NT	602023150F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158300 5'
9609	22089	35018	1.02	0.0E+00	5803069	NT	QV2-HT0898-250700-282-508 HT0898 Homo sapiens cDNA
9617	22032	34962	1.29	0.0E+00	AL042278.1	EST_HUMAN	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9641	22066	34987	1.65	0.0E+00	AI088043.1	EST_HUMAN	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9646	20937	33834	1.24	0.0E+00	11560151	NT	DKFZp434L0120.t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
9646	20937	33835	1.24	0.0E+00	11560151	NT	ow60h01.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14677 KIAA0171 PROTEIN.;
9648	20939	33838	9.68	0.0E+00	AI290909.1	EST_HUMAN	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9648	20939	33839	9.68	0.0E+00	AI290909.1	EST_HUMAN	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9649	20940	33840	3.67	0.0E+00	AW953836.1	EST_HUMAN	gm09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
9670	22017	34947	3.01	0.0E+00	AF153466.1	NT	P28316 60S RIBOSOMAL PROTEIN L23A.;
9681	22093	35003	8.02	0.0E+00	BE255829.1	EST_HUMAN	gm09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
9683	22095	35024	1.38	0.0E+00	BE781382.1	EST_HUMAN	P28316 60S RIBOSOMAL PROTEIN L23A.;
							gm09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
							P28316 60S RIBOSOMAL PROTEIN L23A.;
							EST366028 MAGC resequences, MAGC Homo sapiens cDNA
							Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8
							601109942F1 NIH_MGC.16 Homo sapiens cDNA clone IMAGE:3350722 5'
							601468828F1 NIH_MGC.87 Homo sapiens cDNA clone IMAGE:3870007 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9683	22095	35025	1.38	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_07 Homo sapiens cDNA clone IMAGE:3670007 5'
9685	22097	35026	14.64	0.0E+00	AW163779.1	EST_HUMAN	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072
9688	22110	35038	3.69	0.0E+00	BE283191.1	EST_HUMAN	60S RIBOSOMAL PROTEIN L7A (HUMAN);
9712	22135	35081	5.51	0.0E+00	C06158.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
9712	22135	35062	5.51	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9714	22137	35085	2.41	0.0E+00	BE746215.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9723	22146	35073	2.64	0.0E+00	11437282	NT	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
9723	22146	35074	2.64	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9723	22146	35075	2.64	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9739	22066	34993	1.41	0.0E+00	BE900549.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9757	22180	35092	2.88	0.0E+00	AF018084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9757	22180	35093	2.88	0.0E+00	AF018084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9778	22181	35116	1.34	0.0E+00	BE082977.1	EST_HUMAN	RC2-BT0842-130300-017-g01 BT0842 Homo sapiens cDNA
9792	22185	35133	2.39	0.0E+00	AW500293.1	EST_HUMAN	UHF-BN0-akg-b-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9792	22185	35134	2.39	0.0E+00	AW500293.1	EST_HUMAN	UHF-BN0-akg-b-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9799	22202	35139	1.58	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
9799	22202	35140	1.58	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
9814	22217	35153	1.16	0.0E+00	AB036355.1	NT	Homo sapiens mRNA for neurodin alpha protein, complete cds
9818	22221	35157	2.75	0.0E+00	AW500528.1	EST_HUMAN	UHF-BN0-akg-b-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5'
9851	22254	35190	1.96	0.0E+00	AF009868.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
9866	22269	35208	2.9	0.0E+00	S78466.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9866	22269	35209	2.9	0.0E+00	S78466.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9868	22271	35212	2.75	0.0E+00	BE593320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688680 5'
9881	22284	35224	2.72	0.0E+00	AW353135.1	EST_HUMAN	CM2-CT0311-301169-043-h11 CT0311 Homo sapiens cDNA
9883	22285	35236	0.97	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
9906	22308	35251	2.34	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9906	22308	35252	2.34	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9914	22316	35282	0.95	0.0E+00	AW500636.1	EST_HUMAN	UHF-BP0p-akg-b-12-0-U1.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10186	22897	35594	1.01	0.0E+00	BE568511.1	EST_HUMAN	60146134F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3830177 5'
10223	22624	35591	1.13	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10236	22637	35598	4.66	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10236	22637	35600	4.66	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10237	22638	35601	1.09	0.0E+00	AA704457.1	EST_HUMAN	419b06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450707 3' similar to gb:M14123_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10239	22640	35602	1.45	0.0E+00	M22821.1	NT	Human beta 1,4-galactosyl-transferase mRNA, complete cds
10241	22642	35605	4.47	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4184839 5'
10241	22642	35606	4.47	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4184839 5'
10258	22659	35621	0.98	0.0E+00	BE897148.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10258	22659	35622	0.96	0.0E+00	BE897148.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10292	22693	35657	1.01	0.0E+00	A1631818.1	EST_HUMAN	w336603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10292	22693	35658	1.01	0.0E+00	A1631818.1	EST_HUMAN	Q61204 NOTCH2-LIKE;
10303	22703	35698	1.68	0.0E+00	T03078.1	EST_HUMAN	w336603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10319	22719	35697	1.08	0.0E+00	AU122428.1	EST_HUMAN	Q61204 NOTCH2-LIKE;
10341	22741	35710	2.23	0.0E+00	BF436218.1	EST_HUMAN	FB23A4 Fetal brain, Sireligene Homo sapiens cDNA clone FB23A4 3' end
10342	22742		1.4	0.0E+00	AV654766.1	EST_HUMAN	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002388 5'
10356	22756	35723	4.65	0.0E+00	AW517860.1	EST_HUMAN	rab45a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
10360	22760	35727	5.52	0.0E+00	BE549213.1	EST_HUMAN	AV654765 GLC Homo sapiens cDNA clone GLCDZC07 3'
10365	22765	35754	2.39	0.0E+00	BE761742.1	EST_HUMAN	xt74601.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M69066 MOESIN (HUMAN);
10397	22797	35771	2.24	0.0E+00	BE082720.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
10397	22797	35772	2.24	0.0E+00	BE082720.1	EST_HUMAN	601467419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
10407	22807	35793	4.13	0.0E+00	BE743215.1	EST_HUMAN	RC2-BT0842-150200-012-403 BT0842 Homo sapiens cDNA
10407	22807	35794	4.13	0.0E+00	BE743215.1	EST_HUMAN	RC2-BT0842-150200-012-403 BT0842 Homo sapiens cDNA
10410	22810	35786	1.25	0.0E+00	BE617655.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3836188 5'
10410	22810	35786	1.25	0.0E+00	BE617655.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3836188 5'
10430	22830	35800	0.86	0.0E+00	AB029290.1	NT	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845958 3'
10436	22887		2.06	0.0E+00	AW813783.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845958 3'
10441	22892	35808	5.94	0.0E+00	AW963563.1	EST_HUMAN	Homo sapiens mRNA for actin binding protein ABP620, complete cds
10451	22902	35890	9.88	0.0E+00	11431124	NT	RC3-ST0197-120200-015-403 ST0197 Homo sapiens cDNA
10451	22902	35891	9.88	0.0E+00	11431124	NT	EST1376638 MAGI resequences, MAGH Homo sapiens cDNA
							Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
							Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10455	22906	35885	2.41	0.0E+00	AW057621.1	EST_HUMAN	wy8109.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2653065 3' similar to TR:Q60566 Q60566 VDX;
10462	22912	35892	2.78	0.0E+00	BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) BAYLOR-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917
10465	22915	35894	4.51	0.0E+00	BE306642.1	EST_HUMAN	601888704F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122849 5'
10466	22916	35895	6.81	0.0E+00	BE872908.1	EST_HUMAN	601451502F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3855289 5'
10468	22918	35898	5.81	0.0E+00	BE872908.1	EST_HUMAN	601451502F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3855289 5'
10472	22922	35901	4.75	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10472	22922	35902	4.76	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10484	22934	35912	5.37	0.0E+00	AW404795.1	EST_HUMAN	U1HF-BLO-aam-4.04-0-U1.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
10488	22938	35917	7.07	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10488	22938	35918	7.07	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10489	22939	35919	2.58	0.0E+00	A1891827.1	EST_HUMAN	w132b05.x1 Soares_Diethylstilbestrol (DES) receptor 1E (HTR1E) mRNA
10492	22942	35924	5.39	0.0E+00	BE882109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5'
10495	22945	35926	20.52	0.0E+00	BE891630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919836 5'
10498	22948	35928	1.7	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10498	22948	35929	1.7	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10512	22961	35941	12.56	0.0E+00	BE903304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
10515	18831	31323	2.26	0.0E+00	AA198905.1	EST_HUMAN	zp95b1.1.r1 Stralagene muscle 637209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10533	22980	35960	78.39	0.0E+00	AA809080.1	EST_HUMAN	mw17cd08.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1240718 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);
10534	22981	35961	4.8	0.0E+00	BE783498.1	EST_HUMAN	601588829F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
10542	22989	35969	1.78	0.0E+00	BE729706.1	EST_HUMAN	601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832575 5'
10542	22989	35970	1.78	0.0E+00	BE729706.1	EST_HUMAN	601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832575 5'
10543	22990	35971	31.81	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
10543	22990	35972	31.81	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
10556	23003	35988	17.7	0.0E+00	AA464313.1	EST_HUMAN	zx78c12.1r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:809878 5' similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);
10559	23006	35993	58.2	0.0E+00	AW616055.1	EST_HUMAN	xv04q10.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN);
10564	23011	35998	6.55	0.0E+00	AU135741.1	EST_HUMAN	AU135741 PLAGE1 Homo sapiens cDNA clone PLAGE1002764 5'
10598	23015	36000	5.04	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2946475 3' similar to contains element MSR1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10568	23015	36001	5.04	0.0E+00	AW593333.1	EST_HUMAN	hgt13d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845476 3' similar to contains element MSR1 repetitive element;
10568	23016	36002	5.04	0.0E+00	AW593333.1	EST_HUMAN	hgt13d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845476 3' similar to contains element MSR1 repetitive element;
10570	23017	36003	1.8	0.0E+00	Z34897.1	NT	H.sapiens mRNA for H1 histamine receptor
10571	23018	36004	2.85	0.0E+00	F13089.1	EST_HUMAN	HSC3/C031 normalized infant brain cDNA Homo sapiens cDNA clone c-3ic03
10580	23027	36011	4.99	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10598	23043	36028	29.62	0.0E+00	AW338094.1	EST_HUMAN	xw6601.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832885 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN);
10599	23044	36029	1.83	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B13-ah-a-01-0-UI.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
10599	23044	36030	1.83	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B13-ah-a-01-0-UI.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
10601	12824		63.73	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
10603	23047	36032	2.34	0.0E+00	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
10615	23058	36047	2.88	0.0E+00	BE298449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
10626	23068	36053	2.94	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
10631	23073	36059	3.54	0.0E+00	AA377605.1	EST_HUMAN	EST190347 Synovial sarcoma Homo sapiens cDNA 5' end similar to similar to LERK-2, placenta
10638	23079	36063	2.43	0.0E+00	BE284995.1	EST_HUMAN	601193824F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538012 5'
10848	23088	36072	5.76	0.0E+00	BE792155.1	EST_HUMAN	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5'
10849	23089		221.77	0.0E+00	BF684061.1	EST_HUMAN	602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'
10850	23090	36073	2.31	0.0E+00	BE269288.1	EST_HUMAN	601186342F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544259 5'
10852	23092	36075	19.23	0.0E+00	AU118386.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003488 5'
10853	23093		3.24	0.0E+00	AW236289.1	EST_HUMAN	xn72b01.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02162_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10858	23098	36079	9.69	0.0E+00	A1149809.1	EST_HUMAN	qf43c03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
10658	23098	36080	9.69	0.0E+00	A1149809.1	EST_HUMAN	qf43c03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
10859	23099	36081	2.83	0.0E+00	AW391837.1	EST_HUMAN	QV4-ST0234-121189-032-b06 ST0234 Homo sapiens cDNA
10871	23111		19.02	0.0E+00	AU116808.1	EST_HUMAN	AU116808 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
10874	23114	36089	8.21	0.0E+00	11424728	NT	Homo sapiens insulin receptor (INSR), mRNA
10875	23115	36090	2.97	0.0E+00	A1367350.1	EST_HUMAN	qf65c12.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN.
10875	23115	36081	2.97	0.0E+00	A1367350.1	EST_HUMAN	qf65c12.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN.
10878	23118	36095	86.11	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM00093-170400-191-d08 UM0093 Homo sapiens cDNA
10878	23118	36098	86.11	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM00093-170400-191-d08 UM0093 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10678	23119	36097	3.56	0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4184979 5'
10682	23122	36101	24.76	0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3103310 5'
10688	23128	36108	3.88	0.0E+00	AB007632.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
10691	23130	36111	8.99	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKGSH) gene, exon 15-17
10694	23133	36114	5.71	0.0E+00	BE773036.1	EST_HUMAN	RC1-F10134-170700-012-07 F10134 Homo sapiens cDNA
10694	23133	36115	5.71	0.0E+00	BE773036.1	EST_HUMAN	RC1-F10134-170700-012-07 F10134 Homo sapiens cDNA
10713	23151	36134	118.61	0.0E+00	AA740782.1	EST_HUMAN	063207.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1825412 3' similar to contains element
10716	23154	36138	3.34	0.0E+00	AW46922.1	EST_HUMAN	MSR1 repetitive element;
10723	23161	36145	3.36	0.0E+00	AF252303.1	NT	hca04h04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
10737	23175	36158	4.26	0.0E+00	BE268478.1	EST_HUMAN	Homo sapiens signaling lymphocyte activation molecule (SLAM) gene, exon 2
10737	23175	36159	4.26	0.0E+00	BE268478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533887 5'
10739	23177	36161	5.19	0.0E+00	C05089.1	EST_HUMAN	005089 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4817
10746	23184	36168	3.02	0.0E+00	AA746375.1	EST_HUMAN	065601.1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1309009 5'
10746	23184	36169	3.02	0.0E+00	AA746375.1	EST_HUMAN	065601.1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1309009 5'
10754	23192	36179	2.13	0.0E+00	BE392589.1	EST_HUMAN	601307408F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625560 5'
10756	23194	36179	12.08	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC26
10756	23194	36180	12.08	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC26
10759	23196	36181	3.64	0.0E+00	BF363825.1	EST_HUMAN	QY2-H10698-020800-295-d07 HT0698 Homo sapiens cDNA
10759	23197	36182	9.52	0.0E+00	AL157608.1	EST_HUMAN	DKFZp761J2116.1 1761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5'
10759	23207	36189	4.14	0.0E+00	BE562822.1	EST_HUMAN	601336530F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690390 5'
10771	23209	36191	4.6	0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
10782	23220	36202	2.18	0.0E+00	AV693856.1	EST_HUMAN	AV693856 GKC Homo sapiens cDNA clone GKCCNC03 5'
10789	23227	36210	3.59	0.0E+00	BF366553.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
10809	23245	36229	2.48	0.0E+00	BE182380.1	EST_HUMAN	PMO-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
10809	23245	36230	2.48	0.0E+00	BE182380.1	EST_HUMAN	PMO-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
10812	23248		2.45	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAA008 5'
10829	23266	36251	37.4	0.0E+00	AW406390.1	EST_HUMAN	UI-HF-BLG-acc-c-09-0-UI.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3060089 5'
10832	23267	36253	4.34	0.0E+00	BE898423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
10836	23271	36259	1.81	0.0E+00	AA524458.1	EST_HUMAN	ng45b07.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:937717 3'
10836	23271	36260	1.81	0.0E+00	AA524458.1	EST_HUMAN	ng45b07.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:937717 3'
10839	23273	36263	4.43	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BN0-akg-d-02-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
10839	23273	36264	4.43	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BN0-akg-d-02-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10841	23276	36265	9.81	0.0E+00	BE018293.1	EST_HUMAN	b578c04.y1 NIH_MGC. 10 Homo sapiens cDNA clone IMAGE:3048486 5' similar to gb:Y03945 cds1 POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:U65553 M.musculus mRNA for poly(A) binding protein (MOUSE);
10854	23287	36278	1.94	0.0E+00	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
10863	23296	36290	5.81	0.0E+00	X59314.1	NT	H. sapiens gene for Ig kappa light chain variable region "011"
10877	23310	36307	5.95	0.0E+00	BE897953.1	EST_HUMAN	601440446F1 NIH_MGC. 72 Homo sapiens cDNA clone IMAGE:3925403 5'
10878	23311	36308	8.04	0.0E+00	AI459545.1	EST_HUMAN	ea86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
10878	23311	36309	8.04	0.0E+00	AI459545.1	EST_HUMAN	ea86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
10890	23322	36321	6.13	0.0E+00	AL042278.1	EST_HUMAN	DKFp434L0120_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFp434L0120 5'
10904	23336	36340	2.08	0.0E+00	AI073917.1	EST_HUMAN	cu61d04.x1 NCL CGAP_B12 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;
10904	23336	36341	2.08	0.0E+00	AI073917.1	EST_HUMAN	cu61d04.x1 NCL CGAP_B12 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;
10904	23336	36342	2.08	0.0E+00	AI073917.1	EST_HUMAN	cu61d04.x1 NCL CGAP_B12 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;
10916	23349	36357	3.75	0.0E+00	4769827	NT	Homo sapiens neuridin III (NRXN3) mRNA
10917	23349	36358	18.32	0.0E+00	BF206561.1	EST_HUMAN	601870902F1 NIH_MGC. 19 Homo sapiens cDNA clone IMAGE:4101433 5'
10923	23355	36364	8.95	0.0E+00	AW207734.1	EST_HUMAN	UIH-B12-aga-h-01-QJL81 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
10924	23356	36365	7.89	0.0E+00	AW604975.1	EST_HUMAN	RC0-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA
10924	23356	36366	7.88	0.0E+00	AW604975.1	EST_HUMAN	RC0-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA
10928	23360	36370	9.39	0.0E+00	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
10928	23360	36371	9.39	0.0E+00	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
10929	23381	36372	9.18	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC. 7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B- 55KDA-ASSOCIATED PROTEIN. ;
10929	23381	36373	9.18	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC. 7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B- 55KDA-ASSOCIATED PROTEIN. ;
10948	23379	36389	15.52	0.0E+00	BF093687.1	EST_HUMAN	QVQ-JM0091-120800-385-b12 UM0091 Homo sapiens cDNA
10950	20408	36378	1.93	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
10953	23383	36392	7.21	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
10953	23383	36393	7.21	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA

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Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10984	23393		1.93	0.0E+00	AI703216.1	EST_HUMAN	wd30f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329673 3' similar to SW/CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR.
10971	23400	36410	2.64	0.0E+00	AW673469.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN.
10971	23400	36411	2.64	0.0E+00	AW673469.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN.
10989	23418	36434	7.25	0.0E+00	BF507876.1	EST_HUMAN	UIH-B14-ekb-b-10-0-J1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
10989	23418	36435	7.25	0.0E+00	BF507876.1	EST_HUMAN	UIH-B14-ekb-b-10-0-J1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
10983	23422	36439	5.72	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001381 5'
10987	23428	36443	2.1	0.0E+00	BF086811.1	EST_HUMAN	RC3-GN0089-100800-011-c06 GN0089 Homo sapiens cDNA
10988	23427	36444	30.76	0.0E+00	BE876401.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
10988	23427	36445	30.76	0.0E+00	BE876401.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11002	23431	36449	3.17	0.0E+00	D87682.1	NT	Human mRNA for KIAA0241 gene, partial cds
11007	23435		7.77	0.0E+00	BF240536.1	EST_HUMAN	601876630F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4099710 5'
11018	23445	36463	2.26	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
11018	23445	36464	2.26	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
11024	23451	36470	6.15	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11024	23451	36471	6.15	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11028	23455		2.82	0.0E+00	R00904.1	EST_HUMAN	ye87a08.r1 Soares fetal liver spleen TNF α Homo sapiens cDNA clone IMAGE:124694 5'
11030	23457	36477	9.01	0.0E+00	BE017860.1	EST_HUMAN	bb73h05.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048057 5' similar to SW:CD97_HUMAN P48960 LEUCOCYTE ANTIGEN CD97 PRECURSOR. [1].
11033	23460	36480	1.9	0.0E+00	AA772837.1	EST_HUMAN	aa74g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969942 3'
11045	23471	36496	7	0.0E+00	4503544	NT	Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
11051	23477	36502	4.71	0.0E+00	N08886.1	EST_HUMAN	za68d06.r1 Soares_fetal_Jung_NbHL19W Homo sapiens cDNA clone IMAGE:287707 5' similar to SW:YA35_SCHPO Q09712 HYPOTHETICAL 48.8 KD PROTEIN C18B11.05 IN CHROMOSOME I.;
11051	23477	36503	4.71	0.0E+00	N08886.1	EST_HUMAN	za68d06.r1 Soares_fetal_Jung_NbHL19W Homo sapiens cDNA clone IMAGE:287707 5' similar to SW:YA35_SCHPO Q09712 HYPOTHETICAL 48.8 KD PROTEIN C18B11.05 IN CHROMOSOME I.;
11062	23478	36504	6.01	0.0E+00	BF576267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11054	23480	36506	6.41	0.0E+00	AW328173.1	EST_HUMAN	cd04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:284717 5'
11058	23484		118.03	0.0E+00	M55063.1	NT	Human gamma actin-like pseudogene, complete cds
11062	23488	36513	190.94	0.0E+00	A1680988.1	EST_HUMAN	wf20e11.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
11063	23489	36514	2.92	0.0E+00	BF300990.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11063	23489	36515	2.92	0.0E+00	BF300990.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'

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11070	23498	36523	99.19	0.0E+00	BF392482.1	EST_HUMAN	QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA
11084	23509	36541	2.73	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11084	23509	36542	2.73	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11089	23514		9.98	0.0E+00	BE897051.1	EST_HUMAN	601439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11090	23515		1.76	0.0E+00	4503786	NT	Homo sapiens tyrosine-related kinase (FRK) mRNA
11098	23522	36560	12.49	0.0E+00	8923608	NT	Homo sapiens golgin-like protein (GLP) mRNA
11100	23524		4.1	0.0E+00	BF207892.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081716 5'
11101	23525		1.82	0.0E+00	BE257744.1	EST_HUMAN	601116705F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357384 5'
11112	23585	36608	8.43	0.0E+00	BE208846.1	EST_HUMAN	6014407.Y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:076022 076022 E1B-
11112	23585	36607	8.43	0.0E+00	BE208846.1	EST_HUMAN	6014407.Y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:076022 076022 E1B-
11114	23587	36609	1.99	0.0E+00	AW753028.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN. ;
11119	23572		5.94	0.0E+00	AA558707.1	EST_HUMAN	QV0-CT0225-101289-071-08 CT0225 Homo sapiens cDNA
11120	18115	30472	10.47	0.0E+00	A1834954.1	EST_HUMAN	nl42c08.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-
11121	23573	36615	23.92	0.0E+00	AW327895.1	EST_HUMAN	ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11136	24058	36628	2.41	0.0E+00	AW292776.1	EST_HUMAN	wp05g08.x1 NCI_CGAP_KB12 Homo sapiens cDNA clone IMAGE:2846919 5'
11141	22831	35801	1.85	0.0E+00	4758827	NT	6012808.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
11147	23528	36587	2.59	0.0E+00	BE254058.1	EST_HUMAN	UI-H-BW0-ell-4-07-0-J1.s1 NCI_CGAP_Sub0 Homo sapiens cDNA clone IMAGE:2729509 3'
11149	23530	36588	5.57	0.0E+00	BE968909.2	EST_HUMAN	Homo sapiens neuroxin III (NRXN3) mRNA
11149	23530	36569	5.57	0.0E+00	BE968909.2	EST_HUMAN	601113903F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354600 5'
11150	23531	36570	6.27	0.0E+00	BE186850.1	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11151	23532		2.05	0.0E+00	BF513980.1	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11165	23545	36584	6.62	0.0E+00	AL046540.1	EST_HUMAN	IL6-H10731-020500-077-005 H10731 Homo sapiens cDNA
11165	23545	36585	6.62	0.0E+00	AL046540.1	EST_HUMAN	UI-H-BW1-arm-e-06-0-J1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071121 3'
11173	23563	36594	36.26	0.0E+00	A1923116.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
11176	23592	36632	13.39	0.0E+00	AA760913.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
11176	23592	36633	13.39	0.0E+00	AA760913.1	EST_HUMAN	wn83g03.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452488 3' similar to gb:S37431 LAMININ
11180	23596	36638	5.83	0.0E+00	BE910546.1	EST_HUMAN	RECEPTOR (HUMAN);
							ntz1c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13688
							Q13686 ALKB HOMOLOG PROTEIN. ;
							ntz1c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13688
							Q13686 ALKB HOMOLOG PROTEIN. ;
							601501090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902928 5'

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11187	22839	35811	12.19	0.0E+00	BE678347.1	EST_HUMAN	712712.x1 NCL_CGAP_CL11 Homo sapiens cDNA clone IMAGE:3296919 3' similar to TR:000409 O00409 CHECKPOINT SUPPRESSOR 1.;
11189	22841	35813	9.13	0.0E+00	A1683358.1	EST_HUMAN	166509.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2274521 3' similar to gb:M55942
11181	22843	35815	2.42	0.0E+00	BE615666.1	EST_HUMAN	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (HUMAN);
11191	22843	35816	2.42	0.0E+00	BE615666.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11188	22850	35823	1.98	0.0E+00	AV757420.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11202	22854	35827	8.71	0.0E+00	ALD37746.1	EST_HUMAN	AV757420 BM Homo sapiens cDNA clone BMFAGH03 5'
11203	22855	35828	2.06	0.0E+00	U62789.1	NT	DKFZp564C187_r1 584 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564C187 5'
11208	22860	35834	2.83	0.0E+00	BE683386.1	EST_HUMAN	Human oxytocinase variant 2 mRNA, complete cds
11234	23602	36945	15.82	0.0E+00	L39991.1	NT	601509139F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910833 5'
11234	23602	36946	15.82	0.0E+00	L39991.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11250	23616	36962	3.95	0.0E+00	AU138211.1	EST_HUMAN	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11281	23627	36976	8.99	0.0E+00	BE622317.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'
11287	23652	36700	2.36	0.0E+00	A1699634.1	EST_HUMAN	601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
11295	23660	36706	125.07	0.0E+00	BE748899.1	EST_HUMAN	bm84c10.x5 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165778 3'
11295	23660	36707	125.07	0.0E+00	BE748899.1	EST_HUMAN	601672186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11304	23669	36717	11.1	0.0E+00	AU141882.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11304	23669	36718	11.1	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11307	23672	36721	2.95	0.0E+00	AW006022.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
							wz91h01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:25668226 3' similar to WP.F53H10.2
							CE11040 ZINC FINGER, C2H2 TYPE 1
11308	24659	36722	7.22	0.0E+00	BF002333.1	EST_HUMAN	7h22b10.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458
11322	23686	36735	4.57	0.0E+00	AL043705.1	EST_HUMAN	TRIO.;
11322	23686	36736	4.57	0.0E+00	AL043705.1	EST_HUMAN	DKFZp434L1227_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1227 5'
11326	23690	36742	3.88	0.0E+00	AW387776.1	EST_HUMAN	DKFZp434L1227_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1227 5'
11326	23690	36743	3.88	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-503 ST0118 Homo sapiens cDNA
11329	23693	36745	2.2	0.0E+00	BF699207.1	EST_HUMAN	MR4-ST0118-261099-012-503 ST0118 Homo sapiens cDNA
11334	23698	36751	2.95	0.0E+00	AA435092.1	EST_HUMAN	602120089F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277104 5'
11338	23702		4.2	0.0E+00	AW863777.1	EST_HUMAN	zu03a12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730750 5'
11350	23714	36772	8.91	0.0E+00	11435244	NT	MR3-SN0010-107-103 SN0010 Homo sapiens cDNA
11350	23714	36773	8.91	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11356	23718	36778	5.07	0.0E+00	U36253.1	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11358	23721	36780	13.76	0.0E+00	BE370254.1	EST_HUMAN	Human beta-prime-adaptin (BAM22) gene, exon 5

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11358	23721	36781	13.76	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608923 5'
11374	23736	36784	2.8	0.0E+00	AA488894.1	EST_HUMAN	aa55011.st NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824900 3' similar to gb:M37768 B-LYMPHOCYTE ACTIVATION MARKER BLAST-1 PRECURSOR (HUMAN);
11379	23741	36800	2.17	0.0E+00	BE784758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11381	23743	36801	283.43	0.0E+00	BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
11382	23744	36802	18.78	0.0E+00	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
11387	23749	36808	2.44	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
11387	23749	36809	2.44	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
11389	23751	36810	1.63	0.0E+00	AF063643.1	NT	Homo sapiens glutathione transferase zeta 1 (GSTZ1) gene, exons 6 and 7
11393	23755	36813	50.39	0.0E+00	BE409893.1	EST_HUMAN	601289403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5'
11394	23756	36814	1.79	0.0E+00	BE148650.1	EST_HUMAN	MRO-HT0241-150500-011-702 HT0241 Homo sapiens cDNA
11395	23757	36815	2.53	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11395	23757	36816	2.53	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11396	18315	30748	3.03	0.0E+00	D26535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
11398	18316	30749	3.03	0.0E+00	D26535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
11398	23759	36818	68.43	0.0E+00	BF681641.1	EST_HUMAN	602165722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5'
11398	23759	36819	68.43	0.0E+00	BF681641.1	EST_HUMAN	602165722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5'
11399	23760	36820	1.74	0.0E+00	AF012337.1	NT	Human Endogenous Retrovirus IDDMK1.2-22 envelope protein (env) gene, complete cds
11404	23765	36825	7.69	0.0E+00	BE903372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3658935 5'
11416	23777	36836	4.01	0.0E+00	BF312552.1	EST_HUMAN	601897624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11416	23777	36837	4.01	0.0E+00	BF312552.1	EST_HUMAN	601897624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11417	23778	36838	51.39	0.0E+00	X51755.1	NT	Human lambda-de-immunoglobulin constant region complex (germline)
11417	23778	36839	51.39	0.0E+00	X51755.1	NT	Human lambda-de-immunoglobulin constant region complex (germline)
11448	24660	36866	34.16	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
11449	23808	36866	1.93	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-507 NN0025 Homo sapiens cDNA
11449	23808	36867	1.93	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-507 NN0025 Homo sapiens cDNA
11452	23811	36870	126.53	0.0E+00	BE297175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632568 5'
11465	23823	36887	3.59	0.0E+00	BE744311.1	EST_HUMAN	601576525F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
11465	23823	36888	3.59	0.0E+00	BE744311.1	EST_HUMAN	601576525F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
11467	23825	36890	3.62	0.0E+00	BE257612.1	EST_HUMAN	60113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'
11467	23825	36891	3.62	0.0E+00	BE257612.1	EST_HUMAN	60113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'
11486	23844	36912	1.94	0.0E+00	AW749184.1	EST_HUMAN	PM1-BT0348-151299-001-c11 BT0348 Homo sapiens cDNA

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11486	23844	36913	1.94	0.0E+00	AW749184.1	EST_HUMAN	PM1-BT0348-161298-001-c11 BT0348 Homo sapiens cDNA
11489	23847	36915	1.83	0.0E+00	AW367811.1	EST_HUMAN	MRO-HT0168-271199-005-g03 HT0168 Homo sapiens cDNA
11489	23847	36916	1.83	0.0E+00	AW367811.1	EST_HUMAN	MRO-HT0168-271199-005-g03 HT0168 Homo sapiens cDNA
11482	23850	36919	5.27	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
11492	23850	36920	5.27	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
11508	23868	36942	1.78	0.0E+00	BE250543.1	EST_HUMAN	600843204F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:269898 5'
11520	23878	36961	2.67	0.0E+00	BE257612.1	EST_HUMAN	60113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:335337 5'
11523	23881	36964	1.77	0.0E+00	U69962.3	NT	Homo sapiens CREB-binding protein mRNA, complete cds
11524	23882	36965	3.38	0.0E+00	AU132394.1	EST_HUMAN	AU132394 NT2RP3 Homo sapiens cDNA clone NT2RP3004339 5'
11531	23889	36971	1.85	0.0E+00	AA628180.1	EST_HUMAN	zu90503.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745229 3'
11531	23889	36972	1.85	0.0E+00	AA628180.1	EST_HUMAN	zu90503.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745229 3'
11540	23897	36980	1.85	0.0E+00	BE282840.1	EST_HUMAN	601108662F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2988325 5'
11542	23899	36982	1.82	0.0E+00	AA984839.1	EST_HUMAN	em93g10.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630722 3'
11543	23900	36983	1.87	0.0E+00	11418020	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE), mRNA
11543	23900	36984	1.87	0.0E+00	11418020	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE), mRNA
11546	23903	36987	4.35	0.0E+00	BE747617.1	EST_HUMAN	601677501F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926281 5'
11548	23905	36989	1.98	0.0E+00	AU133203.1	EST_HUMAN	AU133203 NT2RP4 Homo sapiens cDNA clone NT2RP4001639 5'
11548	23905	36990	1.98	0.0E+00	AU133203.1	EST_HUMAN	AU133203 NT2RP4 Homo sapiens cDNA clone NT2RP4001639 5'
11550	23907	36992	3.21	0.0E+00	BE883574.1	EST_HUMAN	601508046F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909659 5'
11550	23907	36993	3.21	0.0E+00	BE883574.1	EST_HUMAN	601508046F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909659 5'
11551	23908	36998	1.73	0.0E+00	AW883916.1	EST_HUMAN	QV3-OT0063-280300-135-g12 OT0063 Homo sapiens cDNA
11566	24982	30448	1.95	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
11578	24781		1.34	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11581	24801		5.57	0.0E+00	AL190993.1	EST_HUMAN	q917b12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
11592	23928		2.78	0.0E+00	AU13099.1	NT	Homo sapiens gene for AF-6, complete cds
11612	23943		5.08	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11614	23946		1.19	0.0E+00	AB016195.1	NT	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)
11621	23950		3.44	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIA00330), mRNA
11640	23984		3.52	0.0E+00	5802973	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
11678	24758	30879	1.21	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11689	24768		4.12	0.0E+00	AL041931.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434K0819 5'
11718	24927		3.14	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
11725	24017		5.38	0.0E+00	AL048644.1	EST_HUMAN	DKFZp434G3218_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G3218 5'
11739	24807		2.02	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
11782	24948		1.98	0.0E+00	N54484.1	EST_HUMAN	W40e08 st Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN;
11788	24063		4	0.0E+00	AF108856.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
11801	13421	25968	4.26	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11801	13421	25969	4.26	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11810	24809		2.83	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
11840	13136		2.88	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA); exon 2 and flanking repeat regions
11877	24569	30851	1.73	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11938	24737	30877	3.71	0.0E+00	AW590082.1	EST_HUMAN	hg31e06.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2847234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
11949	24792		1.48	0.0E+00	BE090210.1	EST_HUMAN	RC6-BT0711-290300-011-D05 BT0711 Homo sapiens cDNA
11968	24767		1.41	0.0E+00	L20493.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
11998	24804		3.18	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12037	24208		3.15	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
12080	24796		1.89	0.0E+00	AI204914.1	EST_HUMAN	an05h04.x1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12116	24258		1.37	0.0E+00	AI904648.1	EST_HUMAN	QV-BT085-020399-103 BT085 Homo sapiens cDNA
12128	24793		1.19	0.0E+00	BE439792.1	EST_HUMAN	HTM1-654F HTM1 Homo sapiens cDNA
12142	14452	26953	1.55	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12142	14452	26954	1.55	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12161	24287	30934	1.48	0.0E+00	AF036365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
12174	14212	26691	3.58	0.0E+00	H30132.1	EST_HUMAN	yc59e08.r1 Soares breast 3NBrBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089
12174	14212	26692	3.58	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYLTRANSEPTIDASE 5 PRECURSOR (HUMAN);
12185	24306		35.58	0.0E+00	D50659.1	NT	yc59e08.r1 Soares breast 3NBrBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089
12189	24309	30808	3.32	0.0E+00	11418189	NT	GAMMA-GLUTAMYLTRANSEPTIDASE 5 PRECURSOR (HUMAN);
12189	24309	30809	3.32	0.0E+00	11418189	NT	Human gamma-cytoplasmic actin (ACTGP6) pseudogene
12189	24309	30809	3.32	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P-1), mRNA
12189	24309	30809	3.32	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P-1), mRNA

Table 4
Single Exon Probes Expressed in Lung

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12192	24312		1.25	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12206	14632	27046	2.07	0.0E+00	4759489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
12251	24352		1.86	0.0E+00	AW684989.1	EST_HUMAN	h186a08.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879154 3'
12300	13783	28239	1.77	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
12307	24387		1.63	0.0E+00	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12333	15828	28246	3.25	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12343	18009	30442	2.07	0.0E+00	6809918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12349	24410		2.31	0.0E+00	AB029800.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
12391	24432	30898	1.59	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
12418	24674		4.26	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12423	13209	25816	1.7	0.0E+00	6809918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12479	14031	28494	1.19	0.0E+00	6912467	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12512	24513		1.46	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12516	24517		3.8	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
12541	24530		1.39	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12557	24542	30842	1.45	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
12585	24563	30847	1.49	0.0E+00	AW025032.1	EST_HUMAN	wu83c07.x1 NCL_CGAP_Kids Homo sapiens cDNA clone IMAGE:2527596 3' similar to TR-Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;contains TAR1.3 TAR1 repetitive element ;

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



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| 60/234,687 | 21 September 2000 (21.09.2000) | US |
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| 0024263.6 | 4 October 2000 (04.10.2000) | GB |
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- (72) Inventors; and
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- (74) Agent: RONNING, Royal, N., Jr.; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).
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- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung is described. Also described are single exon nucleic acid probes expressed in the lung and their use in methods for detecting gene expression.

WO 01/086003 A3

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00665

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

EMBL, EPO-Internal, SEQUENCE SEARCH, WPI Data, PAJ, MEDLINE, BIOSIS, EMBASE, CHEM
ABS Data, INSPEC

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 23254 A (AFFYMETRIX INC ;NAIR ARCHANA (US); LOCKHART DAVID J (US); WARRINGT) 14 May 1999 (1999-05-14) the whole document -/-	1-27

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *G* document member of the same patent family

Date of the actual completion of the international search

12 July 2002

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07. 08. 2002

Name and mailing address of the ISA

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Authorized officer

Knehr, M

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00665

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	BENIT L ET AL: "CLONING OF A NEW MURINE ENDOGENOUS RETROVIRUS, MUERV-L, WITH STRONG SIMILARITY TO THE HUMAN HERV-L ELEMENT AND WITH A GAG CODING SEQUENCE CLOSELY RELATED TO THE FVL RESTRICTION GENE" JOURNAL OF VIROLOGY, THE AMERICAN SOCIETY FOR MICROBIOLOGY, US, vol. 71, no. 7, 1 July 1997 (1997-07-01), pages 5652-5657, XP002037954 ISSN: 0022-538X	13,15, 17-21, 25-27
Y	* see especially nucleic acid sequence and encoded peptide sequence within Fig.2, amino acid residues 965-1120 * abstract; figure 2	1-14, 22-24
X	DATABASE EMBL 'Online! EBI; 27 April 1999 (1999-04-27) DICKHOFF ET AL: "Sequencing of human chromosome 14q31 region" Database accession no. AC007372 XP002182131 sequence	13
X	DATABASE EMBL 'Online! EBI; ADAMS ET AL.: "Use of random BAC end sequence database for sequence ready map building" Database accession no. B57793 XP002185753 Sequence	13
X	DATABASE EMBL 'Online! EBI; 9 May 1997 (1997-05-09) MARRA ET AL.: "The WashU-HHMI Mouse EST Project" Database accession no. AA414703 XP002205620 the whole document	13
Y	CHIN J E ET AL: "Structure and expression of the human MDR (P-glycoprotein) gene family" MOLECULAR AND CELLULAR BIOLOGY, AMERICAN SOCIETY FOR MICROBIOLOGY, WASHINGTON, US, vol. 9, no. 9, September 1989 (1989-09), pages 3808-3820, XP002185923 ISSN: 0270-7306 the whole document	1-14, 22-24
Y	WO 98 30722 A (MACK DAVID H) 16 July 1998 (1998-07-16) * see especially page 63, paragraph 2 * the whole document	1-14, 22-24

-/-

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00665

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	BURGE C ET AL: "Prediction of complete gene structure in human genomic DNA" JOURNAL OF MOLECULAR BIOLOGY, LONDON, GB, vol. 268, no. 1, 25 April 1997 (1997-04-25), pages 78-94, XP002109301 ISSN: 0022-2836 the whole document	1-14, 22-24
Y	DATABASE WPI Section Ch, Week 199936 Derwent Publications Ltd., London, GB; Class B04, AN 1999-422613 XP002183658 "Estimation of protein-coding region in de-oxy-ribo nucleic acid base sequence - useful for medicinal, genetic and pharmacological studies" -& JP 11 169172 A (HITACHI LTD), 29 June 1999 (1999-06-29) abstract	1-14, 22-24
Y	CHURCH D M ET AL: "ISOLATION OF GENES FROM COMPLEX SOURCES OF MAMMALIAN GENOMIC DNA USING EXON AMPLIFICATION" NATURE GENETICS, NEW YORK, NY, US, vol. 6, 1994, pages 98-105, XP000608940 ISSN: 1061-4036 the whole document	1-14, 22-24
A	US 5 618 671 A (LINDSTROEM PER) 8 April 1997 (1997-04-08) column 1, line 60 -column 2, line 19 column 4, line 36 -column 5, line 29; claims	1-27
A	WO 99 67422 A (SMITHKLINE BEECHAM CORP ;LEARY JEFFREY J (US); TAL SINGER RUTH (US) 29 December 1999 (1999-12-29) the whole document	1-27
A	EISEN M B ET AL: "Cluster analysis and display of genome-wide expression patterns" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 95, December 1998 (1998-12), pages 14863-14868, XP002140966 ISSN: 0027-8424 the whole document	1,12

-/-

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00665

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	DATSON N A ET AL: "Scanning for genes in large genomic regions: cosmid based exon trapping of multiple exons in a single product" NUCLEIC ACIDS RESEARCH, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 24, no. 6, 1996, pages 1105-1111, XP002081565 ISSN: 0305-1048 the whole document	1-27
A	DATABASE EMBL 'ONLINE! 'Online! European Molecular Biology Laboratory; 16 December 1998 (1998-12-16) BUETTNER C ET AL.: "The 3'-untranslated region of human type 2 iodothyronine deiodinase mRNA contains a functional selenocysteine insertion sequence element" Database accession no. AF093774 XP002205902 * see especially nucleotides 704-1157 * abstract	13
A	DATABASE EMBL 'Online! European Molecular Biology Laboratory; 15 June 1995 (1995-06-15) HUDSON T: "Human STS WI-7008" Database accession no. G06348 XP002205903 * see especially base pairs 76-550 * abstract	13
P,X	PENN S G ET AL: "Mining the human genome using microarrays of open reading frames." NATURE GENETICS, (2000 NOV) 26 (3) 315-8., XP002183793 the whole document	1
P,A	STEPHAN D A ET AL: "POSITIONAL CLONING UTILIZING GENOMIC DNA MICROARRAYS: THE NIEMANN-PICK TYPE C GENE AS A MODEL SYSTEM" MOLECULAR GENETICS AND METABOLISM, ACADEMIC PRESS, SAN DIEGO, CA, US, vol. 70, no. 1, 2000, pages 10-18, XP001041271 ISSN: 1096-7192 the whole document	1-27

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/00665

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-27 (partially)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first invention in form 206 PCT. If additional fees are paid for the (one or more) as yet unsearched inventions, similar statements about incomplete searches could be issued.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising SEQ ID NOS:1-3 as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Consequently, the search for the sets of probes comprising SEQ ID NOS:1-3 has been limited to SEQ ID NOS:1-3 as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by SEQ ID NOS:1-3. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of SEQ ID NOS:1-3 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (see claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide SEQ ID NOS:25010 and 25011. However, due to the degeneracy of the genetic code, this peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claims impossible. The search has therefore been carried out for those parts of the claims which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred (poly)peptide in table 4 (SEQ ID NOS: 1-3, 12623, 12624, 25010 and 25011).

Likewise, claim 26, which refers to peptides encoded by SEQ ID NOS:1-3 and SEQ ID NOS:12623 and 12624, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claim impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be clear and concise, namely the peptide

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

disclosed, identified by SEQ ID NOS:12623 and 12624.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: Claims 1-27 (partial)

A nucleic acid probe comprising SEQ ID NOS:1 or 2, complementary sequences or fragments thereof, in particular comprising SEQ ID NO:12623, spatially addressable sets of probes comprising said sequence(s), microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by SEQ ID NOS:1,2 and 12623 (in particular the one defined by SEQ ID NO:25010).

Invention 2: Claims 1-27 (partial)

A nucleic acid probe comprising SEQ ID NO:3, complementary sequences or fragments thereof, in particular comprising SEQ ID NO:12624, spatially addressable sets of probes comprising said sequence(s), microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by SEQ ID NO:3 and 12624 (in particular the one defined by SEQ ID NO:25011).

Inventions 3 to 12614: Claims 1-27 (partial)

A nucleic acid probe comprising SEQ ID NO:n (where n ranges from 4-12614 according to the invention number above; as disclosed in table 4), complementary sequences or fragments thereof, in particular comprising the SEQ ID NO. which is listed in the column "Exon Seq. Id. no." in the same row within table 4 that contains Seq. Id. n, spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by SEQ ID NO:n, in particular the one defined by the SEQ ID NO in the column "ORF Seq. Id. no." of the same row where SEQ ID NO:n is listed.

Information on patent family members

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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung is described. Also described are single exon nucleic acid probes expressed in the lung and their use in methods for detecting gene expression.

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